

DIVERSITY ANALYSIS IN COTTON
(*Gossypium hirsutum* L.)

By
B. SARADA
B.Sc. (Ag.)

THESIS SUBMITTED TO THE
ACHARYA N.G.RANGA AGRICULTURAL UNIVERSITY
IN PARTIAL FULFILLMENT 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
RAJENDRANAGAR, HYDERABAD-500 030
2010

CERTIFICATE

Ms. B. SARADA has satisfactorily prosecuted the course of research and that the thesis entitled **“DIVERSITY ANALYSIS IN 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 thereof has not been previously submitted by her for a degree of any University.

Date:

(LAL AHAMED M.)

Place:

Major Advisor
Assistant Professor
Department of Genetics and Plant Breeding
Agricultural College, Bapatla – 522 101

CERTIFICATE

This is to certify that the thesis entitled “**DIVERSITY ANALYSIS IN COTTON (*Gossypium hirsutum* L.)**” submitted in partial fulfillment 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 **Ms. B. SARADA** under my guidance and supervision. The subject of the thesis has been approved by the Student’s Advisory Committee.

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

(LAL AHAMED M.)

Chairman of the Advisory Committee

Thesis approved by the Student’s Advisory Committee

Chairman : **Dr. LAL AHAMED M.** _____

Assistant Professor

Department of Genetics and Plant Breeding

Agricultural College, Bapatla – 522 101

Member : **Dr. V. SATYANARAYANA RAO** _____

Associate Professor

Department of Genetics and Plant Breeding

Agricultural College, Bapatla – 522 101

Member : **Dr. B. SREEKANTH** _____

Assistant Professor

Department of Plant Physiology

Agricultural College, Rajahmundry



Chapter No	Title	Page No.
I	INTRODUCTION	
II	REVIEW OF LITERATURE	
III	MATERIALS AND METHODS	
IV	RESULTS	
V	DISCUSSION	
VI	SUMMARY	
	LITERATURE CITED	
	ANNEXURE	

LIST OF TABLES

S. No.	Title	Page No.
1	Review of literature on genetic variability in cotton (<i>Gossypium hirsutum</i> L.).	
2	Review of literature on heritability ($h^2_{(b)}$) and genetic advance (GA) in cotton (<i>Gossypium hirsutum</i> L.).	
3	Review of literature on the association of component characters with seed cotton yield in cotton (<i>Gossypium hirsutum</i> L.).	
4	Review of literature on association among the yield component characters in cotton (<i>Gossypium hirsutum</i> L.).	
5	Review of literature on direct effects of component characters on seed cotton yield in cotton (<i>Gossypium hirsutum</i> L.).	
6	Genotype name and source of cotton (<i>Gossypium hirsutum</i> L.) germplasm lines employed in the present study.	
7	IBPGR descriptors for morphological traits in cotton (<i>Gossypium hirsutum</i> L.).	
8	Experimental details of present investigation.	
9	Stem and leaf morphological characters descriptors for 60 cotton (<i>Gossypium hirsutum</i> L.) germplasm lines.	
10	Flower and boll morphological characters descriptors for 60 cotton (<i>Gossypium hirsutum</i> L.) germplasm lines.	
11	Analysis of variance for yield and yield components in cotton (<i>Gossypium hirsutum</i> L.).	
12	Mean performance of 60 genotypes for 15 quantitative characters in cotton (<i>Gossypium hirsutum</i> L.).	
13	Mean variability, heritability (broad sense) and genetic advance as per cent of mean for yield and yield components in cotton (<i>Gossypium hirsutum</i> L.) germplasm.	
14	Phenotypic and genotypic correlations of 15 characters in 60 cotton (<i>Gossypium hirsutum</i> L.) genotypes.	
15	Direct and indirect effects (Phenotypic) of yield components on seed	

	cotton yield in 60 genotypes of cotton (<i>Gossypium hirsutum</i> L.).	
16	Direct and indirect effects (Genotypic) of yield components on seed cotton yield in 60 genotypes of cotton (<i>Gossypium hirsutum</i> L.).	
17	Contribution of different characters towards genetic divergence in 60 genotypes of cotton (<i>Gossypium hirsutum</i> L.).	
18	Clustering of 60 genotypes of cotton (<i>Gossypium hirsutum</i> L.) by Tocher's method.	
19	Average intra-and inter-cluster D^2 values among nine clusters in 60 genotypes of cotton (<i>Gossypium hirsutum</i> L.).	
20	The nearest and the farthest cluster from each cluster based on D^2 values using Tocher's method in 60 genotypes of cotton (<i>Gossypium hirsutum</i> L.).	
21	Mean values of nine clusters for 15 characters estimated from 60 genotypes of cotton (<i>Gossypium hirsutum</i> L.) using Tocher's method.	
22	Eigen values, proportion of variance represented by principal components, cumulative per cent variance and component loading of different characters in cotton (<i>Gossypium hirsutum</i> L.).	
23	PCA scores of 60 genotypes of cotton (<i>Gossypium hirsutum</i> L.).	
24	Clustering of 60 cotton (<i>Gossypium hirsutum</i> L.) genotypes by Ward's minimum variance method.	
25	Average intra-and inter-cluster Euclidian ² values among the eight clusters in 60 cotton (<i>Gossypium hirsutum</i> L.) genotypes.	
26	Mean values of eight clusters estimated from 60 genotypes of cotton (<i>Gossypium hirsutum</i> L.) genotypes by Ward's minimum variance method.	
27	Frequency of cotton genotypes for the different morphological characters (Descriptors).	

LIST OF FIGURES

S. No.	Title	Page No.
1	Phenotypic path diagram showing cause and effect relationship of direct effect with seed cotton yield per plant in cotton (<i>Gossypium hirsutum</i> L.).	
2	Genotypic path diagram showing cause and effect relationship of direct effect with seed cotton yield per plant in cotton (<i>Gossypium hirsutum</i> L.).	
3	Dendrogram showing relationship of 60 cotton (<i>Gossypium hirsutum</i> L.) genotypes in nine clusters.	
4	Two dimensional graph showing relative position of 60 cotton (<i>Gossypium hirsutum</i> L.) genotypes based on PCA scores.	
5	Three dimensional graph showing relative position of 60 cotton (<i>Gossypium hirsutum</i> L.) genotypes based on PCA scores.	
6	Dendrogram showing relationship of 60 cotton (<i>Gossypium hirsutum</i> L.) genotypes in eight clusters using Ward's minimum variance method.	
7	Intra-and inter-cluster distance of 60 cotton (<i>Gossypium hirsutum</i> L.) genotypes in eight clusters based on Euclidean ² distance.	

ACKNOWLEDGEMENTS

It is by grace of Almighty, omnipotent blessings of my teachers and parents that I could accomplish and bring to light this humble piece of work.

*I humbly place on record my respect and profound sense of gratitude to the esteemed Chairman of my advisory committee, **Dr. Lal Ahamed M**, Assistant Professor, Department of Genetics and Plant Breeding, Agricultural College, Bapatla for his keen interest, scholarly counsel, constructive suggestions, boundless help and indefatigable guidance which provided me commendable encouragement and shaped my efforts into a successful research work.*

*With a deep sense of reverence, I wish to express my sincere gratitude to **Dr. V.Satyannarayana Rao**, Associate Professor, Department of Genetics and Plant Breeding, Agricultural College, Bapatla for sparing his precious time and giving pragmatic suggestions during the course of my research work, which helped a lot in bringing the thesis to the present format.*

*I cordially offer my unboundful gratitude to **Dr.B.Sreekanth**, Assistant Professor, Dept. of Plant Physiology, Agricultural College, Rajahumandry, member of my Advisory committee for his encouragement in conducting research, valuable comments and meticulous reasoning to refine the dissertation to recon with set standards during the course of investigation and preparation of the thesis.*

*I sincerely extend my profound gratitude to **Dr.C.Panduranga Rao**, Professor and Head of the Department of Genetics and Plant Breeding for his sustained encouragement, constant support and valuable suggestions offered during my post graduation study and cooperation during submission of thesis.*

*I express my deep sense of gratitude to **Dr. J.S.V. Samba Murthy** Professor, Department of Genetics and Plant Breeding, Agricultural College, Bapatla for his cooperation and valuable guidance throughout my research work*

*I sincerely thank **Dr.p.v.Ramkumar**, Professor and **Dr K.V. seethe Ramaiah** Professor, Department of Genetics &, Plant Breeding, for their valuable suggestions and help rendered during my research work.*

*I am very much thankful to **Dr. Gopi Nath**, RARS, Lam, Guntur and **Sri. S. Mukundhan**, Technical Officer, CIRCOT, Gunut for their help rendered in the evaluation of fiber quality.*

*I am also very much thankful to Farm Manager **Dr. Martin Luthar** and Senior Manager sri **K.Venkateswarulu** for their help during my farm operations by providing sufficient labour.*

*From my mere existence on earth to present situation, my every step of life is moulded mud by my mother **Smt.VenkataRatnamma Byra** and father **Sri Purnachandra rao Byra**. I will forever remain indebted to them. Their parenting brings every time the best in every effort of my venture.*

*No wards can express my immense gratitude to my grand mother **Smrajamma Mupperisetty** and grand father **Mastan Mupperisetty** whose affection and valuable suggestions, also been a source of inspiration for me.*

*Single para would not justify my deep affection towards my best five friends **Anuradha, K.K.M, satyamani, Vijayakumari and Divya** for always being there beside me in difficult times during my course of study and giving constant motivation and made my life really enjoyable.*

*I extend my heartfelt thanks to my dear friend **Prasad** for his whole hearted encouragement, cooperation and support throughout my stay at Bapatla during six years of study period in this campus.*

*A Hearty thanks to my seniors **Vijay Kumar G. and K.Vanisree** for the much needed moral support and help during the course of my study.*

*I acknowledge and appreciate my colleagues **Bhanu, Manohar, Rajanna, Bazi, Babji, Sivaparvathi, Usha and Meenakumari** for their support and extended to boost up my morale in carrying out this thesis research work.*

*I also owe my special thanks to my juniors **punyavathi, Tulasi, Dhanalakshmi, Amarnath, Brahmaiah, and Omkar** for providing a helping hand whenever needed.*

*I am thankful to **ANGRAU** for providing financial assistance in the form of fellowship during my course of study.*

Place:

Date:

(B.SARADA)

DECLARATION

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

Date:

(B. SARADA)

Place:

LIST OF SYMBOLS AND ABBREVIATIONS

AICCIP	:	All India Coordinated Cotton Improvement Project
ANOVA	:	Analysis of Variance
ARS	:	Agricultural Research Station
CICR	:	Central Institute for Cotton Research
CV	:	Coefficient of Variation
GA	:	Genetic Advance
GAM	:	Genetic Advance as Per cent of Mean
GAU	:	Gujarat Agricultural University
GCV	:	Genotypic Coefficient of Variation
HAU	:	Haryana Agricultural University
MAU	:	Marathwada 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
^o C	:	Degree Centigrade
Df	:	Degrees of freedom
<i>et al.</i> ,	:	and others
F ₁	:	First generation hybrid of a cross
G	:	Gram
g/in	:	Grams per inch
g/tex	:	Grams per tex
h ² (b)	:	Heritability in broad sense
h ² (n)	:	Heritability in narrow sense
Kg/ha	:	Kilogram per hectare
No.	:	Number
<i>Viz.</i>	:	Namely
2D	:	Two dimensional
3D	:	Three dimensional

Name of the Author : **SARADA BYRA**
Title of Thesis : **DIVERSITY ANALYSIS IN COTTON**
(*Gossypium hirsutum* L.)
Faculty : **AGRICULTURE**
Major Field of Study : **GENETICS AND PLANT BREEDING**
Major Advisor : **Dr. LAL AHAMED M.**
University : **ACHARYA N.G. RANGA AGRICULTURAL
UNIVERSITY**
Year of submission : **2010**

ABSTRACT

The present investigation was carried out during *khariif*, 2009-10 at Agricultural College Farm, Bapatla, with 60 genotypes of cotton (*Gossypium hirsutum* L.).

The variability, genetic divergence, character association and the magnitude of direct and indirect effects of yield component traits with seed cotton yield were studied along with morphological characterization of the germplasm using IBPGR descriptors.

IBPGR descriptors data revealed that variability was present for seventeen characters out of twenty seven descriptors studied and they can be exploited for varietal identification, improvement and IPR protection.

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating the data generated from the diverse material will yield reliable information.

The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the masking effects of the environment. The characters *viz.*, plant height, number of monopodia plant⁻¹, number of bolls plant⁻¹ and seed cotton yield plant⁻¹ exhibited high variability. High heritability coupled with high genetic advance was noted in the case of plant height, number of monopodia plant⁻¹, number of bolls plant⁻¹, boll weight, lint index and seed cotton yield plant⁻¹. This indicates the predominance of additive gene action and hence, simple selection may be effective to some extent.

The correlation and path coefficient analyses together indicated that number of monopodia plant⁻¹, number of bolls plant⁻¹, boll weight and ginning out turn found to have significant positive association with seed cotton yield plant⁻¹. These studies confirmed the existence of true relationship between these characters and yield.

The results of multivariate analysis revealed that the distribution of 60 cotton genotypes into nine clusters in case of D² analysis and into eight clusters in case of agglomerative cluster analysis was at random indicating that the genetic diversity and geographical diversity were not related.

Mahalanobis' D² statistic, indicated that number of monopodia plant⁻¹, 2.5% span length, plant height, micronaire, ginning out turn, bundle strength, lint index, number of bolls plant⁻¹, boll weight and number of sympodia plant⁻¹ contributed maximum towards genetic divergence.

Based on the inter- cluster distances among the groups suggestions were made to attempt crosses after confirming their general combining ability between cluster VII (G-204-13) and cluster V (IC-356932, A-7262, L-614, NH-577, WGP-8, GSHY-01/1338, TXORHY-1-78, ADB-28, TSH-333, NDLH-7122 and NA-777) which had maximum inter cluster distance (128.82) to obtain better heterotic and desirable segregants.

In the principal component method, first 8 principal components explained 87.928 of the variability. The first component explained 21.415% of total variability and was characterized by high number of monopodia plant⁻¹, ginning outturn, seed index, uniformity ratio, bundle strength and lint index.

Agglomerative cluster analysis revealed crosses can be attempted between clusters I (NH-577, WGP-8, IC-356932, A-7262, L-614, and TXORHY-1-78) and cluster VIII (GJHV-01/35) which had wide genetic distance to obtain maximum heterosis.

The genotypes, NH-577, WGP-8, IC-356932, A-7262, L-614 and TXORHY-1-78 showed maximum inter-cluster distance and wide genetic distance in all the three divergence methods. So they can be exploited in hybridization programme for identification desirable segregants.

CHAPTER – I

INTRODUCTION

Cotton is a soft, staple fibre that grows around the seeds of the cotton plant (*Gossypium* sp.), a shrub native to tropical and subtropical regions around the world, including India and Africa. The fibre most often is spun into yarn or thread and used to make a soft, breathable textile, which is the most widely, used natural-fibre cloth in clothing today. The English name which began to be used circa 1400, derives from the Arabic (al) qutun meaning cotton. In the 1800s and 1900s cotton was called "King Cotton" because of the great power it had in the economy.

The cotton genus, *Gossypium* (Malvaceae), comprises 49 species, including 44 diploids and 5 disomic tetraploids distributed throughout the arid and semi-arid regions of Africa, Australia, Central and South America, the Indian subcontinent, Arabia, the Galapagos and Hawaii. The base chromosome number for the genus is 13, and cytogenetically, *Gossypium* genomes, designated A to G and K, and a single disomic AD tetraploid ($2n = 4x = 52$) genome. Two diploid and two tetraploid species are cultivated as sources of lint. The agriculturally superior New World AD-genome species, *G. hirsutum* L. and *G. barbadense* L. have largely supplanted the Old World A-genome species, *G. herbaceum* L. and *G. arboretum* L. and currently are the primary focus of cotton breeders (Chopra 2001).

India has the distinction of growing all the four spinnable lint bearing species of *Gossypium* viz., *G. hirsutum*, *G. barbadense*, *G. arboreum* and *G. herbaceum*. Among the four cultivated species, upland cotton (*G. hirsutum* L.) is known for its production potential, as demonstrated by the release of number of stable varieties and hybrids.

India is the largest cotton growing country with an area of 9.41 million hectares and production of 23.16 million bales of cotton. Average productivity in India is 419 kg lint per hectare. In Andhra Pradesh, cotton is a crop of great economic value and playing a significant role in the socio-economic status of the farmers. It occupies an area of about 1.13 million hectares with an annual production of 3.49 million bales (170kg each) and productivity of 523 kg ha⁻¹ lint (Ministry of Commerce, 2008-09).

Before actual breeding programme is taken up to accomplish the prime objectives in cotton improvement, it is desirable to elicit information on the extent of genetic variability present in the material is very important. Besides, association of characters among themselves and with seed cotton yield are to be worked out, the extent of heritability of these selected traits and magnitude of genetic advance are known to be equally important. Genetic divergence is of considerable practical interest in crop improvement, since plant breeding is the utilization of the crop variability for economic end. So genetic diversity among parents is considered to be an important factor for obtaining heterotic hybrids. The crosses involving genotypes with wider genetic base are likely to generate desirable recombinants in the progeny. The quantification of the degree of divergence present in the population is of immense value in identifying diverse genotypes for recombination breeding programmes. Mahalanobis D² statistics is a powerful tool for quantifying genetic divergence in germplasm collections with respect to characters considered together.

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

In view of the above aspects, the present investigation was carried out with the following objectives.

1. To study variability for yield, yield components and fibre quality traits.
2. To study character association between yield and its components and direct and indirect effect of yield components on yield.
3. To estimate genetic divergence in available germplasm to find out the important characters contributing to the genetic divergence.

CHAPTER - II

REVIEW OF LITERATURE

Cotton (*Gossypium hirsutum* L.) is an important commercial crop of India. It belongs to the family Malvaceae and the genus *Gossypium* consisting of about 50 species. Of these, four species viz., *G. arboreum* L., *G. herbaceum* L., *G. hirsutum* L. and *G. barbadense* L. are cultivated. Among the cultivated species, American cotton varieties viz., *Gossypium hirsutum* L. and intra-hirsutum hybrids occupy more than 75 per cent of the cultivated area, as they are high yielders compared to other species.

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

2.1. Morphological characters (Descriptors)

2.2. Genetic variability

2.3. Heritability and genetic advance as per cent of mean

2.4. Character association

2.5. Path analysis

2.6. Genetic divergence

2.1 Morphological characters (Descriptors)

Germplasm characterization is an important operation for a gene bank. The value of the germplasm collection depends upon the availability of information relative to the accessions.

Morphological and agronomic traits as well as reaction to biotic and abiotic stresses that are known to be in the individual accessions increase the importance of the germplasm. Moreover, systematic description leads to a more efficient use of germplasm in the collection.

Effective use of germplasm in cotton genetic improvement programmes depends on the extent of genetic variation for desirable alleles and the accurate characterization of the variability within and among germplasm accessions in the collection. Genetic diversity is desirable for long term crop improvement with reduction of vulnerability to major crop pests (Poehlman and Sleper, 1995).

Jimmy Xavier Zumba (2004) studied 154 lines from the former USDA cotton breeding programme at Shafter, California and reported the existence of variability for the most of the IBPGR descriptors.

Padmavathi *et al.* (2008) studied on characterization of 60 cotton (*Gossipum hirsutum* L.) germplasm lines and variation was observed for 17 out of 27 descriptors of IBPGR.

2.2. 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 for formulating the efficient breeding programmes. Superior genotypes can be isolated by selection if considerable genetic variation was present within the population. In general the total variability can be partitioned into the heritable and non-heritable components with the help of genetic parameters like genotypic coefficients of variation. The literature on genetic variability studies on cotton is reviewed and presented in Table-1.

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

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

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

Estimates of heritability along with the estimates of genetic advance (GA) are more useful in choice of selection methods rather than heritability or genetic advance alone (Johnson *et al.*, 1955). High heritability coupled with high genetic advance indicates that the improvement could be made for a character by simple selection on phenotypic performance. The literature on heritability (h^2) and genetic advance (GA) is presented in Table-2.

2.4. 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.

2.4.1 Association of component characters with seed cotton yield

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

2.4.2 Association among the yield component characters

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

2.4 Path coefficient analysis

Path coefficient analysis devised by Wright (1921) is a standardized partial regression coefficient, which helps in partitioning 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 formulating 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).

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

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

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

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

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

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

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

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

Jain and Yadav (2001) reported variation in grouping of populations into clusters from environment to environment in their study on 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 involving 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 geographical diversity is not always necessarily associated with genetic diversity.

Kiran (2003) reported that the characters bundle strength followed by seed cotton yield, number of sympodia per plant, 2.5% span length and uniformity ratio contributed maximum 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 which were grouped into 9 clusters.

Ravikumar (2004) indicated maximum contribution of character seed cotton yield per plant towards genetic divergence.

Karunakar Raju *et al.* (2005) assessed genetic divergence of 80 genotypes of upland cotton for 15 traits which 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 which were grouped into 7 clusters.

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

Vijayalaxmi (2008) reported maximum contribution of number of bolls per plant, plant height, number of monopodia per plant, number of sympodia per plant and boll weight towards genetic divergence.

Gopinath *et al.* (2009) reported maximum contribution of boll weight, boll number and 2.5% span length towards total divergence in their study with sixty genotypes of cotton.

Satish *et al.* (2009) reported the geographical diversity and genetic diversity were not related and there were forces other than geographical separation which were responsible for diversity.

2.5.2 Principal component analysis and cluster analysis

Principal component analysis was carried out to transform the inter dependent traits into a set of independent traits as well as to reduce 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 dendrogram.

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

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

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

Vijayalaxmi (2008) used cluster analysis and PCA to estimate genetic divergence in 72 genotypes of upland cotton. PCA identified seven principle components which contributed 87.47% of cumulative variance. The population with high PC₁ values were characterized by high number of bolls per plant, where as population with high PC₂ values were characterized by high boll weight.

Table-1: Review of literature on genetic variability in cotton (*Gossypium hirsutum* L.).

S.No.	Character	Wider genetic variability	Narrow genetic variability
1.	Days to 50% flowering	Ahuja and Tuteja (2000) Laxman and Ganesh (2003)	Reddy (2001) Neelam and Potdukhe (2002) Altaher and Singh (2003b) Narisireddy and Ratnakumari (2004) Karunakar Raju (2005) Prasad <i>et al.</i> (2005) Leela Pratap (2006) Eswararao (2008) Neelima <i>et al.</i> (2008) Padmavathi. (2008) Vijayalaxmi (2008) Srinivasulu (2009)
2.	Plant height (cm)	Neelam and Potdukhe (2002) Laxman and Ganesh (2003) Patnaik <i>et al.</i> (2004) Kale <i>et al.</i> (2006) Tuteja <i>et al.</i> (2006) Kalpande <i>et al.</i> (2008)	Sangeetha (1998) Deshpande and Baig (2003) Leela Pratap (2006) Eswararao (2008) Neelima <i>et al.</i> (2008) Vijayalaxmi (2008)
3.	No. of monopodia per plant	Neelam and Potdukhe (2002) Altaher and Singh (2003b) Kaushik <i>et al.</i> (2003) Ravikumar (2004) Sivaprasad <i>et al.</i> (2004 b) Karunakar Raju (2005) Prasad <i>et al.</i> (2005) Kumari and Chamundeswari (2005) Tuteja <i>et al.</i> (2006) Verma <i>et al.</i> (2006) Gitte <i>et al.</i> (2007) Eswararao (2008) Kalpande <i>et al.</i> (2008) Neelima <i>et al.</i> (2008) Padmavathi. (2008) Vijayalaxmi (2008) Srinivasulu (2009)	Ahuja and Tuteja (2000) Gururajan (2000) Girase and Mehetre (2002)

Contd.....

S.No.	Character	Wider genetic variability	Narrow genetic variability
4.	No.of sympodia per plant	Gururajan (2000) Neelam and Potdukhe (2002) Deshpande and Baig (2003) Tuteja <i>et al.</i> (2003) Tuteja <i>et al.</i> (2006) Gitte <i>et al.</i> (2007) Kalpande <i>et al.</i> (2008) Neelima <i>et al.</i> (2008)	Girase and Mehetre (2002) Laxman and Ganesh (2003) Prasad <i>et al.</i> (2005) Eswararao (2008) Vijayalaxmi (2008)
5.	No. of bolls per plant	Laxman and Ganesh (2003) Gururajan and Sundar (2004) Narisireddy and Ratnakumari (2004) Sivaprasad <i>et al.</i> (2004 b) Kale <i>et al.</i> (2006) Leela Pratap (2006) Tuteja <i>et al.</i> (2006) Gitte <i>et al.</i> (2007) Reddy and Reddy (2007) Padmavathi. (2008)	Girase and Mehetre (2002) Vijayalaxmi (2008)
6.	Boll weight (g)	Kaushik <i>et al.</i> (2003) Laxman and Ganesh (2003) Muthuswamy <i>et al.</i> (2003) Gururajan and Sundar (2004) Sivaprasad <i>et al.</i> (2004 b) Kale <i>et al.</i> (2006) Tuteja <i>et al.</i> (2006) Gitte <i>et al.</i> (2007) Reddy and Reddy (2007) Kalpande <i>et al.</i> (2008)	Reddy (2001) Altaher and Singh (2003b) Eswararao (2008) Neelima <i>et al.</i> (2008) Vijayalaxmi (2008)
7.	Ginning out- turn (%)	Laxman and Ganesh (2003) Muthuswamy <i>et al.</i> (2003) Tuteja <i>et al.</i> (2003) Patnaik <i>et al.</i> (2004) Tuteja <i>et al.</i> (2006) Srinivasulu (2009)	Rao and Reddy (2001) Reddy (2001) Muraleedhar (2005) Prasad <i>et al.</i> (2005) Eswararao (2008) Padmavathi.(2008) Vijayalaxmi (2008)
8.	Seed index (g)	Muthuswamy <i>et al.</i> (2003) Gururajan and Sundar (2004) Patnaik <i>et al.</i> (2004) Ravikumar (2004) Sivaprasad <i>et al.</i> (2004 b)	Rao and Reddy (2001) Reddy (2001) Neelam and Potdukhe (2002) Altaher and Singh (2003b)

Contd.....

S.No.	Character	Wider genetic variability	Narrow genetic variability
			Laxman and Ganesh (2003) Neelima <i>et al.</i> (2008) Vijayalaxmi (2008) Srinivasulu (2009)
9.	Lint index (g)	Laxman and Ganesh (2003) Muthuswamy <i>et al.</i> (2003) Patnaik <i>et al.</i> (2004) Gururajan and Sundar (2004) Sivaprasad <i>et al.</i> (2004 b)	Rao and Reddy (2001) Altaher and Singh (2003b) Vijayalaxmi (2008)
10.	2.5% span length (mm)	Muthuswamy <i>et al.</i> (2003) Gururajan and Sundar (2004) Naphade <i>et al.</i> (2004) Patnaik <i>et al.</i> (2004)	Reddy (2001) Neelam and Potdukhe (2002) Altaher and Singh (2003b) Prasad <i>et al.</i> (2005) Leela Pratap (2006) Tuteja <i>et al.</i> (2006) Verma <i>et al.</i> (2006) Eswararao (2008) Padmavathi. (2008) Vijayalaxmi (2008) Srinivasulu (2009)
11.	Micronaire value (10 ⁻⁶ g/in)	Rao and Reddy (2001) Neelam and Potdukhe (2002) Muthuswamy <i>et al.</i> (2003) Naphade <i>et al.</i> (2004) Patnaik <i>et al.</i> (2004)	Reddy (2001) Altaher and Singh (2003b) Prasad <i>et al.</i> (2005) Eswararao (2008) Vijayalaxmi (2008) Srinivasulu (2009)
12.	Bundle strength (g/tex)	Muthuswamy <i>et al.</i> (2003) Gururajan and Sundar (2004) Naphade <i>et al.</i> (2004) Patnaik <i>et al.</i> (2004) Neelima <i>et al.</i> (2005)	Reddy (2001) Rao and Reddy (2001) Neelam and Potdukhe (2002) Girase and Mehetre (2002) Altaher and Singh (2003b) Karunakar Raju (2005) Prasad <i>et al.</i> (2005) Leela Pratap (2006) Eswararao (2008) Neelima <i>et al.</i> (2008) Padmavathi. (2008) Vijayalaxmi (2008) Srinivasulu (2009)

Contd.....

S.No.	Character	Wider genetic variability	Narrow genetic variability
13.	Uniformity ratio	Patnaik <i>et al.</i> (2004)	Altaher and Singh (2003b) Karunakar Raju (2005) Muraleedhar (2005) Prasad <i>et al.</i> (2005) Leela Pratap (2006) Eswararao (2008) Padmavathi. (2008) Vijayalaxmi (2008) Srinivasulu (2009)
14.	Fibre elongation (%)	—	Valarmathi and Jehangir (1998) Ravi kumar (2004) Muraleedhar (2005) Eswararao (2008) Padmavathi. (2008) Vijayalaxmi (2008) Srinivasulu (2009)
15.	Seed cotton yield per plant (g)	Rao and Reddy (2001) Reddy (2001) Neelam and Potdukhe (2002) Kaushik <i>et al.</i> (2003) Laxman and Ganesh (2003) Muthuswamy <i>et al.</i> (2003) Tuteja <i>et al.</i> (2003) Sivaprasad <i>et al.</i> (2004 b) Gururajan and Sundar (2004) Narisireddy and Ratnakumari (2004) Karunakar Raju (2005) Kumari and Chamundeswari (2005) Leela Pratap (2006) Verma <i>et al.</i> (2006) Gitte <i>et al.</i> (2007) Reddy and Reddy (2007) Padmavathi. (2008) Vijayalaxmi (2008) Srinivasulu (2009)	

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

S. No.	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
1.	Days to 50% flowering	Neelam and Potdukhe (2002)	Sangeetha (1998) Reddy (2001) Muraleedhar (2005) Roy (2006) Do Thi Ha An <i>et al.</i> (2008) Padmavathi. (2008) Srinivasulu(2009)	Vijayalaxmi (2008)	Neelima (2002) Sivaprasad <i>et al.</i> (2004a) Karunakar Raju (2005)
2.	Plant height (cm)	Sangeetha (1998) Neelam and Potdukhe (2002) Pandey <i>et al.</i> (2002) Kale <i>et al.</i> (2006) Roy (2006) Preetha and Raveendran (2007) Sakthi <i>et al.</i> (2007) Do Thi Ha An <i>et al.</i> (2008) Padmavathi. (2008) Neelam and Potdukhe (2002) Srinivasulu (2009)	Verma <i>et al.</i> (2006) Vijayalaxmi (2008)	-	Eswararao (2008) Kumari and Chamundeswari(2005)

Contd...

S. No.	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
3.	No. of monopodia per plant	Girase and Mehetre (2002) Kaushik <i>et al.</i> (2003) Karunakar Raju (2005) Leela Pratap (2006) Verma <i>et al.</i> (2006) Eswararao (2008) Padmavathi. (2008) Vijayalaxmi (2008)	Reddy (2001) Kumari and Chamundeswari(2005) Srinivasulu(2009)	Neelima (2002) Sivaprasad <i>et al.</i> (2004a)	Rao and Reddy (2001)
4.	No. of sympodia per plant	Neelam and Potdukhe (2002) Girase and Mehetre (2002) Kaushik <i>et al.</i> (2003) Ravikumar (2004) Verma <i>et al.</i> (2006) Preetha and Raveendran (2007) Sakthi <i>et al.</i> (2007) Do Thi Ha An <i>et al.</i> (2008) Padmavathi . (2008)	Gururajan (2000) Reddy (2001) Kiran (2003) Vijayalaxmi (2008) Srinivasulu (2009)	-	Rao and Reddy (2001) Sivaprasad <i>et al.</i> (2004a) Kumari and Chamundeswari (2005)

Contd....

S. No.	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
5.	No. of bolls per plant	Rao and Reddy (2001) Reddy (2001) Girase and Mehetre (2002) Neelam and Potdukhe (2002) Kaushik <i>et al.</i> (2003) Ravikumar (2004) Sivaprasad <i>et al.</i> (2004a) Kale <i>et al.</i> (2006) Leela Pratap (2006) Roy (2006) Preetha and Raveendran (2007) Reddy and Reddy (2007) Sakthi <i>et al.</i> (2007) Do Thi Ha An <i>et al.</i> (2008) Padmavathi. (2008) Vijayalaxmi (2008)	Murthy <i>et al.</i> (1994) Gururajan and Sundar (2004) Srinivasulu (2009)	-	-
6.	Boll weight (g)	Neelam and Potdukhe (2002) Neelima (2002)	Gururajan (2000) Gururajan and Sundar (2004)	Sivaprasad <i>et al.</i> (2004a)	Kiran (2003) Kumari and Chamundeswari (2005)

Contd.....

S. No.	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
		Kaushik <i>et al.</i> (2003) Narisireddy and Ratnakumari (2004) Karunakar Raju (2005) Kale <i>et al.</i> (2006) Verma <i>et al.</i> (2006) Roy (2006) Preetha and Raveendran (2007) Sakthi <i>et al.</i> (2007) Do Thi Ha An <i>et al.</i> (2008) Padmavathi . (2008) Vijayalaxmi (2008)	Srinivasulu (2009)		
7.	Ginning outturn (%)	Valarmathi and Jehangir (1998) Gururajan and Sundar (2004)	Gururajan (2000) Rao and Reddy (2001) Neelam and Potdukhe (2002) Karunakar Raju (2005) Leela Pratap (2006) Verma <i>et al.</i> (2006) Vijayalaxmi (2008) Do Thi Ha An <i>et al.</i> (2008)	-	Prasad (2003) Sivaprasad <i>et al.</i> (2004a) Srinivasulu (2009)

Contd.....

S. No.	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
8.	Seed index (g)	Rao and Reddy (2001) Ravikumar (2004) Karunakar Raju (2005) Do Thi Ha An <i>et al.</i> (2008) Padmavathi .(2008) Vijayalaxmi (2008)	Gururajan (2000) Neelam and Potdukhe (2002) Sivaprasad <i>et al.</i> (2004a)	-	Reddy (2001) Gururajan and Sundar (2004) Srinivasulu (2009)
9.	Lint index (g)	Reddy (2001) Neelima (2002) Karunakar Raju (2005) Murthy <i>et al.</i> (2006) Do Thi Ha An <i>et al.</i> (2008) Padmavathi.. (2008) Vijayalaxmi (2008)	Rao and Reddy (2001) Neelam and Potdukhe (2002) Sivaprasad <i>et al.</i> (2004a)	-	Prasad (2003) Srinivasulu (2009)

Contd.....

S. No.	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
10.	2.5% span length (mm)	Rao and Reddy (2001) Reddy (2001) Gururajan and Sundar (2004) Vijayalaxmi (2008)	Kiran (2003) Tuteja <i>et al.</i> (2005a) Verma <i>et al.</i> (2006) Do Thi Ha An <i>et al.</i> (2008) Srinivasulu (2009)	-	Singh <i>et al.</i> (1987) Prasad (2003)
11.	Micronaire value (10 ⁻⁶ g/in)	Rao and Reddy (2001) Do Thi Ha An <i>et al.</i> (2008)	Reddy (2001) Vijayalaxmi (2008)	-	Prasad (2003) Sivaprasad <i>et al.</i> (2004a) Srinivasulu (2009)
12.	Bundle strength (g/tex)	Reddy (2001) Murthy <i>et al.</i> (2006) Do Thi Ha An <i>et al.</i> (2008)	Rao and Reddy (2001) Kiran (2003)	-	Gururajan and Sundar (2004) Sivaprasad <i>et al.</i> (2004a) Muraleedhar (2005) Eswararao (2008) Vijayalaxmi (2008) Srinivasulu (2009)
13.	Uniformity ratio	-	Sangeetha (1998) Neelima (2002) Kiran (2003) Karunakar Raju (2005)	-	Sivaprasad <i>et al.</i> (2004a) Muraleedhar (2005) Vijayalaxmi (2008) Srinivasulu (2009)

Contd.....

S. No.	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
14.	Fibre elongation (%)	Valarmathi and Jehangir (1998) Preetha and Raveendran (2007)	Vijayalaxmi (2008) Srinivasulu (2009)	-	Muraleedhar (2005) Eswararao (2008)
15.	Seed cotton yield/plant (g)	Ahuja and Tuteja (2000) Rao and Reddy (2001) Neelam and Potdukhe (2002) Girase and Mehetre (2002) Pandey <i>et al.</i> (2002) Kaushik <i>et al.</i> (2003) Sivaprasad <i>et al.</i> (2004a) Karunakar Raju (2005) Kumari and Chamundeswari(2005) Kale <i>et al.</i> (2006) Leela Pratap (2006) Tuteja <i>et al.</i> (2006) Verma <i>et al.</i> (2006) Preetha and Raveendran (2007) Reddy and Reddy (2007) Murthy <i>et al.</i> (2006) Roy (2006) Padmavathi. (2008) Vijayalaxmi (2008) Srinivasulu (2009)	Gururajan and Sundar (2004)	-	Jain <i>et al.</i> (1984) Jain (1986)

Table -3: Review of literature on association of component characters with seed cotton yield in cotton (*Gossypium hirsutum* L.).

S. No.	Character	Association	S/NS	Reference
1.	Days to 50% flowering	Positive	S	Ganapathy (2001) Sivaprasad (2003) Muraleedhar (2005) Anandan (2009)
			NS	Murthy (1997) Ravikumar (2004)
		Negative	S	Reddy (2001) Leela Pratap <i>et al.</i> (2007)
			NS	Ladole and Meshram (2000) Altaher and Singh (2003b) Kaushik <i>et al.</i> (2003) Karunakar Raju (2005) Vijayalaxmi (2008) Srinivasulu (2009)
2.	Plant height (cm)	Positive	S	Samanc and Ozkaynak (2000) Tuteja <i>et al.</i> (2006) Kalpande <i>et al.</i> (2008) Padmavathi. (2008) Anandan (2009) Srinivasulu (2009)
			NS	Sumathi and Nadarajan (1995)
		Negative	S	Neelima <i>et al.</i> (2005)
			NS	Pradeep and Sumalini (2005) Vijayalaxmi (2008)
3.	No. of monopodia per plant	Positive	S	Ladole and Meshram (2000) Altaher and Singh (2003b) Kaushik <i>et al.</i> (2003) Padmavathi. (2008) Srinivasulu (2009)
			NS	Neelam and Potdukhe (2002) Altaher and Singh (2003b) Pradeep and Sumalini (2005) Vijayalaxmi (2008)

Contd..

S. No.	Character	Association	S/NS	Reference
		Negative	S	Kiran (2003)
			NS	Reddy (2001) Ravikumar (2004) Karunakar Raju (2005)
4.	No. of sympodia per plant	Positive	S	Altaher and Singh (2003b) Muthu <i>et al.</i> (2004) Ravikumar (2004) Saeed <i>et al.</i> (2004) Neelima <i>et al.</i> (2005) Tuteja <i>et al.</i> (2006) Leela Pratap <i>et al.</i> (2007) Kalpande <i>et al.</i> (2008) Padmavathi (2008) Vijayalaxmi (2008) Anandan (2009) Srinivasulu (2009)
			NS	Ladole and Meshram(2000) Neelam and Potdukhe (2002) Karunakar Raju (2005) Pradeep and Sumalini (2005)
5.	No. of bolls/plant	Positive	S	Kaushik <i>et al.</i> (2003) Sivaprasad (2003) Muthu <i>et al.</i> (2004) Gururajan and Sundar (2004) Saeed <i>et al.</i> (2004) Neelima <i>et al.</i> (2005) Karunakar Raju (2005) Tuteja <i>et al.</i> (2006) Verma <i>et al.</i> (2006) Leela Pratap <i>et al.</i> (2007) Kalpande <i>et al.</i> (2008) Do Thi Ha An <i>et al.</i> (2008) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008) Anandan (2009) Srinivasulu (2009)
			NS	Pradeep and Sumalini (2005)

Contd.

S. No.	Character	Association	S/NS	Reference
		Negative	S	Patil <i>et al.</i> (1991)
6.	Boll weight (g)	Positive	S	Altaher and Singh (2003b) Sivaprasad (2003) Gururajan and Sundar (2004) Muthu <i>et al.</i> (2004) Neelima <i>et al.</i> (2005) Karunakar Raju (2005) Murthy <i>et al.</i> (2006) Do Thi Ha An <i>et al.</i> (2008) Eswararao (2008) Padmavathi (2008) Anandan (2009) Srinivasulu (2009)
			NS	Ladole and Meshram (2000) Reddy (2001) Kaushik <i>et al.</i> (2003) Vijayalaxmi (2008)
		Negative	S	Gururajan (2000) Rao <i>et al.</i> (2001)
			NS	Pradeep and Sumalini (2005) Ravikumar (2004)
7.	Ginning out -turn (%)	Positive	S	Gururajan (2000) Ganapathy (2001) Reddy (2001) Sivaprasad (2003) Tuteja <i>et al.</i> (2005a) Anandan (2009)
			NS	Rao <i>et al.</i> (2001) Neelam and Potdukhe (2002)
		Negative	S	Mandloi <i>et al.</i> (2003) Muthuswamy and Vivek Anandan <i>et.al.</i> , (2004) Srinivasulu (2009)
			NS	Karunakar Raju (2005) Vijayalaxmi (2008)
8.	Seed index (g)	Positive	S	Sivaprasad (2003) Gururajan and Sundar (2004) Muthu <i>et al.</i> (2004) Neelima <i>et al.</i> (2005) Murthy <i>et al.</i> (2006)

Contd..

S. No.	Character	Association	S/NS	Reference
				Do Thi Ha An <i>et al.</i> (2008) Padmavathi (2008) Anandan (2009) Srinivasulu (2009)
		Negative	S	Tyagi (1994b) Gururajan and Sundar (2004)
			NS	Neelam and Potdukhe (2002) Pankaj Rathore <i>et al.</i> (2004) Ravikumar (2004) Karunakar Raju (2005) Tuteja <i>et al.</i> (2005a) Vijayalaxmi (2008) Padmavathi (2008)
9.	Lint index (g)	Positive	S	Reddy (2001) Neelima (2002) Neelam and Potdukhe (2002) Sivaprasad (2003) Muthu <i>et al.</i> (2004) Karunakar Raju (2005) Neelima <i>et al.</i> (2005) Sambamurthy <i>et al.</i> (2006)
			NS	Rao <i>et al.</i> (2001) Ravikumar (2004) Vijayalaxmi (2008)
		Negative	NS	Ladole and Meshram (2000) Mandloi <i>et al.</i> (2003)
10.	2.5% span length (mm)	Positive	S	Rajarathinam <i>et al.</i> (1993) Kiran (2003)
			NS	Rao <i>et al.</i> (2001) Reddy (2001) Neelima (2002) Mandloi <i>et al.</i> (2003)
		Negative	S	Govila and Sharma (1981) Jagtap (1981) Tyagi (1994b) Gururajan and Sundar (2004)
			NS	Neelam and Potdukhe (2002) Ravikumar (2004) Pankaj Rathore <i>et al.</i> (2004)

Contd..

S. No.	Character	Association	S/NS	Reference
				Tuteja <i>et al.</i> (2005a) Karunakar Raju (2005) Vijayalaxmi (2008)
11.	Micronaire value (10 ⁻⁶ g/in)	Positive	S	Reddy (2001) Altaher and Singh (2003b) Karunakar Raju (2005) Neelima <i>et al.</i> (2005) Murthy <i>et al.</i> (2006) Srinivasulu (2009)
			NS	Rao <i>et al.</i> (2001) Neelam and Potdukhe (2002) Mandloi <i>et al.</i> (2003) Pankaj Rathore <i>et al.</i> (2004) Ravikumar (2004) Tuteja <i>et al.</i> (2005a) Vijayalaxmi (2008) Padmavathi (2008)
12.	Bundle strength (g/tex)	Positive	S	Rao <i>et al.</i> (2001)
			NS	Neelima (2002) Neelam and Potdukhe (2002) Mandloi <i>et al.</i> (2003) Padmavathi (2008) Anandan (2009)
		Negative	S	Sangeetha (1998) Rao <i>et al.</i> (2001) Sivaprasad (2003)
			NS	Pankaj Rathore <i>et al.</i> (2004) Ravikumar (2004) Karunakar Raju (2005) Vijayalaxmi (2008) Srinivasulu (2009)

Contd..

S. No.	Character	Association	S/NS	Reference
13.	Uniformity ratio	Positive	S	Sivaprasad (2003) Neelima <i>et al.</i> (2005)
			NS	Karunakar Raju (2005) Srinivasulu (2009)
		Negative	S	Rajarithinam <i>et al.</i> (1993) Vijayalaxmi (2008) Srinivasulu (2009) Anandan (2009)
			NS	Dedaniya and Pethani (1994) Ravikumar (2004) Tuteja <i>et al.</i> (2005 a,b)
14.	Fibre elongation (%)	Positive	N S	Ravi kumar (2004) Muraleedhar (2005) Padmavathi (2008)
		Negative	S	Srinivasulu (2009)
			NS	Vijayalaxmi(2008)

S: Significant

NS: Non-significant

Table- 4: Review of literature on association among component characters of seed cotton yield in cotton (*Gossypium hirsutum* L.).

S. No.	Character	Association	S/NS	Reference
I. Association of days to 50% flowering with				
1.	Plant height (cm)	Positive	S	Murthy (1999) Padmavathi (2008)
			NS	Sangeetha (1998) Srinivasulu (2009) Anandan (2009)
		Negative	S	Dedaniya and Pethani (1994)
			NS	Vijayalaxmi (2008)
2.	No. of monopodia per plant	Positive	S	Altaher and Singh (2003b) Karunakar Raju (2005) Muraleedhar (2005) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000) Reddy (2001) Srinivasulu (2009)
		Negative	NS	Neelam and Potdukhe (2002)
3.	No. of sympodia per plant	Positive	S	Ladole and Meshram (2000) Muraleedhar (2005) Padmavathi (2008)
			NS	Basha (1997) Anandan (2009)
		Negative	S	Altaher and Singh (2003b) Karunakar Raju (2005) Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002) Neelima (2002) Srinivasulu (2009)
4.	No. of bolls/ plant	Positive	S	Muraleedhar (2005) Vijayalaxmi (2008)
			NS	Sangeetha (1998) Anandan (2009)

Contd..

S. No.	Character	Association	S/NS	Reference
		Negative	S	Reddy (2001)
			NS	Ladole and Meshram (2000) Neelam and Potdukhe (2002) Neelima (2002) Karunakar Raju (2005) Srinivasulu (2009) Neelima (2002) Karunakar Raju (2005)
5.	Boll weight (g)	Positive	S	Altaher and Singh (2003b) Sivaprasad (2003)
		Negative	S	Karunakar Raju (2005) Muraleedhar (2005) Leela Pratap <i>et al.</i> (2007) Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000) Neelima (2002) Anandan (2009) Srinivasulu (2009)
6.	Ginning outturn (%)	Positive	S	Neelam and Potdukhe (2002) Karunakar Raju (2005)
			NS	Murthy (1997) Vijayalaxmi (2008)
		Negative	S	Leela Pratap <i>et al.</i> (2007)
			NS	Ladole and Meshram (2000) Reddy (2001) Neelima (2002) Anandan (2009) Srinivasulu (2009)
7.	Seed index (g)	Positive	S	Basha (1997) Karunakar Raju (2005) Leela Pratap <i>et al.</i> (2007)
		Negative	S	Ladole and Meshram (2000) Neelima (2002)

Contd...

S. No.	Character	Association	S/NS	Reference
				Muraleedhar (2005) Vijayalaxmi (2008)
			NS	Reddy (2001) Neelam and Potdukhe (2002) Anandan (2009) Srinivasulu (2009)
8.	Lint index (g)	Positive	S	Karunakar Raju (2005)
			NS	Basha (1997) Neelam and Potdukhe (2002) Anandan (2009)
		Negative	S	Ladole and Meshram (2000) Reddy (2001) Neelima (2002) Leela Pratap <i>et al.</i> (2007)
			NS	Vijayalaxmi (2008) Srinivasulu (2009)
9.	2.5% span length (mm)	Positive	S	Muraleedhar (2005)
			NS	Ladole and Meshram (2000) Neelima (2002) Karunakar Raju (2005) Vijayalaxmi (2008) Srinivasulu (2009)
		Negative	NS	Reddy (2001) Neelam and Potdukhe (2002) Anandan (2009)
10.	Micronaire value (10 ⁻⁶ g/in)	Positive	S	Leela Pratap <i>et al.</i> (2007)
			NS	Sangeetha (1998)
		Negative	S	Altaher and Singh (2003b) Muraleedhar (2005) Vijayalaxmi (2008)

Contd.....

S. No.	Character	Association	S/NS	Reference
			NS	Reddy (2001) Neelima (2002) Neelam and Potdukhe (2002) Anandan (2009) Srinivasulu (2009)
11.	Bundle strength (g/tex)	Positive	S	Sivaprasad (2003) Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002) Srinivasulu (2009)
		Negative	S	Altaher and Singh (2003b) Karunakar Raju (2005)
			NS	Reddy (2001) Neelima (2002)
12.	Uniformity ratio	Positive	S	Neelima (2002) Neelima <i>et al.</i> (2005)
			NS	Sangeetha (1998)
		Negative	NS	Karunakar Raju (2005) Vijayalaxmi (2008)
13.	Fibre elongation (%)	Positive	S	Muraleedhar (2005)
		Negative	S	Vijayalaxmi (2008)
			NS	Vijayalaxmi (2008) Anandan (2009)
II. Association of plant height with				
1.	No. of monopodia per plant	Positive	S	Neelam and Potdukhe (2002) Padmavathi (2008)
			NS	Srinivasulu(2009)
		Negative	NS	Sangeetha (1998) Pradeep and Sumalini (2005) Vijayalaxmi (2008)
2.	No. of sympodia per plant	Positive	S	Samanc and Ozkaynak (2000) Muthu <i>et al.</i> (2004) Tuteja <i>et al.</i> (2006) Verma <i>et al.</i> (2006)

Contd.....

S. No.	Character	Association	S/NS	Reference
				Leela Pratap <i>et al.</i> (2007) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Pradeep and Sumalini (2005) Anandan (2009) Srinivasulu (2009)
3.	No. of bolls/plant	Positive	S	Samanc and Ozkaynak (2000) Muthu <i>et al.</i> (2004) Tuteja <i>et al.</i> (2006) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Sangeetha (1998) Anandan (2009) Srinivasulu(2009)
		Negative	NS	Pradeep and Sumalini (2005)
4.	Boll weight (g)	Positive	NS	Pradeep and Sumalini (2005) Vijayalaxmi (2008)
			S	Gnana Arul Samuel Rajan (1997)
		Negative	NS	Tyagi (1994a) Sangeetha (1998) Anandan (2009) Srinivasulu (2009)
5.	Ginning outturn (%)	Positive	NS	Vijayalaxmi (2008) Anandan (2009)
		Negative	S	Tyagi (1994a)
			NS	Kowsalya and Raveendran (1996) Sangeetha (1998) Srinivasulu (2009)
6.	Seed index (g)	Positive	S	Muthu <i>et al.</i> (2004) Padmavathi (2008)
			NS	Sumathi and Nadarajan (1995) Sangeetha (1998) Padmavathi (2008)

Contd....

S. No.	Character	Association	S/NS	Reference
				Vijayalaxmi (2008) Anandan (2009)
		Negative	NS	Tyagi (1994a) Srinivasulu (2009)
			S	Leela Pratap <i>et al.</i> (2007)
7.	Lint index (g)	Positive	NS	Sumathi and Nadarajan (1995) Padmavathi (2008) Vijayalaxmi (2008) Anandan (2009)
		Negative	NS	Sangeetha (1998) Srinivasulu (2009)
8.	2.5% span length (mm)	Positive	S	Muthu <i>et al.</i> (2004) Verma <i>et al.</i> (2006)
			NS	Sumathi and Nadarajan (1995) Vijayalaxmi (2008) Anandan (2009)
		Negative	NS	Sangeetha (1998) Srinivasulu (2009)
9.	Micronaire value(10^{-6} g/in)	Positive	NS	Sangeetha (1998) Vijayalaxmi (2008)
		Negative	NS	Dedaniya and Pethani (1994) Srinivasulu (2009) Anandan (2009)
			S	Tyagi (1994a)
10.	Bundle strength (g/tex)	Positive	S	Vijayalaxmi (2008)
			NS	Kowsalya and Raveendran (1996) Srinivasulu (2009)
		Negative	NS	Sangeetha (1998) Anandan (2009)

Contd....

S. No.	Character	Association	S/NS	Reference
11.	Uniformity ratio	Positive	NS	Dedaniya and Srinivasulu (2009) Pethani (1994) Sangeetha (1998) Srinivasulu (2009)
		Negative	S	Padmavathi (2008) Vijayalaxmi (2008)
			NS	Anandan,(2009)
12.	Fibre elongation (%)	Positive	S	Vijayalaxmi (2008)
		Negative	NS	Srinivasulu (2009) Anandan (2009)
III. Association of no. of monopodia per plant with				
1.	No.of sympodia per plant	Positive	S	Leela Pratap <i>et al.</i> (2007) Padmavathi (2008)
			NS	Ladole and Meshram (2000) Reddy (2001) Neelima (2002) Kaushik <i>et al.</i> (2003) Srinivasulu(2009)
		Negative	S	Verma <i>et al.</i> (2006) Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002) Pradeep and Sumalini (2005)
2.	No.of bolls/plant	Positive	S	Ladole and Meshram (2000) Kaushik <i>et al.</i> (2003) Verma <i>et al.</i> (2006) Leela Pratap <i>et al.</i> (2007) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Neelima (2002) Neelam and Potdukhe (2002) Srinivasulu (2009)
		Negative	NS	Reddy (2001)
3.	Boll weight (g)	Positive	S	Basha (1997)

Contd.....

S.NO	Character	Association	S/NS	Reference
			NS	Ladole and Meshram (2000) Reddy (2001) Neelima (2002)
		Negative	NS	Murthy (1997) Sangeetha (1998) Kaushik <i>et al.</i> (2003) Pradeep and Sumalini (2005) Vijayalaxmi (2008) Srinivasulu (2009)
			S	Leela Pratap <i>et al.</i> (2007)
4.	Ginning outturn (%)	Positive	S	Gururajan (2000) Muthu <i>et al.</i> (2004) Leela Pratap <i>et al.</i> (2007) Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000) Reddy (2001) Neelima (2002) Srinivasulu (2009)
		Negative	NS	Neelam and Potdukhe (2002)
5.	Seed index (g)	Positive	NS	Ladole and Meshram (2000) Reddy (2001) Neelima (2002)
		Negative	S	Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002) Karunakar Raju (2005) Srinivasulu (2009)
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) Srinivasulu (2009)

Contd..

7.	2.5% span length (mm)	Positive	S	Reddy (2001) Sivaprasad (2003)
			NS	Ladole and Meshram (2000) Neelam and Potdukhe (2002) Srinivasulu (2009)
		Negative	NS	Neelima (2002) Vijayalaxmi (2008)
			S	Verma <i>et al.</i> (2006)
8.	Micronaire value (10 ⁻⁶ g/in)	Positive	NS	Neelima (2002)
		Negative	NS	Reddy (2001) Neelam and Potdukhe (2002)
			S	Muraleedhar (2005) Vijayalaxmi (2008)
9.	Bundle strength (g/tex)	Positive	NS	Neelam and Potdukhe (2002) Neelima (2002) Vijayalaxmi (2008) Srinivasulu (2009)
			S	Muraleedhar (2005)
		Negative	NS	Sangeetha (1998) Reddy (2001)
10.	Uniformity ratio	Negative	NS	Sangeetha (1998) Neelima (2002)
			S	Vijayalaxmi (2008)
		Positive	S	Altaher and Singh (2003b)
			NS	Karunakar Raju (2005) Srinivasulu (2009)
11.	Fibre elongation (%)	Positive	S	Muraleedhar (2005)
			NS	Srinivasulu(2009)
		Negative	S	Vijayalaxmi (2008)
IV. Association of number of sympodia per plant with				
1.	Number of bolls/plant	Positive	S	Altaher and Singh (2003b) Sivaprasad (2003) Muthu <i>et al.</i> (2004)

Contd..

S. No.	Character	Association	S/NS	Reference
				Muthuswamy and Vivekanandan (2004) Neelima <i>et al.</i> (2005) Tuteja <i>et al.</i> (2006) Eswararao (2008) Padmavathi (2008)
		Positive	NS	Ladole and Meshram (2000) Ganapathy (2001) Kaushik <i>et al.</i> (2003) Pradeep and Sumalini (2005) Anandan (2009) Srinivasulu (2009)
		Negative	NS	Karunakar Raju (2005) Vijayalaxmi (2008)
2.	Boll weight (g)	Positive	S	Neelima (2002) Altaher and Singh (2003b)
			NS	Neelima <i>et al.</i> (2005) Vijayalaxmi (2008) Srinivasulu (2009)
		Negative	S	Rao <i>et al.</i> (2001) Leela Pratap <i>et al.</i> (2007)
			NS	Pradeep and Sumalini (2005) Anandan (2009)
3.	Ginning outturn (%)	Positive	S	Muthu <i>et al.</i> (2004) Muthuswamy and Vivekanandan (2004) Neelima <i>et al.</i> (2005) Padmavathi (2008)
			NS	Reddy (2001) Vijayalaxmi (2008) Anandan (2009)
		Negative	S	Altaher and Singh (2003b)
			NS	Basha (1997) Murthy (1997) Vijayalaxmi (2008)

Contd...

S. No.	Character	Association	S/NS	Reference
				Srinivasulu(2009)
4.	Seed index (g)	Positive	S	Ladole and Meshram (2000) Neelam and Potdukhe (2002) Altaher and Singh (2003b) Muthu <i>et al.</i> (2004) Neelima <i>et al.</i> (2005)
			NS	Reddy (2001) Neelima (2002) Vijayalaxmi (2008) Anandan (2009)
		Negative	S	Rao <i>et al.</i> (2001) Muthuswamy and Vivekanandan (2004) Muraleedhar (2005)
			NS	Srinivasulu(2009)
5.	Lint index (g)	Positive	S	Ladole and Meshram (2000) Neelam and Potdukhe (2002) Neelima (2002) Muthu <i>et al.</i> (2004) Neelima <i>et al.</i> (2005) Karunakar Raju (2005) Padmavathi (2008)
			NS	Reddy (2001) Vijayalaxmi (2008) Anandan (2009)
		Negative	NS	Rao <i>et al.</i> (2001) Srinivasulu (2009)
			S	Muraleedhar (2005)
6.	2.5% span length (mm)	Positive	NS	Reddy (2001) Neelam and Potdukhe (2002)
			S	Verma <i>et al.</i> (2006)
		Negative	NS	Ladole and Meshram (2000) Rao <i>et al.</i> (2001)

Contd.....

S. No.	Character	Association	S/NS	Reference
				Neelima (2002) Karunakar Raju (2005) Vijayalaxmi (2008) Srinivasulu (2009)
			S	Muraleedhar (2005)
7.	Micronaire value (10 ⁻⁶ g/in)	Positive	S	Altaher and Singh (2003b) Karunakar Raju (2005) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Sangeetha (1998) Rao <i>et al.</i> (2001)
				Reddy (2001) Neelima (2002) Neelam and Potdukhe (2002)
		Negative	NS	Srinivasulu (2009)
8.	Bundle strength (g/tex)	Positive	S	Rao <i>et al.</i> (2001) Altaher and Singh (2003b) Muthu <i>et al.</i> (2004)
			NS	Neelam and Potdukhe (2002) Neelima (2002) Srinivasulu (2009)
		Negative	NS	Reddy (2001) Karunakar Raju (2005) Vijayalaxmi (2008)
9.	Uniformity ratio	Negative	NS	Neelima (2002)
		Positive	S	Karunakar Raju (2005) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)
10.	Fibre elongation (%)	Positive	NS	Vijayalaxmi (2008) Srinivasulu (2009) Anandan (2009)

Contd...

S. No.	Character	Association	S/NS	Reference
		Negative	S	Muthu <i>et al.</i> (2004)
			NS	Muraleedhar (2005)
V. Association of number of bolls per plant with				
1.	Boll weight (g)	Positive	S	Neelima (2002) Altaher and Singh (2003b) Neelima <i>et al.</i> (2005)
		Negative	S	Rao <i>et al.</i> (2001) Karunakar Raju (2005) Padmavathi (2008) Vijayalaxmi (2008) Anandan (2009)
			NS	Ladole and Meshram (2000) Reddy (2001) Kaushik <i>et al.</i> (2003) Pradeep and Sumalini (2005) Srinivasulu (2009)
2.	Ginning outturn (%)	Positive	S	Ganapathy (2001) Muthu <i>et al.</i> (2004) Leela Pratap <i>et al.</i> (2007) Anandan (2009)
			NS	Vijayalaxmi (2008) Srinivasulu (2009)
		Negative	S	Karunakar Raju (2005)
			NS	Sangeetha (1998)
3.	Seed index (g)	Positive	S	Neelam and Potdukhe (2002) Neelima (2002) Muthu <i>et al.</i> (2004) Neelima <i>et al.</i> (2005) Anandan (2009)
			NS	Reddy (2001) Srinivasulu (2009)
		Negative	S	Rao <i>et al.</i> (2001) Muraleedhar (2005) Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000)

Contd...

S. No.	Character	Association	S/NS	Reference
4.	Lint index (g)	Positive	S	Neelima (2002) Neelam and Potdukhe (2002) Muthu <i>et al.</i> (2004) Neelima <i>et al.</i> (2005) Anandan (2009)
			NS	Reddy (2001) Srinivasulu (2009)
		Negative	S	Murthy (1997) Karunakar Raju <i>et al.</i> (2005) Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000) Rao <i>et al.</i> (2001) Neelam and Potdukhe (2002) Neelima (2002)
5.	2.5% span length (mm)	Positive	NS	Ladole and Meshram (2000) Rao <i>et al.</i> (2001) Reddy (2001) Neelam and Potdukhe (2002) Sakthi <i>et al.</i> (2007) Srinivasulu (2009)
		Negative	NS	Neelima (2002) Vijayalaxmi (2008) Anandan (2009)
			S	Tyagi (1994a) Muraleedhar (2005)
6.	Micronaire value (10^{-6} g/in)	Positive	S	Reddy (2001) Neelima (2002) Altaher and Singh (2003b) Muthu <i>et al.</i> (2004) Karunakar Raju (2005) Sakthi <i>et al.</i> (2007) Eswararao (2008) Anandan (2009)

Contd....

S. No.	Character	Association	S/NS	Reference
			NS	Rao <i>et al.</i> (2001) Neelam and Potdukhe (2002)
		Negative	S	Leela Pratap <i>et al.</i> (2007) Vijayalaxmi (2008)
7.	Bundle strength (g/tex)	Positive	S	Rao <i>et al.</i> (2001) Altaher and Singh (2003b) Muthu <i>et al.</i> (2004)
			NS	Reddy (2001) Neelam and Potdukhe (2002) Neelima (2002) Vijayalaxmi (2008) Srinivasulu (2009)
		Negative	S	Sangeetha (1998)
			NS	Karunakar Raju (2005) Anandan (2009)
8.	Uniformity ratio	Positive	S	Muthu <i>et al.</i> (2004)
			NS	Srinivasulu (2009)
		Negative	S	Vijayalaxmi (2008)
			NS	Sangeetha (1998) Neelima (2002) Anandan (2009)
9.	Fibre elongation (%)	Negative	S	Muthu <i>et al.</i> (2004) Vijayalaxmi (2008)
			NS	Muraleedhar (2005) Anandan (2009)
		Positive	NS	Srinivasulu (2009)
VI. Association of boll weight (g) with				
1.	Ginning outturn (%)	Positive	S	Reddy (2001) Muthuswamy and Vivekanandan (2004) Karunakar Raju (2005)
			NS	Neelima (2002) Srinivasulu (2009)
		Negative	NS	Murthy (1997) Ladole and Meshram (2000) Vijayalaxmi (2008) Anandan (2009)

Contd..

S. No.	Character	Association	S/NS	Reference
2.	Seed index (g)	Positive	S	Ladole and Meshram (2000) Altaher and Singh (2003b) Sivaprasad (2003) Muthu <i>et al.</i> (2004) Karunakar Raju (2005) Neelima <i>et al.</i> (2005) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Anandan (2009)
		Negative	NS	Srinivasulu (2009)
3.	Lint index (g)	Positive	S	Neelima (2002) Altaher and Singh (2003b) Sivaprasad (2003) Muthuswamy and Vivekanandan (2004) Neelima <i>et al.</i> (2005) Karunakar Raju (2005) Padmavathi (2008) Vijayalaxmi (2008)
		Negative	NS	Anandan (2009) Srinivasulu (2009)
4.	2.5% span length (mm)	Positive	NS	Rao <i>et al.</i> (2001) Reddy (2001) Anandan (2009) Srinivasulu (2009)
			S	Sivaprasad (2003) Verma <i>et al.</i> (2006) Vijayalaxmi (2008)
		Negative	NS	Neelima (2002)
5.	Micronaire value (10 ⁻⁶ g/in)	Negative	S	Rao <i>et al.</i> (2001) Neelima (2002)
			NS	Sangeetha (1998) Vijayalaxmi (2008) Anandan (2009) Srinivasulu (2009)
		Positive	S	Tyagi (1994a)
			NS	Sangeetha (1998) Reddy (2001)
6.	Bundle strength (g/tex)	Positive	NS	Neelima (2002) Muthuswamy and Vivekanandan (2004) Vijayalaxmi (2008) Anandan, (2009)

Contd...

S. No.	Character	Association	S/NS	Reference
			S	Muraleedhar (2005)
		Negative	S	Rao <i>et al.</i> (2001)
			NS	Sangeetha (1998) Reddy (2001) Srinivasulu (2009)
7.	Uniformity ratio	Negative	S	Neelima (2002) Muraleedhar (2005) Eswararao (2008)
			NS	Vijayalaxmi (2008)
8.	Fibre elongation (%)	Positive	S	Vijayalaxmi (2008)
			NS	Muraleedhar (2005) Srinivasulu (2009)
VII. Association of ginning outturn with				
1	Seed index (g)	Positive	NS	Reddy (2001) Neelima (2002) Mandloi <i>et al.</i> (2003) Altaher and Singh (2003b) Leela Pratap <i>et al.</i> (2007) Padmavathi (2008) Anandan (2009) Srinivasulu (2009)
		Negative	S	Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000) Rao <i>et al.</i> (2001) Neelam and Potdukhe (2002)
2.	Lint index (g)	Positive	S	Reddy (2001) Neelima (2002) Altaher and Singh (2003b) Mandloi <i>et al.</i> (2003) Muthu <i>et al.</i> (2004) Karunakar Raju (2005) Leela Pratap <i>et al.</i> (2007) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Rao <i>et al.</i> (2001) Neelam and Potdukhe (2002) Anandan (2009)
		Negative	NS	Srinivasulu (2009)

Contd..

S. No.	Character	Association	S/NS	Reference
3.	2.5% span length (mm)	Positive	S	Sivaprasad (2003)
			NS	Ladole and Meshram (2000) Rao <i>et al.</i> (2001) Reddy (2001) Neelima (2002)
		Negative	S	Muthu <i>et al.</i> (2004) Padmavathi (2008)
			NS	Mandloi <i>et al.</i> (2003) Neelam and Potdukhe (2002) Vijayalaxmi (2008) Anandan (2009) Srinivasulu (2009)
4.	Micronaire value (10 ⁻⁶ g/in)	Positive	S	Rao <i>et al.</i> (2001) Muthu <i>et al.</i> (2004) Padmavathi (2008)
			NS	Reddy (2001) Neelam and Potdukhe (2002) Neelima (2002)
		Negative	S	Vijayalaxmi (2008)
			NS	Mandloi <i>et al.</i> (2003) Karunakar Raju (2005) Anandan (2009) Srinivasulu (2009)
5.	Bundle strength (g/tex)	Positive	S	Mandloi <i>et al.</i> (2003) Murthy <i>et al.</i> (2006)
			NS	Rao <i>et al.</i> (2001) Reddy (2001) Neelima (2002) Vijayalaxmi (2008) Srinivasulu (2009)
		Negative	S	Neelam and Potdukhe (2002) Padmavathi (2008)
			NS	Neelam and Potdukhe (2002) Anandan (2009)
6.	Uniformity ratio	Positive	S	Muthu <i>et al.</i> (2004) Karunakar Raju (2005) Padmavathi (2008)
			NS	Sangeetha (1998)

Contd..

S. No.	Character	Association	S/NS	Reference
				Srinivasulu (2009)
		Negative	S	Altaher and Singh (2003b)
			NS	Neelima (2002) Vijayalaxmi (2008) Anandan (2009)
7.	Fibre elongation (%)	Positive	NS	Muraleedhar (2005) Anandan (2009) Srinivasulu (2009)
		Negative	NS	Vijayalaxmi (2008)
			S	Padmavathi (2008)
VIII. Association of seed index (g) with				
1.	Lint index (g)	Positive	S	Mandloi <i>et al.</i> (2003) Altaher and Singh (2003b) Muthu <i>et al.</i> (2004) Karunakar Raju (2005) Neelima <i>et al.</i> (2005) Leela Pratap <i>et al.</i> (2007) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002) Anandan (2009)
		Negative	NS	Srinivasulu (2009)
2.	2.5% span length (mm)	Positive	S	Rao <i>et al.</i> (2001) Karunakar Raju (2005) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002) Anandan (2009) Srinivasulu (2009)
		Negative	NS	Ladole and Meshram (2000) Neelima (2002) Mandloi <i>et al.</i> (2003)
3.	Micronaire value (10^{-6} g/in)	Positive	S	Sivaprasad (2003) Eswararao (2008) Vijayalaxmi (2008)
			NS	Reddy (2001) Neelam and Potdukhe (2002) Neelima (2002)

Contd..

S. No.	Character	Association	S/NS	Reference
		Negative	NS	Rao <i>et al.</i> (2001) Mandloi <i>et al.</i> (2003) Anandan (2009) Srinivasulu (2009)
4.	Bundle strength (g/tex)	Positive	S	Muthu <i>et al.</i> (2004) Padmavathi (2008)
			NS	Sangeetha (1998) Neelima (2002) Neelam and Potdukhe (2002) Altaher and Singh (2003b) Anandan (2009)
		Negative	S	Rao <i>et al.</i> (2001)
			NS	Reddy (2001) Vijayalaxmi (2008) Srinivasulu (2009)
5.	Uniformity ratio	Positive	NS	Sangeetha (1998) Vijayalaxmi (2008)
		Negative	S	Neelima (2002) Muraleedhar (2005)
			NS	Anandan (2009) Srinivasulu (2009)
6.	Fibre elongation (%)	Positive	S	Vijayalaxmi (2008)
		Negative	S	Muthu <i>et al.</i> (2004)
			NS	Muraleedhar (2005) Anandan (2009) Srinivasulu (2009)
IX. Association of lint index (g) with				
1.	2.5% span length (mm)	Positive	S	Muthu <i>et al.</i> (2004) Murthy <i>et al.</i> (2006) Vijayalaxmi (2008)
			NS	Reddy (2001)
		Negative	NS	Ladole and Meshram (2000) Neelam and Potdukhe (2002) Neelima (2002) Mandloi <i>et al.</i> (2003) Anandan (2009) Srinivasulu (2009)
2.	Micronaire value (10 ⁻⁶ g/in)	Positive	S	Reddy (2001) Neelima (2002) Neelam and Potdukhe (2002) Eswararao (2008)

Contd..

S. No.	Character	Association	S/NS	Reference
			NS	Karunakar Raju (2005) Vijayalaxmi (2008) Anandan (2009)
		Negative	NS	Rao <i>et al.</i> (2001) Srinivasulu (2009)
			S	Mandloi <i>et al.</i> (2003)
3.	Bundle strength (g/tex)	Positive	S	Muthu <i>et al.</i> (2004) Murthy <i>et al.</i> (2006)
			NS	Neelima (2002) Vijayalaxmi (2008) Anandan (2009)
		Negative	NS	Reddy (2001) Neelam and Potdukhe (2002) Mandloi <i>et al.</i> (2003) Karunakar Raju (2005) Srinivasulu (2009)
4.	Uniformity ratio	Positive	NS	Karunakar Raju (2005) Vijayalaxmi (2008) Anandan (2009) Srinivasulu (2009)
		Negative	S	Muthu <i>et al.</i> (2004)
			NS	Sangeetha (1998) Neelima (2002)
5.	Fibre elongation (%)	Positive	S	Vijayalaxmi (2008)
			NS	Muraleedhar (2005) Srinivasulu (2009)
		Negative	S	Muthu <i>et al.</i> (2004)
			NS	Anandan (2009)
X. Association of 2.5% span length with				
1.	Micronaire value (10 ⁻⁶ g/in)	Negative	S	Neelam and Potdukhe (2002) Altaher and Singh (2003b) Karunakar Raju (2005) Leela Pratap <i>et al.</i> (2007) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Neelima (2002)
		Positive	S	Mandloi <i>et al.</i> (2003) Muthuswamy and Vivekanandan (2004)

Contd.

S. No.	Character	Association	S/NS	Reference
			NS	Reddy (2001) Tuteja (2005b) Anandan (2009) Srinivasulu (2009)
2.	Bundle strength (g/tex)	Positive	S	Neelam and Potdukhe (2002)
			NS	Mandloi <i>et al.</i> (2003) Muthuswamy and Vivekanandan (2004) Muthu <i>et al.</i> (2004) Pankaj Rathore <i>et al.</i> (2004) Karunakar Raju (2005) Tuteja <i>et al.</i> (2005 b) Padmavathi (2008) Vijayalaxmi (2008) Anandan (2009)
		Negative	NS	Rao <i>et al.</i> (2001) Reddy (2001) Neelima (2002) Srinivasulu (2009)
			S	Rao <i>et al.</i> (2001)
3.	Uniformity ratio	Positive	NS	Neelima (2002)
			S	Sivaprasad (2003)
		Negative	S	Altaher and Singh (2003b) Karunakar Raju (2005) Leela Pratap <i>et al.</i> (2007) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Muthu <i>et al.</i> (2004) Tuteja <i>et al.</i> (2005b) Anandan, (2009) Srinivasulu (2009)
XI. Association of micronaire value with				
1.	Bundle strength (g/tex)	Positive	S	Neelima (2002)
			NS	Rao <i>et al.</i> (2001) Reddy (2001) Mandloi <i>et al.</i> (2003) Srinivasulu (2009)

Contd..

S. No.	Character	Association	S/NS	Reference
		Negative	S	Karunakar Raju (2005) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002) Tuteja <i>et al.</i> (2005 b) Anandan (2009)
2.	Uniformity ratio	Positive	S	Altaher and Singh (2003b) Pankaj Rathore <i>et al.</i> (2004) Karunakar Raju (2005) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Muthu <i>et al.</i> (2004) Srinivasulu (2009)
		Negative	S	Tuteja <i>et al.</i> (2005a)
			NS	Sangeetha (1998) Neelima (2002) Anandan (2009)
3.	Fibre elongation (%)	Negative	S	Muraleedhar (2005)
		Positive	S	Muthuswamy and Vivekanandan (2004) Ravikumar (2004)
			NS	Anandan (2009) Srinivasulu (2009)
XII. Association of bundle strength (g/tex) with				
1.	Uniformity ratio	Positive	S	Gnana Arul Samuel Rajan (1997)
			NS	Sangeetha (1998)
		Negative	S	Tuteja <i>et al.</i> (2005a) Leela Pratap <i>et al.</i> (2007) Padmavathi (2008) Vijayalaxmi (2008) Srinivasulu (2009)
			NS	Neelima (2002)
2.	Fibre elongation (%)	Positive	S	Kamal <i>et al.</i> (2002) Muthuswamy and Vivekanandan (2004) Ravi kumar (2004) Muraleedhar (2005) Padmavathi (2008) Vijayalaxmi (2008)

Contd.

S. No.	Character	Association	S/NS	Reference
		Negative	S	Muthu <i>et al.</i> (2004)
			NS	Anandan (2009) Srinivasulu (2009)
XIII. Association of uniformity ratio with				
1.	Fibre elongation (%)	Negative	S	Muraleedhar (2005)
			NS	Vijayalaxmi (2008) Anandan (2009)
		Positive	NS	Srinivasulu (2009)

S: Significant

NS: Non-significant

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

S. No.	Character	Positive Direct effect	Negative Direct effect
1.	Days to 50% flowering	Sangeetha (1998) Tuteja <i>et al.</i> (2006) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)	Gururajan (2000) Muthu <i>et al.</i> (2004) Anandan(2009)
2.	Plant height (cm)	Reddy (2001) Altaher and Singh (2003b) Sivaprasad (2003) Ahuja <i>et al.</i> (2004) Muthu <i>et al.</i> (2004) Eswararao (2008) Anandan (2009) Srinivasulu (2009)	Ladole and Meshram (2000) Karunakar Raju (2005) Verma <i>et al.</i> (2006) Padmavathi (2008) Vijayalaxmi (2008)
3.	No. of monopodia per plant	Gururajan (2000) Reddy (2001) Kaushik <i>et al.</i> (2003) Altaher and Singh (2003a) Muthu <i>et al.</i> (2004) Eswararao (2008) Srinivasulu (2009)	Ladole and Meshram (2000) Sivaprasad (2003) Karunakar Raju (2005) Tuteja <i>et al.</i> (2006) Verma <i>et al.</i> (2006) Padmavathi (2008) Vijayalaxmi (2008)
4.	No. of sympodia per plant	Ladole and Meshram (2000) Rao <i>et al.</i> (2001) Kaushik <i>et al.</i> (2003) Neelima <i>et al.</i> (2005) Verma <i>et al.</i> (2006) Leela Pratap <i>et al.</i> (2007) Padmavathi (2008) Vijayalaxmi (2008) Anandan (2009) Srinivasulu (2009)	Sumathi and Nadarajan (1995) Gururajan (2000) Reddy(2001) Sivaprasad (2003) Muthu <i>et al.</i> (2004) Karunakar Raju (2005) Tuteja <i>et al.</i> (2006) Eswararao (2008)

Contd.....

S. No.	Character	Positive Direct effect	Negative Direct effect
5.	No. of bolls/plant	Altaher and Singh (2003b) Sivaprasad (2003) Ahuja <i>et al.</i> (2004) Muthu <i>et al.</i> (2004) Gururajan and Sundar (2004) Saeed <i>et al.</i> (2004) Karunakar Raju (2005) Neelima <i>et al.</i> (2005) Verma <i>et al.</i> (2006) Leela Pratap <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008) Anandan (2009) Srinivasulu (2009)	Kaushik <i>et al.</i> (2003) Tuteja <i>et al.</i> (2006)
6.	Boll weight (g)	Neelima (2002) Altaher and Singh (2003b) Kaushik <i>et al.</i> (2003) Muthu <i>et al.</i> (2004) Gururajan and Sundar (2004) Karunakar Raju (2005) Sakthi <i>et al.</i> (2007) Padmavathi (2008) Anandan (2009) Srinivasulu (2009)	Ladole and Meshram (2000) Verma <i>et al.</i> (2006) Eswararao (2008) Vijayalaxmi (2008)
7.	Ginning out- turn (%)	Gururajan (2000) Reddy (2001) Muthu <i>et al.</i> (2004) Tuteja <i>et al.</i> (2006) Verma <i>et al.</i> (2006) Leela Pratap <i>et al.</i> (2007) Vijayalaxmi (2008) Anandan (2009)	Ladole and Meshram (2000) Altaher and Singh (2003b) Sivaprasad (2003) Gururajan and Sundar (2004) Karunakar Raju (2005) Eswararao (2008) Padmavathi (2008) Srinivasulu (2009)

Contd.....

S. No.	Character	Positive Direct effect	Negative Direct effect
8.	Seed index (g)	Gururajan (2000) Rao <i>et al.</i> (2001) Reddy (2001) Sivaprasad (2003) Murthy <i>et al.</i> (2006) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008) Anandan (2009) Srinivasulu (2009)	Ladole and Meshram (2000) Neelima (2002) Altaher and Singh (2003a) Gururajan and Sundar (2004) Karunakar Raju (2005)
9.	Lint index (g)	Reddy (2001) Altaher and Singh (2003b) Gururajan and Sundar (2004) Neelima <i>et al.</i> (2005) Karunakar Raju (2005) Sakthi <i>et al.</i> (2007) Eswararao (2008) Vijayalaxmi (2008) Anandan (2009)	Sivaprasad (2003) Muthu <i>et al.</i> (2004) Leela Pratap <i>et al.</i> (2007) Padmavathi (2008)
10.	2.5% span length (mm)	Ladole and Meshram (2000) Muthu <i>et al.</i> (2004) Karunakar Raju (2005) Tuteja <i>et al.</i> (2006) Vijayalaxmi (2008)	Reddy (2001) Neelima (2002) Sivaprasad (2003) Gururajan and Sundar (2004) Verma <i>et al.</i> (2006) Eswararao (2008) Padmavathi (2008)
11.	Micronaire value (10 ⁻⁶ g/in)	Rao <i>et al.</i> (2001) Reddy (2001) Sivaprasad (2003) Muthu <i>et al.</i> (2004) Neelima <i>et al.</i> (2005) Murthy <i>et al.</i> (2006) Leela Pratap <i>et al.</i> (2007) Padmavathi (2008) Vijayalaxmi (2008) Srinivasulu (2009)	Dedaniya and Pethani (1994) Karunakar Raju (2005) Eswararao (2008) Anandan (2009)

Contd.....

S. No.	Character	Positive Direct effect	Negative Direct effect
12.	Bundle strength (g/tex)	Sivaprasad (2003) Murthy <i>et al.</i> (2006) Padmavathi (2008)	Muthu <i>et al.</i> (2004) Gururajan and Sundar (2004) Karunakar Raju (2005) Eswararao (2008) Vijayalaxmi (2008)
13.	Uniformity ratio	Sivaprasad (2003) Karunakar Raju (2005) Murthy <i>et al.</i> (2006) Eswararao (2008) Vijayalaxmi (2008)	Muthu <i>et al.</i> (2004) Leela Pratap <i>et al.</i> (2007) Padmavathi (2008) Anandan (2009)
14.	Fibre elongation (%)	Muthu <i>et al.</i> (2004)	Muraleedhar (2005) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008) Anandan (2009) Srinivasulu (2009)

CHAPTER –III

MATERIALS AND METHODS

The present investigation entitled “Diversity analysis in cotton (*Gossypium hirsutum* L.)” was taken up during *kharif* 2009-10 at Agricultural College Farm, Bapatla, Andhra Pradesh. The site of the experiment is situated at 15⁰54’ North and 80⁰3’ East longitude at an altitude of 5.49 m above mean sea level. The soils are black cotton type with clay texture. The annual rainfall and the weather parameters prevailed during crop season are presented in Annexure-I.

3.1 MATERIALS

The experimental material used in the present study comprised of 60 germplasm lines obtained from all over India. . The source of origin of these genotypes is presented in Table-6. International Bureau of Plant Genetic Resources (IBPGR) descriptor list of morphological traits was used to characterize the given germplasm and presented in Table-7.

3.2 METHODS

3.2.1 Experimental Technique

The detailed experimental technique for the present investigation is furnished in Table-8.

Table-8: Experimental details of the present investigation

Location	:	Agricultural College Farm, Bapatla
Season	:	<i>Kharif</i> , 2009-10
Entries	:	60
Design	:	Randomized block design
Replications	:	3
Plot size	:	2 rows of 6 m length
Spacing	:	120 cm between rows and 60 cm within rows
Fertilizers	:	90 N: 45 P ₂ O ₅ : 45 K ₂ O kg ha ⁻¹
Plant protection	:	Need base

3.2.2 Recording Observations

For the characterization of cotton germplasm, the study was divided into four parts. The first data collection was done on days to 50% flowering and the second data was collected for stem, leaf and flower characteristics during peak flowering stage, the third data was collected during peak boll development and the fourth data for quality parameters of the cotton fiber was collected after ginning.

Data were collected by selecting randomly ten plants per genotype per replication and were used for the differentiation of the germplasm lines based on IBPGR descriptors. The descriptors recorded for the present investigation are stem pigmentation, stem hairiness, leaf shape, leaf lobe number, leaf size, leaf colour, leaf pubescence, leaf appearance, leaf gossypol glands, leaf nectaries, leaf petiole pigmentation, bract shape, bract number of serration, flower sepal pigmentation, petal colour, petal spotting, position of stigma, filament colouration, anther colour, boll bearing habit, boll size, boll colour, boll shape, boll surface, boll prominence at tip, boll opening and plant habit.

The data were also recorded on 10 randomly selected competitive plants per entry per replication and labeled for recording observations on yield and yield component traits.

However, the data on days to 50% flowering, ginning out turn (%), bundle strength (g/tex), uniformity ratio, 2.5% Span length (mm), micronaire (10g/inch), uniformity ratio and fibre elongation (%) were recorded on plot basis. To estimate fibre quality parameters composite sample of kapas was obtained from each genotype per replication and ginned for seed and lint and the lint sample was used for estimating the fibre properties. The data on the following yield and yield component traits and quality parameters were recorded.

3.2.2.1 Days to 50% flowering

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

3.2.2.2 Plant height (cm)

Measured in centimeters from the base to the top of the apical bud at the time of harvest.

3.2.2.3 Number of monopodia plant⁻¹

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

3.2.2.4 Number of sympodia plant⁻¹

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

3.2.2.5 Number of bolls plant⁻¹

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

3.2.2.6 Boll weight (g)

The boll weight in grams was obtained by taking the average weight of 20 randomly collected bolls per plot.

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 Seed index (g)

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

3.2.2.9 Lint index (g)

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

3.2.2.10 2.5% Span length (mm)

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

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

The fibre fineness was measured with Sheffield micronaire using spacer technique. In micronaire instrument, air is passed through a fibre plug of 3.24 m compressed in a cylinder of specific dimension. The dimension of airflow reflected by the fibre plug is measured in a calibrated scale.

3.2.2.12 Bundle strength (g/tex)

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

3.2.2.13 Uniformity ratio

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

3.2.2.14 Fibre elongation (%)

It is fibre extensibility measured with the help of premier HFT 9000V 2.1.3 SP High volume instrument.

3.2.2.15 Seed cotton yield plant⁻¹ (g)

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

3.3 STATISTICAL ANALYSIS

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

3.3.1 Analysis of variance

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

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

Where,

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

μ = General mean

b_i = Effect of i^{th} block

t_j = Effect of j^{th} genotype

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

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

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

Where, r = Number of replications

t = Number of genotypes

df = Degrees of freedom

SS = Sum of squares

MSS = Mean sum of squares

σ^2_e = Error variance

σ^2_g = Variance due to genotypes

σ^2_r = Variance due to replications

M/ r = Mean sum of squares due to replications

M/ t = Mean sum of squares due to treatments

M/ e = Mean sum of squares due to error

The test of significance was carried out against the corresponding error degrees of freedom using 'F' table values given by Fisher and Yates (1963).

3.3.2 Estimation of genetic parameters

3.3.2.1. Coefficient of Variation

Phenotypic and Genotypic Coefficients of Variation (PCV and GCV) were computed according to Burton (1952).

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

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

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

Low = Less than 10 per cent

Moderate = 10-20 per cent

High = More than 20 per cent

3.3.2.2. Heritability in broad sense [h^2 (b)]

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

$$h^2 (b) = \frac{\text{Genotypic variance } (\sigma_g^2)}{\text{Phenotypic variance } (\sigma_p^2)} \times 100$$

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

Low = 0 – 30 per cent

Moderate = 31-60 per cent

High = 61 per cent and above

3.3.2.3. Genetic advance (GA)

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

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

Where,

k= Selection differential at 5% selection intensity which accounts to a

constant value of 2.06

h^2 (b) = Heritability in broad sense

σ_p = Phenotypic standard deviation

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

$$\text{GAM} = \frac{\text{Genetic Advance}}{\text{Grand mean } (\bar{X})} \times 100$$

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

Low = Less than 10 per cent

Moderate = 10-20 per cent

High = More than 20 per cent

in the j^{th} genotype

3.3.3 Correlation Analysis

Analysis of Covariance

Analysis of Covariance was computed by following procedure.

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

Where,

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

M = General mean

t_i = True effect of i^{th} treatment

b_j = True effect of j^{th} block

b_{yx} = Regression coefficient of y on x

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

e_{ij} = Random error

The structure of analysis of covariance is as follows

Source	df	SSY	SSX	SPXY	MSSY	MSSX	MSPXY
Replications	(r-1)	RY	RX	RXY	ry	rx	rxxy
Genotypes	(t-1)	TY	TX	TXY	ty	tx	txy
Error	(r-1)(t-1)	EY	EX	EXY	ey	ex	exy

Where,

df = Degrees of freedom

SS = Sum of squares

SP = Sum of products

MSS = Mean sum of squares

MSP = Mean sum of products

r = Number of replications

t = Number of genotypes

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

$(X_i.X_j) g$ = Genotypic covariance between i^{th} and j^{th} characters

MSPr = Mean sum of products of genotypes

MSPe = Error mean sum of products

Phenotypic covariance $(X_i.X_j) p = (Xi.Xj) g + e_i e_j$

$(X_i.X_j) p$ = Phenotypic covariance between i^{th} and j^{th} characters

$(X_i.X_j) g$ = Genotypic covariance between i^{th} and j^{th} characters

$e_i e_j$ = Environmental covariance between i^{th} and j^{th} characters

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

Phenotypic coefficients of correlation (r_p)

$$r(x_i.x_j)p = \frac{\text{Cov}(x_i.x_j)p}{\sqrt{V(x_i)p.V(x_j)p}}$$

Where,

$r (X_i.X_j)p$ = Phenotypic correlation between i^{th} and j^{th} characters

COV $(X_i.X_j) p$ = Phenotypic covariance between i^{th} and j^{th} characters

$V (X_i) p$ = Phenotypic variance of i^{th} character

$V (X_j) p$ = Phenotypic variance of j^{th} character

Genotypic coefficient of correlation (r_g)

$$r(x_i, x_j)_g = \frac{Cov(x_i, x_j)_g}{\sqrt{V(x_i)_g \cdot V(x_j)_g}}$$

Where,

$r(X_i, X_j)_g$ = Genotypic correlation between i^{th} and j^{th} characters

$COV(X_i, X_j)_g$ = Genotypic covariance between i^{th} and j^{th} characters

$V(X_i)_g$ = Genotypic variance of i^{th} character

$V(X_j)_g$ = Genotypic variance of j^{th} character

3.3.3.1 Test of significance

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

3.3.4 Path coefficient analysis

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

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

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

Where,

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

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

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

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

$$\begin{array}{ccc}
\mathbf{A} & & \mathbf{C} & & \mathbf{B} \\
\left[\begin{array}{c} r_{1y} \\ r_{2y} \\ \cdot \\ \cdot \\ r_{ky} \end{array} \right] & = & \left[\begin{array}{cccccc} 1 & r_{12} & r_{13} & \cdot & \cdot & r_{1k} \\ r_{21} & 1 & r_{23} & \cdot & \cdot & r_{2k} \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ r_{k1} & r_{k2} & r_{k3} & \cdot & \cdot & 1 \end{array} \right] & \cdot & \left[\begin{array}{c} P_{1y} \\ P_{2y} \\ \cdot \\ \cdot \\ P_{ky} \end{array} \right]
\end{array}$$

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

$$\text{Where } (C)^{-1} = \left[\begin{array}{cccccc} C_{11} & C_{12} & \cdot & \cdot & \cdot & C_{1k} \\ C_{21} & C_{22} & \cdot & \cdot & \cdot & C_{2k} \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ C_{k1} & C_{k2} & \cdot & \cdot & \cdot & C_{kk} \end{array} \right]$$

Then direct effects were calculated as follows,

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

$$P_{2y} = \sum_{i=1}^K C_{2i} \cdot r_{iy}$$

$$P_{ky} = \sum_{i=1}^K C_{ki} \cdot r_{iy}$$

3.3.4.1 Residual effect

In plant breeding, it is very difficult to have complete knowledge of all components 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.

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

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

3.3.5 Genetic divergence

3.3.5.1 Mahalanobis' D^2 analysis

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

3.3.5.1.1 Test of significance

Variations were calculated for all the characters investigated and test of significance was done. Analysis of covariance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme, 1978). After testing the difference

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

$$\hat{\Lambda} = \frac{(E)}{(E+V)}$$

Where,

$\hat{\Lambda}$ = Wilk's criterion

(E) = Determinant of error matrix and

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

$$V(\text{Stat}) = -m \log_e \hat{\Lambda} = -\left(n - \frac{P+Q+1}{2}\right) \log_e \hat{\Lambda}$$

Where,

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

n = Degrees of freedom for error + varieties

$$\log_e \hat{\Lambda} = 2.3026 \log_{10} \hat{\Lambda}$$

P = Number of variables or characters (15)

Q = Number of varieties – 1 (or d.f for populations 59)

V (Stat) is distributed as χ^2 with PQ (885= 15x59) degrees of freedom. The value of 'V' statistic was 3748.49 in the present investigation.

Transformation of correlated variables

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

3.3.5.1.2 Computation of D^2 values

For the given combination of i and j genotypes, the mean deviation *i.e.*, $Y_{it}-Y_{jt}$ for $t=1, 2, \dots, p$ variables are computed and the D^2 values were calculated as

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

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.

3.3.5.1.3 Testing the significance of D^2 values

The D^2 value obtained for a pair of population is taken as calculated value of χ^2 and is tested against the tabulated value of χ^2 for P degrees of freedom where P is the number of characters considered *i.e.* 15 in the present study.

3.3.5.1.4 Contribution of individual characters towards divergence

In all combinations, each character was ranked on the basis of their contribution towards divergence between two entries ($d_i = Y_{it} - Y_{jt}$). Rank 1 is given to the highest mean difference and the 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.

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

Where,

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

M = All possible combinations of number of genotypes considered.

i.e. 1770 in the present study.

3.3.5.1.5 Grouping of genotypes into various clusters

The grouping of genotypes into different clusters was done using the Tocher's method as described by Rao (1952). The criterion was that the two varieties belonging to the same cluster at least on an average show a smaller D^2 value than those belonging to different clusters. For this purpose D^2 values of all combinations of each genotype were arranged in ascending order of magnitude in a tabular form as described by Singh and Chaudhary (1977).

To start with, two populations having the closest distance from each other were considered, to which the third population having the smallest D^2 value from the first two populations was added. Similarly, the next nearest fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population there was an abrupt increase in the average D^2 , that population was not considered for including in that cluster.

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

3.3.5.1.6 Average intra- cluster distance

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

3.3.5.1.7 Average inter-cluster distance

Clusters were taken one by one and the distances from other clusters were calculated.

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

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

Where,

D^2 = difference in the mean values between two populations when all the characters are considered simultaneously.

n_1 and n_2 are number of genotypes of two clusters.

3.3.5.2 Principal component analysis and cluster analysis

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

of same scale, a variance – covariance matrix can be used. In the present study, PCA was performed on the correlation matrix of traits, thereby removing the effects of scale (Jackson, 1991).

3.3.5.2.1 Eigen values and eigen vectors

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

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

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:

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

Where,

A_{ij} are found such that Y_j is uncorrelated Y_1, Y_2, \dots, Y_{j-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 $(S) = \lambda_1 + \lambda_2 + \dots + \lambda_p$.

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

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

Where S_i is the standard deviation of X_i .

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

$$\text{Principal component} = ax_1 + bx_2 + \dots + hx_8$$

Where, a, b, \dots are coefficients and x_1, x_2, \dots 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.

3.3.5.2.2 Cluster analysis

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

3.3.5.2.2.1. 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.

3.3.5.2.2.2. Standardizing the data matrix

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

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

$$Z_{ij} = \frac{\bar{X}_{ij} - \bar{X}_j}{S_{ij}}$$

Where

$$\bar{X}_j = \sum_{i=1}^n X_{ij} / n$$

$$S_{ij} = \sqrt{\sum_{i=1}^n \frac{X_{ij} - \bar{X}_j}{n-1}}$$

For

i= genotypes *i.e.*, 60

j = total variables *i.e.*, 15

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

3.3.5.2.2.3. Computing the resemblance matrix

A resemblance coefficient, which measures the overall 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 within cluster sum of squares is minimized over all partitions obtained by combining 2 clusters from previous stage.

3.3.5.2.3 Complete linkage diagram

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

Sorenson (1948) first developed the method, complete linkage dendrogram. This method was based on the distance matrix D .

Table 7: IBPGR Descriptors of Botanical Traits

Stem pigmentation	Stem hairiness	Leaf shape	Leaf lobe number	Leaf size
1 = Absent	1 = Absent	1 = Palmate(Normal)	1 = One	3 = Small
9 = Present	3 = Sparse	2 = Semi-digitate(Semi-okra)	2 = Three	5 = Medium
	5 = Medium	3 = Digitate(Okra)	3 = Five	7 = Large
	7 = Strong	4 = Lanceolate(Super okra)	4 = Seven	

Leaf colour	Leaf pubescence	Leaf appearance	Leaf gossypol glands	Leaf nectaries	Leaf petiole pigmentation
1 = Light green	1 = Absent	1 = Cup	1 = Absent	1 = Absent	1 = Absent
2 = Green	5 = Medium	2 = Flat	9 = Present	9 = Present	9 = Present
3 = Light red	9 = Strong				
4 = Dark red					

Bract	Bract – number of serrations	Sepal pigmentation	Petal colour	Petal spotting
1 = Normal	3 = Few	1 = Absent	1 = white	1 = Absent
3 =Frego	5 = Medium	9 = Present	2 = Cream	9 = Present
	7 = Many		3 = Yellow	
			4 = Pink	
			5 =Red	
			6 =Bicolor	

Position of stigma	Filament colouration	Anther colour	Boll bearing habit	Boll size	Boll colour
1 = Embedded	1 = Absent	1 = white	1 = Solitary	3 = Small	1 =Green
2 = Exerted	9 = Present	2 = Cream	2 = Cluster	5 = Medium	2 = Red
		3 = Yellow		7 = Large	
		4 = Purple			

Boll shape	Boll surface	Boll prominence of tip	Boll opening	Plant habit
1 = Rounded	1 = Smooth	1 = Blunt	3 = Open	3 = Prostrate
2 = Ovate	2 = Pitted	2 = pointed	5 = Semi-open	5 = Compact
3 = Elliptic			7 = Close	7 = Erect

Table -6: Name and source of cotton (*Gossypium hirsutum* L.) germplasm employed in the present study

S. No.	Genotype	Source
1	NDLH-575	RARS, Nandyal(Andhra Pradesh).
2	NH-577	AICCIP.
3	NDLH-779	RARS, Nandyal(Andhra Pradesh).
4	NDLH-849	RARS, Nandyal(Andhra Pradesh).
5	KDCAKD	HAU, Hissar (Haryana).
6	TSH-333	GAU, Surat (Gujarat).
7	WGP-8	CICR, Nagpur (Maharashtra).
8	IC-356932	AICCIP
9	TXLAMA	ARS, Hagari.
10	A-7262	RARS, Lam (Andhra Pradesh).
11	IH-07	UAS, Dharwad (Karnataka).
12	NDLH-7122	RARS, Nandyal(Andhra Pradesh).
13	CPD-1050	UAS, Dharwad(Karnataka).
14	G-204-13	GAU, Surat (Gujarat).
15	GSHY01/1338	CICR, Coiminator (Tamil Nadu).
16	NDLH-1101	RARS, Nandyal(Andhra Pradesh).
17	CPD-478	NAU, Surat (Gujarat).
18	CCH-18	UAS, Raichur (Karnataka).
19	KH-121	RARS, Lam (Andhra Pradesh).
20	GJHV-01/35	NAU, Surat (Gujarat).
21	NDL-770	RARS, Nandyal(Andhra Pradesh).
22	H1-1117/08	NA.
23	NA-777	RAU, Sri Ganga Nagar (Rajasthan).
24	NDLH-152	RARS, Nandyal (Andhra Pradesh).
25	MALE223/08	NA
26	TXORHY1-78	CICR, Sirsa
27	H-1226/08	NA.
28	L-614	RARS, Lam (Andhra Pradesh).
29	Female223/08	NA.
30	H-1236/08	NA.

CHAPTER - IV

RESULTS

The data were collected on 60 cotton germplasm lines, which were collected from different parts of the country. The characters studied to know the diversity among the germplasm lines were days to 50% flowering, plant height (cm), no. of monopodia plant⁻¹, no. of sympodia plant⁻¹, no. of bolls plant⁻¹, boll weight (g), ginning outturn (%), seed index (g), lint index (g), 2.5% span length (mm), micronaire (10⁻⁶g/inch), bundle strength (g/tex), uniformity ratio, fibre elongation (%) and seed cotton yield plant⁻¹. Along with these characters, morphological characters of stem, leaf, flower and boll data were also collected to systematically characterize the germplasm lines using IBPGR descriptors. The results obtained are presented here under the following headings:-

4.1 Morphological characterization using IBPGR descriptors

4.2 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 MORPHOLOGICAL CHARACTERIZATION USING IBPGR DESCRIPTORS

The data were collected on stem, leaf, flower and boll parameters. Variability was observed for seventeen parameters out of twenty seven descriptors studied. No plant of any genotype studied showed a deviation to characteristics from the mentioned descriptors in Tables 9-10. Stem pigmentation was observed in only one line (Tx Lama). Stem hairiness was sparse in 7 lines and medium in 53 lines.

Among the leaf characteristics, variation was observed for leaf shape, leaf lobes, leaf colour and leaf pubescence. No variation was observed for leaf size (Large type), leaf appearance (Flat), leaf gossypol glands and leaf nectarines. Leaf shape was palmate in 53 lines, okra in 4 lines and super okra in 3 lines. Leaf lobes were 3 in 39 lines and 5 in 21 lines.

Leaf colour was green in 59 lines and dark red in only one line (Tx Lama). 58 lines showed medium leaf pubescence and only 2 lines showed strong leaf pubescence. Petiole pigmentation was absent in 56 lines and present in 4 lines. For bract and bract having no. of serrations no variation *i.e.*, normal bract and many serrations on bract were observed.

Sepal pigmentation was absent in 59 lines and present in only one line *i.e.*, Tx Lama (red pigmentation). Petal colour was cream in 55 lines, yellow in 4 lines and bicolour in only one line (Tx Lama). Petal spot was absent in 56 lines and present in 4 lines. Stigma position was exerted in 47 lines and embedded in 13 lines. Filament colouration was absent in 57 lines and present in 3 lines. Anther colour was cream in 43 lines; yellow in 16 lines and purple in only one line (Tx Lama).

Boll bearing habit in all the lines was solitary. Boll size was small in 6 lines and medium in 54 lines. Boll colour was green in 59 lines and red in one line (Tx Lama). Boll shape was round in 10 lines, ovate in 44 lines and elliptic in 6 lines. Boll surface was smooth in all the lines. Boll tip was blunt in 8 lines and 52 lines had pointed one. Boll opening (open) and plant habit (erect type) showed no variation among all the lines.

The quantitative characters data was obtained from the experimental trial conducted at Agricultural college farm, Bapatla, during *kharif* 2009-10. The results of statistical analysis of the 60 cotton genotypes were presented here under.

ANALYSIS OF VARIANCE

The analysis of variance revealed significant differences among the genotypes for all the 15 characters indicating the presence of significant genetic variability in the genotypes studied and are furnished in Table –11.

4.2 VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The estimates of individual genotypes along with character wise 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 Tables 12 and 13 and described character- wise hereunder.

4.2.1 Days to 50% flowering

The number of days to 50% flowering ranged from 49.67 (Tx Lama and TSH-333) to 62.33 (MALE-2097/08, NH-630 and TCH-1705) days with a mean of 55.74 days. The estimates of PCV (6.17) and GCV (5.30) were low. High heritability (73.97) coupled with low genetic advance as per cent of mean (9.40) was observed for days to 50% flowering.

4.2.2 Plant height (cm)

The range of variation for this character varied from 58.18 (NA-777) to 157.90 cm (PH-348) with a mean of 102.12 cm. The estimates of PCV (21.88) and GCV (20.69) were high. High heritability (89.35) coupled with high genetic advance as per cent of mean (40.28) was observed for plant height.

4.2.3 Number of monopodia plant⁻¹

The number of monopodia per plant ranged from 0.12 (TXORHY-1-78) to 2.83 (GJHV-01/35) with a mean of 1.06. The estimates of PCV (50.11) and GCV (49.08) were high. High heritability (95.92) and high genetic advance as per cent of mean (99.02) were observed for this trait.

4.2.4 Number of sympodia plant⁻¹

The number of sympodia per plant ranged from 9.11 (Tx Lama) to 18.80 (PH-348) with a mean of 14.77. The estimates of PCV (16.28) and GCV (12.57) were moderate and moderate heritability (59.68) coupled with moderate genetic advance as per cent of mean (20.01) was recorded for number of sympodia per plant.

4.2.5 Number of bolls plant⁻¹

The number of bolls per plant ranged from 17.28 (Tx Lama) to 51.18 (WGP-8) with a mean of 32.67. It showed high PCV (22.03) and moderate GCV (18.61). High heritability (71.33) coupled with high genetic advance as per cent of mean (32.37) was observed for this character.

4.2.6 Boll weight (g)

The mean boll weight ranged from 2.90g (ADB-28) to 5.57g (Male-2097/08, NARASIMHA and NDLH-1938) with a mean of 4.06g. The estimates of PCV (17.21) and GCV (15.47) were moderate. High heritability (80.75) and high genetic advance as per cent of mean (28.63) were recorded for this trait.

4.2.7 Ginning outturn (%)

The range of variation among the genotypes for this trait was 27.05 (Male-223/08) to 43.48 (NA-777) with a mean of 34.63. It showed moderate PCV (11.84) and low GCV (9.69). High heritability (66.96) coupled with moderate genetic advance as per cent of mean (16.33) was recorded for this trait.

4.2.8 Seed index (g)

Seed index was in the range of 7.10g (NA-777) to 11.33g (CPS-141) with a mean of 9.34g. The estimates of PCV (11.92) and GCV (10.31) were moderate. High heritability (74.84) and moderate genetic advance as per cent of mean (18.37) were observed for this trait.

4.2.9 Lint index (g)

The range of variation observed for this character was from 3.30g (GSHY-01/1338) to 6.87g (NDLH-7122) with a mean of 4.96g. The estimates of PCV (16.40) and GCV (14.33) were moderate. High heritability (76.37) coupled with high genetic advance as per cent of mean (25.80) was observed for lint index.

4.2.10 2.5% Span length (mm)

The mean span length ranged from 23.59mm (TSH-333) to 30.54mm (KDCAKD) with a mean of 27.42mm. The estimates of PCV (7.21) and GCV (4.94) were low. Moderate heritability (47.01) coupled with low genetic advance as per cent of mean (6.98) was observed for this trait.

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

The range of variation for the character was 3.37×10^{-6} g/in (A-7262) to 5.35×10^{-6} g/in (CPS-141) with a mean of 4.36×10^{-6} g/in. The estimate of PCV (12.0) was moderate and GCV (9.79) was low. High heritability (66.58) coupled with moderate genetic advance as per cent of mean (16.46) was recorded for this trait.

4.2.12 Bundle strength (g/tex)

The range of variation for bundle strength was from 18.77 g/tex (NA-777) to 24.07 g/tex (CPD-1050) with a mean of 21.34 g/tex. The estimates of PCV (5.54) and GCV (4.13) were low. Moderate heritability (55.56) coupled with low genetic advance as per cent of mean (6.34) was recorded for this trait.

4.2.13 Uniformity Ratio (%)

The range of variation was 42.77 (L-713) to 53.63 (NDLH-849) with a mean of 48.69 for this character. The estimates of PCV (6.57) and GCV (4.60) were low. Moderate heritability (48.79) coupled with low genetic advance as per cent of mean (6.63) was observed for uniformity ratio.

4.2.14 Fibre elongation (%)

The range of variation was 5.30 (NDLH-849, H1-1117/08, H-1226/08, Female-223/08 and H-1236/08) to 5.60 (GSHV-01/1338, KH-121, H-1098-1/08, L-713 and CNDTS-55) with a mean of 5.47 for this character. The estimates of PCV (1.74) and GCV (1.51) were low. High heritability (75.58) coupled with low genetic advance as per cent of mean (2.70) was observed for uniformity ratio.

4.2.15 Seed cotton yield plant⁻¹ (g)

The range of variation was from 57.86g (TXORHY-1-78) to 179.02g (NDLH-1101) with a mean of 109.49g. The estimate of PCV (22.42) was high and GCV (20.30) was moderate. High heritability (82.01) coupled with high genetic advance as per cent of mean (37.87) was observed for seed cotton yield per plant.

4.3 CHARACTER ASSOCIATION

The phenotypic and genotypic correlation coefficients among characters and with seed cotton yield were estimated and presented in Table 14.

4.3.1 Days to 50% flowering

Genotypic correlations revealed that this trait showed significant positive association with number of monopodia/plant (0.1308* and 0.1480*), number of sympodia per plant (0.1344* and 0.1338*), boll weight (0.2113** and 0.2548**), seed index (0.1515** and 0.2026**) both at phenotypic and genotypic levels.

It also showed significant negative association with ginning outturn (-0.1712** and -0.2514**) and fibre elongation (-0.1619**and -0.1798**) at both levels and at genotypic level only with number of bolls per plant (-0.1623**) and uniformity ratio (-0.1893**).

4.3.2 Plant height (cm)

Plant height showed significant positive association with number of sympodia per plant (0.5121** and 0.7191**), seed index (0.2856** and 0.3326**), micronaire (0.2797** and 0.3338**) bundle strength (0.1812** and 0.2514**) and uniformity ratio (0.2289** and 0.2877**) at both phenotypic and genotypic levels. It also showed significant negative association with ginning outturn (-0.2363** and -0.3135**) at both levels.

4.3.3 Number of monopodia plant⁻¹

This character showed significant positive association with boll weight (0.1987** and 0.2207**), lint index (0.1721** and 0.2162**) and seed cotton yield per plant (0.2428** and 0.2504**) both at phenotypic and genotypic levels.

It showed significant negative association with number of sympodia plant (-0.1606**) and uniformity ratio (-0.1673**) at genotypic level only. It also showed significant positive association with ginning outturn (0.1770**) at genotypic level only.

4.3.4 Number of sympodia plant⁻¹

This trait showed significant positive association with boll weight (0.1569**) at genotypic level only and seed index (0.2125** and 0.2364**), micronaire (0.2528** and 0.5245**), uniformity ratio (0.2464** and 0.4081**) and seed cotton yield per plant (0.1653** and 0.1786**) both at phenotypic and genotypic levels.

It showed significant negative association with fibre elongation (-0.1483* and -0.1587**) both at phenotypic and genotypic levels. It showed significant negative association with ginning outturn (-0.1456*) at genotypic level only.

4.3.5 Number of bolls plant⁻¹

It showed significant positive association with seed cotton yield per plant (0.4136** and 0.5092**) at both phenotypic and genotypic levels.

It showed significant negative association with boll weight (-0.3110** and -0.3894**), seed index (-0.2866** and -0.3893**), lint index (-0.2063** and -0.2466**) and bundle strength (-0.1338* and -0.1839**) both at phenotypic and genotypic levels.

4.3.6 Boll weight (g)

It showed significant positive association with ginning outturn (0.1521** and 0.2061**), seed index (0.1863** and 0.2571**), lint index (0.3153** and 0.4081**), 2.5% span length (0.1462* and 0.2290**), micronaire (0.1318* and 0.1593**), bundle strength (0.1513** and 0.2450**), uniformity ratio (0.1552** and 0.1897**) and seed cotton yield per plant (0.5670** and 0.6599**) both at phenotypic and genotypic levels.

It showed significant negative association with fibre elongation (-0.2918** and -0.3656**) both at phenotypic and genotypic levels.

4.3.7 Ginning out-turn (%)

It showed significant positive association with lint index (0.7534** and 0.7368**) and seed cotton yield per plant (0.1605** and 0.2540**) both at phenotypic and genotypic levels.

It showed significant negative association with seed index (-0.4432** and -0.3851**) and bundle strength (-0.1612** and -0.2717**) both at phenotypic and genotypic levels. 2.5% span length (-0.2197**) and fibre elongation (-0.2178**) recorded negative association at genotypic level only.

4.3.8 Seed index (g)

It showed significant positive association with lint index (0.2435** and 0.3318**) and micronaire (0.1709** and 0.2613**) both at phenotypic and genotypic levels.

It showed significant positive association with 2.5% span length (0.1577**) and bundle strength (0.2411**) only at genotypic level.

4.3.9 Lint index (g)

It showed significant positive association with seed cotton yield per plant (0.1689** and 0.2318**) both at phenotypic and genotypic levels.

It showed significant negative association with fibre elongation (-0.2130** and -0.3114**) both at phenotypic and genotypic levels.

4.3.10 2.5% Span length (mm)

It showed significant positive association with bundle strength (0.1548** and 0.2648**) while uniformity ratio (-0.1500** and -0.3956**) showed negative association both at phenotypic and genotypic levels.

It showed negative association with micronaire (-0.2699**) while, positive association with seed cotton yield per plant (0.1526**) at genotypic level only.

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

It showed significant positive association with uniformity ratio (0.5099** and 0.7912**) whereas fibre elongation (-0.3365** and -0.5363**) showed negative association both at phenotypic and genotypic levels.

3.12 Bundle strength (g/tex)

It showed significant positive association with fibre elongation (0.1521** and 0.3192**) both at phenotypic and genotypic levels.

4.4.13 Uniformity ratio (%)

It showed significant positive association with seed cotton yield per plant (0.2022** and 0.2158**) both at phenotypic and genotypic levels.

It showed significant negative association with fibre elongation (-0.3020** and -0.5355**) both at phenotypic and genotypic levels.

4.4.14 Fibre elongation (%)

It showed significant negative association with seed cotton yield per plant (-0.2834** and -0.3372**) both at phenotypic and genotypic levels.

4.3.15 Seed cotton yield plant⁻¹ (g)

It showed significant positive association with number of monopodia per plant (0.2428** and 0.2504**), number of sympodia per plant (0.1653** and 0.1786**), number of bolls per plant (0.4136** and 0.5092**), boll weight (0.5670** and 0.6599**), ginning outturn (0.1605** and 0.2540**), lint index (0.1689** and 0.2318**), uniformity ratio (0.2022** and 0.2158**) whereas fibre elongation (-0.2834** and -0.3372**) showed negative association both at phenotypic and genotypic levels.

It showed significant positive association with 2.5% span length (0.1526**) at genotypic level only.

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-15 and 16, respectively. The phenotypic and genotypic path diagrams are given in Fig.-1 and 2, respectively.

Path coefficient analysis revealed that seed cotton yield per plant was directly and positively influenced by number of bolls per plant (0.6401 and 0.9605), boll weight (0.7100 and 1.0776), micronaire (0.0218 and 0.1930) and bundle strength (0.0546 and 0.1049) both at phenotypic and genotypic levels, respectively.

Days to 50% flowering (-0.0215 and -0.1061), uniformity ratio (-0.0021 and -0.3544) and fibre elongation (-0.0640 and -0.1279) exerted direct negative effects on seed cotton yield per plant.

Number of bolls per plant exerted indirect positive effects on seed cotton yield *via* plant height (0.0150 and 0.0047), number of monopodia per plant (0.0126 and 0.0026), number of sympodia per plant (0.0470 and 0.0937) and uniformity ratio (0.0779 and 0.0977) at phenotypic and genotypic levels, respectively.

Boll weight showed its indirect effects through days to 50% flowering (0.1500 and 0.2746), plant height (0.0632 and 0.1131), number of monopodia per plant (0.1410 and 0.2379), number of sympodia per plant (0.0583 and 0.1691), ginning outturn (0.1080 and 0.2221), seed index (0.1323 and 0.2771), lint index (0.2239 and 0.4397), 2.5% span length (0.1038 and 0.2468), micronaire (0.0936 and 0.1716), bundle strength (0.1075 and 0.2640) and uniformity ratio (0.1102 and 0.2044) at phenotypic and genotypic levels, respectively.

Micronaire through days to 50% flowering (0.0006 and 0.0114), plant height (0.0036 and 0.0644), number of sympodia per plant (0.0032 and 0.1012), boll weight (0.0017 and 0.0307), seed index (0.0022 and 0.0504), lint index (0.0011 and 0.0125) and uniformity ratio (0.0065 and 0.1527) exerted its indirect effects on seed cotton yield per plant at phenotypic and genotypic levels, respectively.

Bundle strength through plant height (0.0099 and 0.0264), number of sympodia per plant (0.0070 and 0.0210) and boll weight (0.0083 and 0.0257), seed index (0.0063 and 0.0253) and fibre elongation (0.0083 and 0.0335) at phenotypic and genotypic levels, respectively exerted positive indirect effects on seed cotton yield per plant *via* bundle strength.

The direct and indirect effects along with phenotypic correlation coefficients for each yield component character are presented hereunder character wise.

4.4.1 Days to 50% flowering

The direct contribution of this character on seed cotton yield per plant was negative (-0.0215). The indirect effects *via* plant height (0.0020), number of monopodia per plant (0.0138), number of sympodia per plant (0.0118), boll weight (0.1500), seed index (0.0244), lint index (0.0167), micronaire (0.0006), uniformity ratio (0.0003) and fibre elongation (0.0104) were positive. While, number of bolls per plant (-0.0595), ginning outturn (-0.0430), 2.5% span length (-0.0001) and bundle strength (-0.0020) showed negative indirect effects. This trait had positive phenotypic correlation with seed cotton yield per plant (0.1038).

4.4.2 Plant height (cm)

The direct contribution of this character on seed cotton yield per plant was negative (-0.0542). The indirect effects *via* number of monopodia per plant (-0.0033), ginning outturn (-0.0594) and uniformity ratio (-0.0005) were negative. While, days to 50% flowering (0.0008), number of sympodia per plant (0.0450), number of bolls per

plant (0.0150), boll weight (0.0632), seed index (0.0460), lint index (0.0085), micronaire (0.0036), bundle strength (0.0099) and fibre elongation (0.0056) showed positive indirect effects. This trait had positive phenotypic correlation with seed cotton yield per plant (0.0803).

4.4.3 Number of monopodia plant⁻¹

The direct contribution of this character on seed cotton yield per plant was positive (0.1057). The indirect effects through plant height (0.0017), number of bolls per plant (0.0126), boll weight (0.1410), ginning outturn (0.0307), seed index (0.0082) and uniformity ratio (0.0002) were positive. While, days to 50% flowering (-0.0028), number of sympodia per plant (-0.0096), lint index (-0.0326), 2.5% span length (-0.0001), micronaire (-0.0012), bundle strength (-0.0051) and fibre elongation (-0.0060) showed negative indirect effects. This trait had positive significant phenotypic correlation with seed cotton yield per plant (0.2428**).

4.4.4 Number of sympodia plant⁻¹

The direct contribution of this character on seed cotton yield per plant was positive (0.0879). The indirect effects *via* number of bolls per plant (0.0470), boll weight (0.0583), seed index (0.0342), micronaire (0.0032), bundle strength (0.0070) and fibre elongation (0.0095) were positive. While, days to 50% flowering (-0.0029), plant height (-0.0278), number of monopodia per plant (-0.0116), ginning outturn (-0.0286), lint index (-0.0106) and uniformity ratio (-0.0005) showed negative indirect effects. This trait had significant positive phenotypic correlation with seed cotton yield per plant (0.1653**).

4.4.5 Number of bolls plant⁻¹

The direct contribution of this character on seed cotton yield per plant was positive (0.6401). The indirect effects through days to 50% flowering (0.0020), number of monopodia per plant (0.0021), number of sympodia per plant (0.0065), lint index (0.0391) and fibre elongation (0.0012) were positive while, plant height (-0.0013), boll weight (-0.2208), ginning out turn (-0.0015), seed index (-0.0461), 2.5% span length (-0.0001), bundle strength (-0.0073) and uniformity ratio (-0.0003) showed negative indirect effects. This trait had significant positive phenotypic correlation with seed cotton yield per plant (0.4136**).

4.4.6 Boll weight (g)

The direct contribution of this character on seed cotton yield per plant was positive (0.7100). The indirect effects *via* number of monopodia per plant (0.0210), number of sympodia per plant (0.0072), ginning out turn (0.0382), seed index (0.0300), 2.5% span length (0.0003), micronaire (0.0017), bundle strength (0.0083) and fibre elongation (0.0187) were positive. While, days to 50% flowering (-0.0045), plant height (-0.0048), number of bolls per plant (-0.1990), lint index (-0.0597) and uniformity ratio (-0.0003) showed negative indirect effects. This trait had significant positive phenotypic correlation with seed cotton yield per plant (0.5670**).

4.4.7 Ginning out-turn (%)

The direct contribution of this character on seed cotton yield per plant was positive (0.2513). The indirect effects *via* days to 50% flowering (0.0037), plant height (0.0128), number of monopodia per plant (0.0129), boll weight (0.1080), uniformity ratio

(0.0001) and fibre elongation (0.0089) were positive. While, number of sympodia per plant (-0.1000), number of bolls per plant (-0.0037), seed index (-0.0714), lint index (-0.1427), 2.5% span length (-0.0002), micronaire (-0.0004) and bundle strength (-0.0088) showed negative indirect effects. This trait had positive significant phenotypic correlation with seed cotton yield per plant (0.1605**).

4.4.8 Seed index (g)

The direct contribution of this character on seed cotton yield per plant was positive (0.1610). The indirect effects *via* number of monopodia per plant (0.0054), number of sympodia per plant (0.0187), boll weight (0.1323), 2.5% span length (0.0002), micronaire (0.0022), bundle strength (0.0063) and fibre elongation (0.0060) was positive. While, days to 50% flowering (-0.0033), plant height (-0.0155), number of bolls per plant (-0.1834), ginning outturn (-0.1114), lint index (-0.0461) and uniformity ratio (-0.0001) showed negative indirect effects. This trait had negative nonsignificant phenotypic correlation with seed cotton yield per plant (-0.0277).

4.4.9 Lint index (g)

The direct contribution of this character on seed cotton yield per plant was negative (-0.1894). The indirect effects through days to 50% flowering (0.0019), plant height (0.0024), number of monopodia per plant (0.0182), number of sympodia per plant (0.0049), boll weight (0.2239), ginning outturn (0.1893), seed index (0.0392), micronaire (0.0001) and fibre elongation (0.0136) were positive. While, number of bolls per plant (-0.1320), 2.5% span length (-0.0001) and bundle strength (-0.0043) showed negative indirect effects. This trait had positive significant phenotypic correlation with seed cotton yield per plant (0.1689**).

4.4.10 2.5% Span length (mm)

Direct contribution of this character on seed cotton yield per plant was positive (0.0023). The indirect effects through days to 50% flowering (0.0007), plant height (0.0003), number of sympodia per plant (0.0013), boll weight (0.1038), seed index (0.0134), lint index (0.0047) and uniformity ratio (0.0003) were positive while, the characters *viz.*, number of monopodia per plant (-0.0034), number of bolls per plant (-0.0239), ginning outturn (-0.0203), micronaire (-0.0013), bundle strength (-0.0085) and fibre elongation (-0.0001) showed negative indirect effects. This trait had positive non significant phenotypic correlation with seed cotton yield per plant (0.0861).

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

The direct contribution of this character on seed cotton yield per plant was positive (0.0128). The indirect effects through number of sympodia per plant (0.0222), boll weight (0.0936), seed index (0.0275) and fibre elongation (0.0215) were positive. While, days to 50% flowering (-0.0010), plant height (-0.0152), number of monopodia per plant (-0.0098), number of bolls per plant (-0.0007), ginning outturn (-0.0077), lint index (-0.0163), 2.5% span length (-0.0002), bundle strength (-0.0064) and uniformity ratio (-0.0010) showed negative indirect effects. This trait had positive nonsignificant phenotypic correlation with seed cotton yield per plant (0.1194).

4.4.12 Bundle strength (g/tex)

The direct contribution of this character on seed cotton yield per plant was positive (0.0546). The indirect effects *via* days to 50% flowering (0.0008), number of sympodia per plant (0.0112), boll weight (0.1075), seed index (0.0187), lint index (0.0150) and 2.5% span length (0.0003) were positive, while the characters, plant height (-0.0098), number of monopodia per plant (-0.0099), number of bolls per plant (-0.0856), ginning outturn (-0.0405), micronaire (-0.0015), uniformity ratio (-0.0003) and fibre elongation (-0.0097) showed negative indirect effects. This trait had positive non significant phenotypic correlation with seed cotton yield per plant (0.0513).

4.4.13 Uniformity ratio (%)

The direct contribution of this character on seed cotton yield per plant was negative (-0.0021). The indirect effects *via* days to 50% flowering (0.0027), number of sympodia per plant (0.0217), number of bolls per plant (0.0779), boll weight (0.1102), seed index (0.0111), lint index (0.0045), micronaire (0.0065) and fibre elongation (0.0193) were positive. While, the characters, plant height (-0.0124), number of monopodia per plant (-0.0115), ginning outturn (-0.0181), 2.5% Span length (-0.0003) and bundle strength (-0.0073) showed negative indirect effects. This trait had significant positive phenotypic correlation with seed cotton yield per plant (0.2022**).

4.4.14 Fibre elongation (%)

The direct contribution of this character on seed cotton yield per plant was negative (-0.0640). The indirect effects through days to 50% flowering (0.0035), plant

height (0.0048), number of monopodia per plant (0.0099), lint index (0.0403), bundle strength (0.0083) and uniformity ratio (0.0006) were positive while, the characters, number of sympodia per plant (-0.0130), number of bolls per plant (-0.0124), boll weight (-0.2072), ginning outturn (-0.0348), seed index (-0.0151) and micronaire (-0.0043) showed negative indirect effects. This trait had significant negative phenotypic correlation with seed cotton yield per plant (-0.2834**).

The residual effects at both phenotypic and genotypic levels were 0.5225 and 0.6957, respectively.

4.5. GENETIC DIVERGENCE

The quantitative assessment of genetic divergence was carried out for 60 genotypes for all the 15 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 λ'

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* λ' . 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. The value of 'V' statistic was 3748.49 in the present investigation.

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 15 contributing characters is presented in Table -17. The maximum contribution towards genetic divergence was by number of monopodia plant⁻¹ (39.72), followed by plant height (16.55), fibre elongation (8.93), boll weight (7.23), seed index (5.65), seed cotton yield plant⁻¹ (5.31), days to 50% flowering (4.24), number of bolls plant⁻¹ (3.16), lint index (2.26), ginning outturn (2.20), bundle strength (1.64), micronaire (1.47), 2.5% Span length (1.24), number of sympodia plant⁻¹ (0.28) and uniformity ratio (0.11).

4.5.1.3 Grouping of genotypes into various clusters

The 60 genotypes were grouped into 9 clusters using 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 60 genotypes into 9 clusters was presented in Table-18. 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 Chaudhary (1977) are presented in the Table-19. The proximity and divergence among 9 clusters are indicated in Table-20.

The maximum intra-cluster distance was 48.25 for cluster IX, followed by 47.97 for cluster V, followed by 37.36 for cluster III, 23.44 for cluster II, followed by 14.935 for cluster I, while, it was zero for clusters IV, VI, VII and VIII.

Cluster I was close to cluster IV (24.93) followed by Cluster III (28.07) and it was farthest from cluster IX (94.17) followed by cluster VII (91.36).

Cluster II was nearer to cluster I (28.94) followed by cluster IV (36.82) and it was farthest from cluster IX (68.18) followed by cluster VII (57.23).

Cluster III was nearer to cluster I (28.07) followed by cluster IV (50.35) and it was farthest from cluster IX (105.32) followed by cluster VII (98.78).

Cluster IV was nearer to cluster I (24.93) followed by cluster II (36.82) while it was farthest from cluster IX (112.56) followed by cluster VII (111.91).

Cluster V was nearer to cluster IV (37.08) followed by cluster I (42.18) and it was farthest from cluster VII (128.82) followed by cluster IX (125.35).

Cluster VI was nearer to cluster VII (19.27) followed by cluster IX (37.74) and was farthest from cluster V (87.97) followed by cluster III (79.84).

Cluster VII was nearer to cluster VI (19.27) followed by cluster IX (31.82) and was farthest from cluster V (128.82) followed by IV (111.91).

Cluster VIII was nearer to cluster II (40.01) followed by cluster I (41.05) and was farthest from cluster IX (112.41) followed by cluster VII (84.38).

Cluster IX was nearer to cluster VII (31.82) followed by cluster VI (37.74) and was farthest from cluster V (125.35) followed by cluster IV (112.56).

4.5.1.5 Cluster Mean Values

The cluster mean values for 15 characters are presented in Table-21. The data indicated a wide range of mean values between the characters.

Days to 50% flowering had a range of 53.00 for cluster VIII to 57.17 for cluster II; plant height had a range of 73.05 for cluster VI to 125.68 for cluster III; number of monopodia per plant range varied from 0.58 for cluster V to 2.21 for cluster VII ; number of sympodia per plant range varied from 12.29 for cluster IX to 16.08 for cluster III; number of bolls per plant range varied from 28.72 for cluster VII to 42.84 for cluster VIII; boll weight ranged from 3.40 for cluster IV to 4.96 for cluster VIII; ginning outturn ranged from 33.23 for cluster III to 40.12 for cluster VIII; seed index range varied from 8.18 for cluster V to 9.91 for cluster IV; lint index ranged from 4.66 for cluster V to 6.46 for cluster VIII; 2.5% Span length range varied from 25.36 for cluster VII to 28.37 for cluster IV; micronaire ranged from 3.87 for cluster VI to 4.98 for cluster VIII; bundle strength range varied from 19.40 for cluster VI to 21.89 for cluster III; uniformity ratio ranged from 46.73 for cluster IX to 53.43 for cluster VIII; fibre elongation range varied from 5.30 for clusters IV to 5.53 for clusters VII; seed cotton yield ranged from 92.71 for cluster IV to 179.02 for cluster VIII.

4.5.2 Application of principal component analysis in genetic divergence

In principal component analysis on correlation matrix the standardization of columns (here characters) created 15 new variables for 60 genotypes without changing their relative positions. These 15 new variables are the principal components ($PC_1, PC_2, \dots, PC_{15}$). Each principal component is a linear combination of the 15 attributes of data matrix. The loading values are scaled or standardized in such a manner that the sum of square of loadings within a principal component is equal to one. The loadings are viewed as weights defining the contribution of characters in respective principal components. Like regression coefficients, loadings sign (+ / -) is indicative of the direction of contribution. But unlike regression only the relative contribution is important, so all signs can be changed without affecting the analysis (Jackson, 1991).

The loadings for first principal component were chosen so as to make its variance as large as possible. Loadings of second principal component were chosen such that the variance of PC_2 is as large as possible, subject to the constraint that PC_1 and PC_2 are uncorrelated. The process was continued to create 15 principal components, but PC's having eigen value less than one is not having any practical significance (Legendre and Legendre, 1984).

Principal components (eigen value greater than one), eigen values (Latent Root), per cent variability, cumulative per cent variability and component loading of different characters are presented in Table-22.

In the present study, the first eight principal components with eigen values more than one contributed 87.928 per cent towards the total variability. The principal component with eigen values less than one were considered as nonsignificant. It was therefore inferred that the essential features of data set had been represented in the first eight principal components. The first principal component contributed maximum towards variability (21.415%). Characters *viz.*, number of monopodia per plant (0.419), ginning outturn (0.352), seed index (0.298), uniformity ratio (0.262), bundle strength (0.229) and lint index (0.223) had positive loading while negative loading of number of bolls per plant (-0.318), 2.5% Span length (-0.317), number of sympodia per plant (-0.296) and seed cotton yield per plant (-0.247) explained the maximum variance in first principal component (PC₁).

The second principal component (PC₂) described 14.688 per cent of total variance and it was reflected by significant positive loading of boll weight (0.486), number of sympodia per plant (0.396), plant height (0.395), bundle strength (0.337), seed index (0.256), micronaire (0.251) and days to 50% flowering (0.213) and negative loading was observed with number of bolls per plant (-0.248).

The third principal component (PC₃) was characterized by 12.154 per cent contribution towards the total variability. Characters *viz.*, 2.5% Span length (0.406), seed cotton yield per plant (0.359), lint index (0.336), boll weight (0.263) and seed index (0.242) were positively loaded while, plant height (-0.436), micronaire (-0.303), number of monopodia per plant (-0.250) and fibre elongation (-0.201) were negatively loaded on total variance.

The fourth principal component (PC₄) was characterized by conspicuously high loading of fibre elongation (0.409), days to 50% flowering (0.319), bundle strength (0.296) and 2.5% Span length (0.263) which were positively loaded while micronaire

(-0.396), number of bolls per plant (-0.345), ginning outturn (-0.325), seed cotton yield per plant (-0.288) and uniformity ratio (-0.240) were negatively loaded. Contribution of this principal component towards the total variability was 11.501 per cent.

Similarly, fifth principal component (PC₅) contributed 9.401 percent towards total variability of the study material. High loading value of uniformity ratio (0.414), micronaire (0.390) and 2.5% Span length (0.233) was observed, while seed cotton yield per plant (-0.433), ginning outturn (-0.342), number of monopodia per plant (-0.303), boll weight (-0.237), and plant height (-0.211) were negatively loaded.

PC₆ was characterized by high positive loading value of days to 50% flowering (0.619). While lint index (-0.514), seed index (-0.307) and number of sympodia per plant (-0.302) were negatively loaded. Contribution of this principal component towards the total variability was 7.191 per cent.

Similarly, principal components seventh (PC₇) and eighth (PC₈) contributed 6.730 per cent and 4.849 per cent, respectively towards total variability of the study material. Seed index (0.275) was positively loaded while, bundle strength (-0.526), uniformity ratio (-0.514), fibre elongation (-0.479) and number of bolls per plant (-0.256), were negatively loaded in seventh principal component. While, PC₈ was characterized by high loading value of days to 50% flowering (0.499), number of bolls per plant (0.422), lint index (0.422) and micronaire (0.243) on positive side while, boll weight (-0.352) and uniformity ratio (-0.334) were negatively loaded. The PCA scores for 60 cotton genotypes in the first three principal components were computed and were considered as three axes as X, Y and Z and squared distance of each genotype from these

three axes were calculated and are presented in Table-23. These three PCA scores for 60 genotypes were plotted on graph to get two dimensional and three dimensional scatter diagram (Fig. - 4 and Fig.-5).

4.5.3 Cluster analysis

The 60 genotypes of cotton were grouped into various clusters based on agglomerative hierarchical cluster analysis. 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 Euclidean² distance computed from PCA scores of genotypes.

The 60 genotypes were grouped into 8 clusters. The distribution of genotypes into 8 clusters is presented in Table-24. The mutual relationship between clusters is represented diagrammatically (Fig.-7) by taking average intra and inter-cluster Euclidean² distances.

4.5.3.1 Average intra- and inter- cluster Euclidean² distance values

The average intra-and inter-cluster Euclidean² distances were estimated based on Ward's minimum variance method and are presented in the Table-25.

By Ward's method, the 60 genotypes were grouped into 8 clusters. Of the 8 clusters formed, cluster VIII had minimum intra cluster Euclidean² distance value of 0.000 followed by cluster IV (41.688) and cluster III (59.247). The inter cluster Euclidean² distances varied from 86.296 (between cluster II and cluster III) to 755.558 (cluster I and VIII).

Cluster I was comprised of 6 genotypes. It was nearest to cluster II (147.958) followed by cluster IV (119.526) and farthest from cluster VIII (755.55) followed by cluster VII (344.60).

Cluster II was (the largest one) comprised of 12 genotypes. It was closest to cluster III (86.29) followed by cluster IV (94.25) and farthest from cluster VIII (477.95) followed by cluster VII (227.17).

Cluster III was comprised of 8 genotypes. It was closest to cluster II (86.29) followed by cluster IV (99.54) and farthest from cluster VIII (410.81) followed by cluster VII (225.77).

Cluster IV was comprised of 8 genotypes. It was nearest to cluster II (94.25) followed by cluster V (96.26) and farthest from cluster VIII (515.66) followed by cluster VII (260.52).

Cluster V was comprised of 8 genotypes and was closest to cluster IV (96.26) followed by cluster VI (105.59) and farthest from cluster VIII (427.13) followed by cluster VII (252.66).

Cluster VI consisted of 10 genotypes. It was nearest to cluster IV (96.07) followed by cluster V (105.59) and farthest from cluster VIII (341.405) followed by cluster I (181.82).

Cluster VII was comprised of 7 genotypes. It was closest to cluster VI (160.02) followed by cluster VIII (196.52) and farthest from cluster I (344.60) followed by cluster IV (260.52).

Cluster VIII was consisted of only one genotype. It was closest to cluster VII (196.52) followed by cluster VI (341.40) and farthest from cluster I (755.55) followed by cluster IV (515.66).

4.5.3.2 Cluster means

Cluster means were computed for all the 15 characters studied on pooled basis and are presented in Table -26.

Cluster I recorded low mean value for characters, plant height (74.51), number of monopodia per plant (0.32), boll weight (3.51), seed index (8.17), lint index (4.45) and micronaire (3.87).

Cluster II recorded low mean values for days to 50% flowering (54.41) and ginning outturn (33.318) and high mean value for number of bolls per plant (37.24) and fibre elongation (5.53).

Cluster III recorded high mean values for plant height (130.91), number of sympodia per plant (16.92) and low mean values for number of bolls per plant (28.95) and seed cotton yield per plant (88.55).

Cluster IV registered high mean value for 2.5% Span length (28.20) and uniformity ratio (50.73) and low mean value for fibre elongation (5.33).

Cluster V recorded high mean value for boll weight (5.22) and bundle strength (22.15). Cluster VI registered high mean value for seed index (10.23) only.

Cluster VII recorded low mean value for number of sympodia per plant (12.47), uniformity ratio (46.88) and high mean value for fibre elongation (5.510).

Cluster VIII recorded high mean value for days to 50% flowering (61.66), number of monopodia per plant (2.83), ginning outturn (38.14), lint index (5.66), micronaire (4.75) and seed cotton yield per plant (140.07). Low mean value was registered for 2.5% Span length (25.74) and bundle strength (20.23).

Table 9. : Stem and leaf morphological descriptors in 60 cotton (*Gossypium hirsutum* L.) germplasm lines.

S.No	Genotype	Stem pigmentation	Stem hairiness	Leaf shape	Leaf lobes	Leaf colour	Leaf pubescence	Petiole pigmentation
		1= absent	3= Sparse	1=Palmate	2= three	2= green	5= medium	1= absent
		9= present	5= medium	3=okra	3= five	4= dark red	9= strong	9=present
			4=super okra					
1	NDLH-575	1	5	1	3	2	5	1
2	NH-777	1	5	1	2	2	5	1
3	NDLH-779	1	5	1	2	2	5	1
4	NDLH-849	1	5	1	2	2	5	1
5	KDCAKD	1	5	1	2	2	5	1
6	TSH-333	1	3	1	3	2	5	1
7	WGP-8	1	5	1	2	2	5	1
8	IC-356932	1	5	1	2	2	5	1
9	TXLAMA	9	5	3	3	4	5	9
10	A-7262	1	3	1	2	2	5	1
11	IH-07	1	5	4	3	2	5	1
12	NDLH-7122	1	5	1	3	2	5	1
13	CPD-1050	1	3	1	2	2	5	1
14	G-204-13	1	5	1	3	2	5	1
15	GSHY-01/1338	1	5	1	3	2	9	1
16	NDLH-1101	1	5	1	2	2	5	1
17	CPD-478	1	3	1	2	2	5	1
18	CCH-18	1	5	1	2	2	5	1
19	KH-121	1	5	1	3	2	5	1
20	GJHV-01/35	1	3	1	2	2	5	1
21	NDL-770	1	5	1	2	2	5	9
22	H1-1117/08	1	5	1	2	2	5	1
23	NA-777	1	5	1	3	2	5	1
24	NDLH-152	1	5	1	3	2	5	1
25	MALE-223/08	1	5	1	3	2	5	1
26	TXORHY-1-78	1	5	4	3	2	5	1
27	H-1226/08	1	5	1	2	2	5	1
28	L-614	1	5	1	2	2	5	1
29	Female-223/08	1	3	4	3	2	5	9
30	H-1236/08	1	5	3	2	2	5	1

Contd.....

S.No	Genotype	Stem pigmentation	Stem hairiness	Leaf shape	Leaf lobes	Leaf colour	Leaf pubescence	Petiole pigmentation
		1= absent	3= Sparse	1=Palmate	2= three	2= green	5= medium	1= absent
		9= present	5= medium	3=okra	3= five	4= dark red	9= strong	9=present
				4=super okra				
31	NH-452	1	5	1	2	2	5	1
32	NDLH-1906	1	5	1	2	2	5	1
33	H-1098/08	1	5	1	2	2	5	1
34	Female-287/08	1	5	1	2	2	5	1
35	H-1098-1/08	1	5	3	2	2	5	1
36	MALE-2097/08	1	5	3	2	2	5	1
37	HS-6/08	1	5	1	3	2	5	1
38	TIDEWATER5-3	1	3	1	3	2	5	1
39	AKH-9331	1	5	1	2	2	9	1
40	L-713	1	5	1	2	2	5	1
41	NH-630	1	5	1	2	2	5	1
42	P-21-15	1	5	1	2	2	5	1
43	NH-545	1	5	1	2	2	5	9
44	F-2170	1	5	1	2	2	5	1
45	CPD-821	1	5	1	2	2	5	1
46	NA-1325	1	5	1	3	2	5	1
47	L-801	1	5	1	2	2	5	1
48	TCH-1705	1	5	1	2	2	5	1
49	GBHV-156	1	5	1	3	2	5	1
50	CPS-141	1	5	1	2	2	5	1
51	CSH-3129	1	5	1	2	2	5	1
52	PH-348	1	5	1	3	2	5	1
53	ADB-28	1	5	1	2	2	5	1
54	ARBH-225	1	5	1	2	2	5	1
55	CNDTS-55	1	5	1	3	2	5	1
56	NH-615	1	5	1	3	2	5	1
57	NARASIMHA	1	5	1	3	2	5	1
58	SIVANAMELI	1	5	1	2	2	5	1
59	NDLH-1905	1	5	1	2	2	5	1
60	NDLH-1938	1	5	1	2	2	5	1

Table 10. : Flower and boll morphological characters descriptors for 60 cotton (*Gossypium hirsutum* L.) germplasm lines

S.No	Genotype	Sepal pig	Petal colour	Petal spot	Stigma position	Filament colour	Anther colour	Boll size	Boll colour	Boll shape	Boll tip
		1=absent	2=cream	1=absent	1=embedded	1=absent	2=cream	5= medium	1= Green	1=Round	1=blunt
		9=present	3=yellow	9=present	2=exserted	9=present	3=yellow	3=Small	2=Red	2=ovate	2= pointed
			6=bicolour			4=purple	4= purple			3=elliptic	
1	NDLH-575	1	2	1	2	1	2	5	1	1	1
2	NH-577	1	3	1	2	1	3	5	1	3	2
3	NDLH-779	1	2	1	1	1	3	5	1	2	2
4	NDLH-849	9	2	1	2	1	3	5	1	3	2
5	KDCAKD	1	3	1	2	1	3	5	1	2	2
6	TSH-333	1	2	1	2	1	3	5	1	2	2
7	WGP-8	1	2	9	2	9	2	5	1	2	2
8	IC-356932	1	2	1	2	1	2	5	1	2	2
9	TXLAMA	9	6	1	2	1	4	5	2	1	2
10	A-7262	1	2	1	2	1	3	5	1	2	2
11	IH-07	1	2	1	2	1	2	5	1	2	2
12	NDLH-7122	9	2	1	1	1	2	5	1	2	2
13	CPD-1050	1	2	1	2	1	2	5	1	1	2
14	G-204-13	1	2	1	2	1	2	5	1	3	2
15	GSHY01/1338	1	3	1	2	1	2	5	1	3	2
16	NDLH-1101	1	2	1	1	1	2	5	1	2	2
17	CPD-478	1	2	1	2	1	2	5	1	1	1
18	CCH-18	1	2	1	1	1	3	5	1	2	2
19	KH-121	1	2	1	2	1	2	5	1	2	2
20	GJHV-01/35	1	2	1	2	1	2	5	1	1	2
21	NDL-770	1	2	1	2	1	2	5	1	1	1
22	H1-1117/08	1	2	1	2	1	3	5	1	1	1
23	NA-777	1	3	1	1	1	2	3	1	2	2
24	NDLH-152	1	2	1	2	1	2	3	1	2	1
25	MALE-223/08	1	2	1	1	1	3	5	1	2	2
26	TXORHY-1-78	1	2	1	1	1	3	5	1	2	2
27	H-1226/08	1	2	1	2	1	2	5	1	2	2
28	L-614	1	2	1	2	1	2	5	1	3	2
29	FEMALE223/08	1	2	1	1	1	2	5	2	2	2
30	H-1236/08	1	2	1	1	1	2	3	1	1	1

Contd.....

		Sepal pig	Petal colour	Petal spot	Stigma position	Filament colour	Anther colour	Boll size	Boll colour	Boll shape	Boll tip
		1=absent	2=cream	1=absent	1=embedded	1=absent	2=cream	5= medium	1= Green	1=Round	1=blunt
		9=present	3=yellow	9=present	2=exserted	9=present	3=yellow	3=Small	2=Red	2=ovate	2= pointed
			6=bicolour			4=purple	4= purple			3=elliptic	
S.No	Genotype										
31	NH-452	1	3	1	2	1	3	5	1	2	2
32	NDLH-1906	1	2	1	2	1	3	5	1	2	2
33	H-1098/08	1	3	1	2	1	3	5	1	3	2
34	FEMALE287/08	1	2	1	1	1	3	5	1	2	2
35	H-1098-1/08	1	2	1	1	1	3	5	1	2	2
36	MALE-2097/08	1	3	1	2	1	2	5	1	3	2
37	HS-6/08	1	2	1	1	1	2	5	1	1	2
38	TIDEWATER5-3	1	2	1	1	1	3	5	1	1	2
39	AKH-9331	1	2	1	2	1	2	5	1	1	2
40	L-713	1	2	1	2	1	2	5	1	3	2
41	NH-630	1	3	9	2	1	3	5	1	2	2
42	P-21-15	1	2	1	1	1	2	5	1	1	2
43	NH-545	1	2	1	2	1	2	5	1	2	2
44	F-2170	1	2	1	2	1	2	5	1	2	2
45	CPD-821	1	3	1	2	1	2	5	1	3	2
46	NA-1325	1	2	1	2	1	2	5	1	2	2
47	L-801	1	2	1	2	1	2	5	1	2	2
48	TCH-1705	1	2	1	2	1	3	5	1	3	2
49	GBHV-156	1	2	1	2	1	3	5	1	2	2
50	CPS-141	1	2	1	2	1	3	5	1	2	2
51	CSH-3129	1	3	1	2	1	2	5	1	2	2
52	PH-348	1	2	1	2	1	3	5	1	2	2
53	ADB-28	1	2	1	2	1	2	5	1	2	2
54	ARBH-225	1	2	1	2	1	3	5	1	2	2
55	CNDTS-55	1	2	1	2	1	3	5	1	2	2
56	NH-615	1	2	1	2	1	2	5	1	1	2
57	NARASIMHA	1	2	1	1	1	3	3	1	2	2
58	SIVANAMELI	1	2	1	2	1	2	5	1	2	2
59	NDLH-1905	1	3	1	2	1	2	3	1	2	2
60	NDLH-1938	1	2	1	2	1	3	5	1	3	2

Table-11: Analysis of variance for yield and yield components in cotton (*Gossypium hirsutum* L.).

Source	d.f.	Days to 50% flowering	Plant height (cm)	No. of monopodia plant ⁻¹	No. of sympodia plant ⁻¹	No. of bolls plant ⁻¹	Boll weight (g)	Ginning-outturn (%)	Seed index (g)
Mean squares									
Replications	2	8.5056	114.6796	0.0095	4.6491	41.9074	0.0756	16.1837	0.8224
Varieties	59	29.3005**	1392.0132**	0.8175**	12.6751**	125.6876**	1.2749**	39.2923**	3.0941**
Error	118	3.0762	53.1852	0.0114	2.3300	14.8482	0.0938	5.5505	0.3118

Source	d.f.	Lint index (g)	2.5% Span length (mm)	Micronaire (10 ⁻⁶ g/in)	Bundle strength (g/tex)	Uniformity ratio	Fibre elongation (%)	Seed cotton yield plant ⁻¹ (g)
Mean squares								
Replications	2	0.2846	4.7307	0.0416	1.4074	8.7816	0.0005	294.3890
Varieties	59	1.6716**	7.5806**	0.6380**	2.9522**	20.2813**	0.0226**	1590.1259**
Error	118	0.1563	2.0703	0.0914	0.6213	5.2288	0.0022	108.3632

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

Table -12: Mean performance of 15 characters in 60 genotypes of cotton (*Gossypium hirsutum* L.).

S.No	Genotype	Days to 50% flowering	Plant height (cm)	No. of monopodia Plant ⁻¹	No. of sympodia Plant ⁻¹	No.of bolls Plant ⁻¹	Boll weight (g)	Ginning Out turn (%)	Seed index (g)
1	NDLH-575	57.33	106.19	0.30	15.17	30.96	4.57	35.70	9.31
2	NH-577	54.33	80.80	0.33	13.15	39.72	3.80	36.88	7.27
3	NDLH-779	53.67	119.47	1.10	15.73	40.92	3.70	33.61	9.50
4	NDLH-849	53.67	112.29	0.93	15.30	38.69	3.80	34.38	9.80
5	KDCAKD	55.67	77.10	1.93	13.73	42.41	3.40	33.96	8.17
6	TSH-333	49.67	99.27	1.27	12.33	38.40	3.47	38.20	8.20
7	WGP-8	50.33	79.50	0.47	15.30	51.18	3.27	35.37	8.10
8	IC-356932	54.67	71.37	0.23	12.83	34.58	3.07	33.53	9.03
9	TXLAMA	49.67	62.61	1.63	9.11	17.28	4.27	34.38	8.97
10	A-7262	58.67	80.92	0.37	11.57	24.62	3.80	31.51	9.93
11	IH-07	56.67	89.09	1.58	13.37	30.05	4.67	34.46	11.10
12	NDLH-7122	52.67	87.62	0.75	17.07	29.14	4.40	41.10	9.85
13	CPD-1050	59.67	121.13	0.75	16.13	26.34	4.67	27.79	10.13
14	G-204-13	54.33	86.37	2.21	15.60	28.72	4.37	39.08	9.53
15	GSHY-01/1338	57.33	83.77	1.00	15.23	49.83	3.10	31.28	7.20
16	NDLH-1101	53.00	108.63	1.05	15.83	42.84	4.97	40.12	9.66
17	CPD-478	55.67	71.08	1.05	14.77	29.47	4.33	39.81	9.58
18	CCH-18	57.67	98.15	2.18	13.60	45.57	3.57	37.41	7.47
19	KH-121	57.67	98.98	0.95	15.53	41.41	3.57	33.10	9.20
20	GJHV-01/35	61.67	104.41	2.83	14.60	31.04	4.97	38.15	9.20
21	NDL-770	55.33	121.65	0.80	16.30	25.77	3.17	35.56	11.12
22	H1-1117/08	55.67	82.95	0.60	15.10	34.06	3.40	33.84	9.91
23	NA-777	56.33	58.18	1.17	12.40	28.52	3.50	43.48	7.10
24	NDLH-152	54.67	113.99	0.73	13.57	29.32	4.57	34.38	9.39
25	MALE-223/08	58.33	111.09	0.90	15.43	32.73	3.50	27.05	11.18
26	TXORHY-1-78	54.33	66.55	0.12	11.50	19.85	3.67	32.10	7.17
27	H-1226/08	55.67	110.74	1.27	13.77	32.18	4.13	35.62	10.61
28	L614	59.33	67.92	0.43	11.03	33.57	3.47	42.07	7.53
29	FEMALE-223/08	55.67	110.84	1.10	14.60	32.94	4.33	35.07	8.40
30	H-1236/08	54.67	116.68	0.57	14.20	38.83	3.57	36.16	9.31

S.No	Genotype	Days to 50% flowering	Plant height (cm)	No.of monopodia Plant ⁻¹	No.of sympodia Plant ⁻¹	No.of Bolls plant ⁻¹	Boll weight (g)	Ginning Out turn (%)	Seed index (g)
31	NH-452(RENUKA)	54.33	123.62	1.14	16.57	23.31	3.73	38.80	8.79
32	NDLH-1906	54.67	113.45	0.52	16.20	31.09	4.33	34.24	9.94
33	H-1098/08	61.33	107.23	0.65	17.63	27.73	5.33	30.24	9.94
34	FEMALE287/08	58.33	111.37	1.37	17.90	27.52	5.07	36.29	9.79
35	H-1098-1/08	53.67	118.95	0.58	15.40	33.81	3.83	35.26	9.83
36	MALE-2097/08	62.33	117.11	0.77	17.47	27.37	5.57	31.65	10.16
37	HS-6/08	54.33	107.75	1.13	15.07	31.48	5.03	41.32	7.77
38	TIDEWATER-5-3	53.67	76.96	1.17	11.07	29.61	4.33	32.02	10.33
39	AKH-9331	56.00	73.05	1.82	12.47	34.45	4.57	39.94	9.20
40	L-713	59.33	82.82	2.22	10.43	26.50	3.43	30.70	10.37
41	NH-630	62.33	95.58	1.17	13.27	34.52	3.67	30.89	10.17
42	P-21-15	54.67	131.72	1.23	14.33	43.30	3.80	33.60	8.78
43	NH-545	55.67	120.94	1.07	13.83	37.49	3.67	30.33	9.57
44	F-2170	60.67	141.14	1.03	16.63	26.43	4.23	32.72	10.50
45	CPD-821	54.33	133.04	1.17	17.83	36.71	3.43	30.83	8.90
46	NA-1325	56.33	108.90	0.90	14.33	32.63	3.50	33.99	10.23
47	L-801	56.67	118.18	0.90	15.67	28.27	3.66	33.44	9.00
48	TCH-1705	62.33	84.49	1.27	16.53	32.25	4.37	32.95	9.57
49	GBHV-156	54.33	131.67	1.20	16.20	28.81	4.37	31.77	9.70
50	CPS-141	55.67	85.94	0.90	15.43	28.90	4.20	33.37	11.33
51	CSH-3129	59.67	98.01	1.23	16.47	33.51	4.13	28.30	9.94
52	PH-348	53.00	157.90	1.20	18.80	28.82	3.70	34.34	9.78
53	ADB-28	54.00	126.33	0.33	18.73	36.43	2.90	30.83	8.64
54	ARBH-225	52.00	127.18	1.00	17.67	29.08	3.73	35.57	9.47
55	CNDTS-55	52.33	133.37	1.52	13.70	32.90	4.60	30.57	9.49
56	NH-615	51.33	107.13	0.80	15.00	31.57	3.60	35.60	9.14
57	NARASIMHA	59.67	95.02	1.37	15.97	29.80	5.57	41.05	8.33
58	SIVANAMELI	51.67	89.61	1.35	14.27	31.47	4.37	32.67	9.83
59	NDLH-1905	53.00	95.17	0.87	14.90	33.70	4.10	32.26	9.45
60	NDLH-1938	52.67	114.14	0.90	12.50	29.69	5.57	36.96	9.67
	Mean	55.74	102.12	1.06	14.77	32.67	4.06	34.63	9.34
	C.V.	3.15	7.14	10.12	10.34	11.80	7.55	6.80	5.98
	C.D at 5%	2.84	11.79	0.17	2.47	6.23	0.50	3.81	0.90

S.No	Genotype	Lint index (g)	2.5%Span length (mm)	Micronaire (10 ⁻⁶ g/In)	Bundle strength (g/tex)	Uniformity ratio	Fibre elongation (%)	Seed cotton yield plant ⁻¹ (g)
1	NDLH-575	5.13	27.50	3.88	20.83	48.43	5.33	130.15
2	NH-577	4.23	25.51	4.25	20.47	49.53	5.43	119.15
3	NDLH-779	4.77	29.61	4.75	20.77	49.03	5.57	110.14
4	NDLH-849	5.13	29.00	5.23	20.93	53.63	5.30	115.50
5	KDCAKD	4.20	30.54	3.57	21.20	43.33	5.53	122.23
6	TSH-333	5.07	23.59	4.40	21.30	50.17	5.57	115.89
7	WGP-8	4.43	27.78	3.70	21.17	46.90	5.57	141.00
8	IC-356932	4.60	28.57	3.53	21.00	46.70	5.50	83.50
9	TXLAMA	4.70	28.97	3.50	21.43	46.30	5.57	64.61
10	A-7262	4.57	28.25	3.37	21.33	44.67	5.53	73.67
11	IH-07	5.83	28.36	4.33	21.30	46.53	5.50	127.09
12	NDLH-7122	6.87	26.69	4.23	21.30	49.27	5.33	107.73
13	CPD-1050	4.03	28.09	4.35	24.07	47.73	5.57	110.41
14	G-204-13	6.13	25.36	4.20	21.20	48.60	5.53	114.94
15	GSHY-01/1338	3.30	27.40	4.17	20.57	48.40	5.60	119.74
16	NDLH-1101	6.47	25.53	4.99	20.67	53.43	5.40	179.02
17	CPD-478	6.33	28.22	3.99	20.93	44.57	5.53	109.09
18	CCH-18	4.47	24.92	4.16	20.73	51.90	5.43	122.86
19	KH-121	4.56	26.44	4.19	23.30	51.30	5.60	119.70
20	GJHV-01/35	5.67	25.75	4.75	20.23	49.37	5.37	140.07
21	NDL-770	6.13	27.48	4.17	22.77	47.80	5.53	64.92
22	H1-1117/08	5.07	28.37	4.67	20.60	51.00	5.30	92.71
23	NA-777	5.47	25.31	4.74	18.77	48.00	5.47	80.14
24	NDLH-152	4.90	27.88	4.82	20.67	52.33	5.37	110.32
25	MALE-223/08	4.07	25.81	4.85	20.87	51.33	5.43	91.88
26	TXORHY-1-78	3.40	25.49	4.65	21.36	50.60	5.53	57.86
27	H-1226/08	5.87	27.03	4.91	21.43	46.00	5.30	115.58
28	L614	5.47	27.00	3.76	20.10	42.97	5.47	92.45
29	FEMALE-223/08	4.53	28.18	4.66	21.60	50.83	5.30	121.90
30	H-1236/08	5.27	27.43	4.54	20.77	48.60	5.30	104.39

S.No	Genotype	Lint index (g)	2.5%Span length (mm)	Micronaire (10 ⁻⁶ g/In)	Bundle Strength (g/tex)	Uniformity ratio	Fibre elongation (%)	Seed cotton yield plant ¹ (g)
31	NH-452(RENUKA)	5.57	25.29	4.21	23.20	49.57	5.53	74.12
32	NDLH-1906	5.13	28.48	4.91	20.93	50.07	5.40	117.57
33	H-1098/08	4.30	28.63	4.41	21.33	51.40	5.37	133.78
34	FEMALE287/08	5.57	27.75	3.92	21.37	47.93	5.50	125.98
35	H-1098-1/08	5.37	27.20	4.19	21.63	47.43	5.60	95.06
36	MALE-2097/08	4.77	26.17	4.90	21.67	47.27	5.43	133.38
37	HS-6/08	5.47	28.07	4.16	22.47	49.73	5.43	141.23
38	TIDEWATER-5-3	4.83	26.54	4.56	22.33	48.69	5.53	110.40
39	AKH-9331	6.13	27.04	3.88	19.40	47.30	5.43	130.92
40	L-713	4.60	27.18	3.51	20.47	42.77	5.60	74.68
41	NH-630	4.53	27.06	3.94	21.80	46.37	5.53	104.16
42	P-21-15	4.43	27.50	4.16	21.57	45.83	5.47	130.70
43	NH-545	4.17	24.53	4.24	21.30	50.50	5.47	105.78
44	F-2170	5.10	26.67	4.33	20.43	51.10	5.40	98.80
45	CPD-821	4.00	24.09	4.89	20.93	51.83	5.50	98.49
46	NA-1325	5.27	27.78	4.85	21.93	46.50	5.53	99.29
47	L-801	4.43	28.99	4.72	21.73	46.33	5.53	99.48
48	TCH-1705	4.70	29.57	4.46	23.53	45.83	5.40	121.27
49	GBHV-156	4.53	28.16	4.54	20.13	49.27	5.47	103.94
50	CPS-141	5.67	24.63	5.35	20.87	52.80	5.47	98.37
51	CSH-3129	4.13	29.47	5.08	20.57	51.57	5.40	116.98
52	PH-348	5.10	27.36	4.76	20.03	49.00	5.50	86.26
53	ADB-28	3.87	26.83	4.54	22.10	49.37	5.53	73.95
54	ARBH-225	5.23	27.29	4.14	22.30	47.07	5.50	90.03
55	CNDTS-55	4.20	29.07	3.43	22.60	44.10	5.60	131.98
56	NH-615	5.07	30.16	4.30	20.65	49.70	5.53	94.07
57	NARASIMHA	5.80	29.89	4.56	22.39	49.17	5.47	142.19
58	SIVANAMELI	4.77	29.52	4.28	22.27	50.67	5.50	116.37
59	NDLH-1905	4.50	28.82	4.61	21.45	51.00	5.40	113.65
60	NDLH-1938	5.67	29.12	4.42	23.29	52.13	5.40	147.66
	Mean	4.96	27.42	4.36	21.34	48.69	5.47	109.49
	C.V.	7.97	5.25	6.94	3.69	4.70	0.86	9.51
	C.D at 5%	0.64	2.33	0.49	1.27	3.70	0.08	16.83

Table -13: Mean, variability, heritability (broad sense) and genetic advance as per cent of mean for yield and yield components in cotton (*Gossypium hirsutum* L.)

S NO.	Characters	Mean	Range		Coefficient Variation		Heritability (%) (Broad sense)	Genetic advance as per cent of mean (at 5% level)
			Minimum	Maximum	PCV (%)	GCV (%)		
1	Days to 50% flowering	55.74	49.67	62.33	6.17	5.30	73.97	9.40
2	Plant height (cm)	102.12	58.18	157.90	21.88	20.69	89.35	40.28
3	No. of monopodia plant ⁻¹	1.06	0.12	2.83	50.11	49.08	95.92	99.02
4	No. of sympodia plant ⁻¹	14.77	9.11	18.80	16.28	12.57	59.68	20.01
5	No. of bolls plant ⁻¹	32.67	17.28	51.18	22.03	18.61	71.33	32.37
6	Boll weight (g)	4.06	2.90	5.57	17.21	15.47	80.75	28.63
7	Ginning outturn (%)	34.63	27.05	43.48	11.84	9.69	66.96	16.33
8	Seed index (g)	9.34	7.10	11.33	11.92	10.31	74.84	18.37
9	Lint index (g)	4.96	3.30	6.87	16.40	14.33	76.37	25.80
10	2.5% span length (mm)	27.42	23.59	30.54	7.21	4.94	47.01	6.98
11	Micronaire (10 ⁻⁶ g/inch)	4.36	3.37	5.35	12.00	9.79	66.58	16.46
12	Bundle strength (g/tex)	21.34	18.77	24.07	5.54	4.13	55.56	6.34
13	Uniformity ratio (%)	48.69	42.77	53.63	6.57	4.60	48.97	6.63
14	Fibre elongation (%)	5.47	5.30	5.60	1.74	1.51	75.58	2.70
15.	Seed cotton yield plant ⁻¹ (g)	109.49	57.86	179.02	22.42	20.30	82.01	37.87

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

Table -14: Phenotypic (above diagonal) and genotypic (below diagonal) correlation of 15 characters in 60 cotton (*Gossypium hirsutum* L.) genotypes.

Character	Days to 50% flowering	Plant height	No. of monopodia plant ⁻¹	No. of sympodia plant ⁻¹	No. of bolls plant ⁻¹	Boll weight	Ginning outturn	Seed index	Lint index	2.5% Span length	Micro-naire	Bundle strength	Uniformity ratio	Fibre elongation	Seed cotton yield plant ⁻¹
Days to 50% flowering	--	-0.0361	0.1308*	0.1344*	-0.0930	0.2113**	-0.1712**	0.1515**	-0.0882	-0.0322	0.0456	-0.0373	-0.1263	-0.1619**	0.1038
Plant height	-0.0379	--	-0.0311	0.5121**	0.0235	0.0890	-0.2363**	0.2856**	-0.0451	-0.0060	0.2797**	0.1812**	0.2289**	-0.0879	0.0803.
No. of monopodia plant ⁻¹	0.1480*	-0.0362	--	-0.1095	0.0197	0.1987**	0.1221	0.0511	0.1721**	-0.0326	-0.0924	-0.0937	-0.1091	0.0941	0.2428**
No. of sympodia plant ⁻¹	0.1338*	0.7191**	-0.1606**	--	0.0734	0.0821	-0.1137	0.2125**	0.0561	0.0150	0.2528**	0.1279	0.2464**	-0.1483*	0.1653**
No. of bolls plant ⁻¹	-0.1623**	0.0049	0.0027	0.0976	--	-0.3110**	-0.0058	-0.2866**	-0.2063**	-0.0373	-0.0011	-0.1338*	0.1216	-0.0194	0.4136**
Boll weight	0.2548**	0.1050	0.2207**	0.1569**	-0.3894**	--	0.1521**	0.1863**	0.3153**	0.1462*	0.1318*	0.1513**	0.1552**	-0.2918**	0.5670**
Ginning outturn	-0.2514**	-0.3135**	0.1770**	-0.1456*	0.0294	0.2061**	--	-0.4432**	0.7534**	-0.0808	-0.0307	-0.1612**	-0.0719	-0.1387*	0.1605**
Seed index	0.2026**	0.3326**	0.0481	0.2364**	-0.3893**	0.2571**	-0.3851**	--	0.2435**	0.0832	0.1709**	0.1160	0.0691	-0.0940	-0.0277
Lint index	-0.1217	-0.0783	0.2162**	0.0580	-0.2466**	0.4081**	0.7368**	0.3318**	--	-0.0246	0.0860	-0.0791	-0.0236	-0.2130**	0.1689**
2.5% Span length	0.0255	-0.0422	-0.0864	0.0347	-0.0952	0.2290**	-0.2197**	0.1577*	-0.0977	--	-0.1055	0.1548**	-0.1500**	0.0018	0.0861
Micronaire	0.0592	0.3338**	-0.1032	0.5245**	0.0079	0.1593**	-0.1190	0.2613**	0.0649	-0.2699**	--	-0.1166	0.5099**	-0.3365**	0.1194
Bundle strength	0.0390	0.2514**	-0.1126	0.2003**	-0.1839**	0.2450**	-0.2717**	0.2411**	-0.0813	0.2648**	-0.1093	--	-0.1331	0.1521**	0.0513
Uniformity ratio	-0.1893**	0.2877**	-0.1673**	0.4081**	0.1017	0.1897**	-0.0322	0.0214	-0.0096	-0.3956**	0.7912**	0.0229	--	-0.3020**	0.2022**
Fibre elongation	-0.1798**	-0.0958	0.1065	-0.1587**	0.0113	-0.3656**	-0.2178**	-0.1343	-0.3114**	-0.0690	-0.5363**	0.3192**	-0.5355**	--	-0.2834**
Seed cotton yield plant ⁻¹	0.1036	0.1007	0.2504**	0.1786**	0.5092**	0.6599**	0.2540**	-0.0590	0.2318**	0.1526**	0.1376	0.0885	0.2158**	-0.3372**	--

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

Table -15: Direct and indirect effects (phenotypic) of yield components on seed cotton yield in 60 genotypes of cotton (*Gossypium hirsutum* L.).

Character	Days to 50% flowering	Plant height	No.of monopodia plant ⁻¹	No.of sympodia plant ⁻¹	No.of bolls plant ⁻¹	Boll weight	Ginning outturn	Seed index	Lint index	2.5%Span length	Micronaire	Bundle strength	Uniformity ratio	Fibre elongation	Correlation with seed cotton yield plant ⁻¹
Days to 50% flowering	-0.0215	0.0020	0.0138	0.0118	-0.0595	0.1500	-0.0430	0.0244	0.0167	-0.0001	0.0006	-0.0020	0.0003	0.0104	0.1038
Plant height	0.0008	-0.0542	-0.0033	0.0450	0.0150	0.0632	-0.0594	0.0460	0.0085	0.0000	0.0036	0.0099	-0.0005	0.0056	0.0803
No.of monopodia plant ⁻¹	-0.0028	0.0017	0.1057	-0.0096	0.0126	0.1410	0.0307	0.0082	-0.0326	-0.0001	-0.0012	-0.0051	0.0002	-0.0060	0.2428**
No. of sympodia plant ⁻¹	-0.0029	-0.0278	-0.0116	0.0879	0.0470	0.0583	-0.0286	0.0342	-0.0106	0.0000	0.0032	0.0070	-0.0005	0.0095	0.1653**
No. of bolls plant ⁻¹	0.0020	-0.0013	0.0021	0.0065	0.6401	-0.2208	-0.0015	-0.0461	0.0391	-0.0001	0.0000	-0.0073	-0.0003	0.0012	0.4136**
Boll weight	-0.0045	-0.0048	0.0210	0.0072	-0.1990	0.7100	0.0382	0.0300	-0.0597	0.0003	0.0017	0.0083	-0.0003	0.0187	0.5670**
Ginning outturn	0.0037	0.0128	0.0129	-0.0100	-0.0037	0.1080	0.2513	-0.0714	-0.1427	-0.0002	-0.0004	-0.0088	0.0001	0.0089	0.1605**
Seed index	-0.0033	-0.0155	0.0054	0.0187	-0.1834	0.1323	-0.1114	0.1610	-0.0461	0.0002	0.0022	0.0063	-0.0001	0.0060	-0.0277
Lint index	0.0019	0.0024	0.0182	0.0049	-0.1320	0.2239	0.1893	0.0392	-0.1894	-0.0001	0.0011	-0.0043	0.0000	0.0136	0.1689**
2.5% Span length	0.0007	0.0003	-0.0034	0.0013	-0.0239	0.1038	-0.0203	0.0134	0.0047	0.0023	-0.0013	-0.0085	0.0003	-0.0001	0.0861
Micronaire	-0.0010	-0.0152	-0.0098	0.0222	-0.0007	0.0936	-0.0077	0.0275	-0.0163	-0.0002	0.0128	-0.0064	-0.0010	0.0215	0.1194
Bundle strength	0.0008	-0.0098	-0.0099	0.0112	-0.0856	0.1075	-0.0405	0.0187	0.0150	0.0003	-0.0015	0.0546	-0.0003	-0.0097	0.0513
Uniformity ratio	0.0027	-0.0124	-0.0115	0.0217	0.0779	0.1102	-0.0181	0.0111	0.0045	-0.0003	0.0065	-0.0073	-0.0021	0.0193	0.2022**
Fibre elongation	0.0035	0.0048	0.0099	-0.0130	-0.0124	-0.2072	-0.0348	-0.0151	0.0403	0.0000	-0.0043	0.0083	0.0006	-0.0640	0.2834**

*=Significant at 5% level **=Significant at 1% level, Bold and diagonal values indicate direct effects, Residual effect= 0.5225

Table -16: Direct and indirect effects (genotypic) of yield components on seed cotton yield in 60 genotypes of cotton (*Gossypium hirsutum* L.).

Character	Days to 50% flowering	Plant height	No.of monopodia plant ⁻¹	No.of sympodia plant ⁻¹	No.of bolls Plant ⁻¹	Boll weight	Ginning outturn	Seed index	Lint index	2.5%Span length	Micro-naire	Bundle strength	Uniformity ratio	Fibre elongation	Correla-tion with seed cotton yield plant ⁻¹
Days to 50% flowering	-0.1061	-0.0014	-0.0011	-0.0143	-0.1559	0.2746	0.0911	-0.0476	-0.0380	-0.0034	0.0114	0.0041	0.0671	0.0230	0.1036
Plant height	0.0040	0.0376	0.0003	-0.0768	0.0047	0.1131	0.1137	-0.0782	-0.0244	0.0056	0.0644	0.0264	-0.1020	0.0123	0.1007
No. of monopodia plant ⁻¹	-0.0157	-0.0014	-0.0074	0.0172	0.0026	0.2379	-0.0642	-0.0113	0.0674	0.0114	-0.0199	-0.0118	0.0593	-0.0136	0.2504**
No. of sympodia plant ⁻¹	-0.0142	0.0271	0.0012	-0.1068	0.0937	0.1691	0.0528	-0.0556	0.0181	-0.0046	0.1012	0.0210	-0.1446	0.0203	0.1786**
No. of bolls plant ⁻¹	0.0172	0.0002	0.0000	-0.0104	0.9605	-0.4196	-0.0106	0.0915	-0.0769	0.0126	0.0015	-0.0193	-0.0360	-0.0014	0.5092**
Boll weight	-0.0270	0.0040	-0.0016	0.0168	-0.3740	1.0776	-0.0747	-0.0604	0.1272	-0.0303	0.0307	0.0257	-0.0672	0.0468	0.6599**
Ginning outturn	0.0267	-0.0118	-0.0013	0.0156	0.0282	0.2221	-0.3626	0.0905	0.2297	0.0291	-0.0230	-0.0285	0.0114	0.0279	0.2540**
Seed index	-0.0215	0.0125	-0.0004	-0.0252	-0.3739	0.2771	0.1396	-0.2351	0.1034	-0.0209	0.0504	0.0253	-0.0076	0.0172	-0.0590
Lint index	0.0129	-0.0029	-0.0016	-0.0062	-0.2369	0.4397	-0.2671	-0.0780	0.3118	0.0129	0.0125	-0.0085	0.0034	0.0398	0.2318**
2.5%Span length	-0.0027	-0.0016	0.0006	-0.0037	-0.0914	0.2468	0.0797	-0.0371	-0.0305	-0.1323	-0.0521	0.0278	0.1402	0.0088	0.1526**
Micronaire	-0.0063	0.0126	0.0008	-0.0560	0.0076	0.1716	0.0431	-0.0614	0.0202	0.0357	0.1930	-0.0115	-0.2804	0.0686	0.1376
Bundle strength	-0.0041	0.0095	0.0008	-0.0214	-0.1766	0.2640	0.0985	-0.0567	-0.0253	-0.0350	-0.0211	0.1049	-0.0081	-0.0408	0.0885
Uniformity ratio	0.0201	0.0108	0.0012	-0.0436	0.0977	0.2044	0.0117	-0.0050	-0.0030	0.0523	0.1527	0.0024	-0.3544	0.0685	0.2158**
Fibre elongation	0.0191	-0.0036	-0.0008	0.0170	0.0108	-0.3940	0.0790	0.0316	-0.0971	0.0091	-0.1035	0.0335	0.1898	-0.1279	-0.3372**

*=Significant at 5% level **=Significant at 1% level, Bold and diagonal values indicate direct effects, Residual effect= 0.6957

Table -17: Contribution of different characters towards genetic divergence in 60 genotypes of cotton (*Gossypium hirsutum* L.)

Source	Times ranked first	Contribution % towards divergence
Days to 50% flowering	75	4.24
Plant height (cm)	293	16.55
No. of monopodia plant ⁻¹	703	39.72
No. of sympodia plant ⁻¹	5	0.28
No. of bolls plant ⁻¹	56	3.16
Boll weight (g)	128	7.23
Ginning outturn (%)	39	2.20
Seed index (g)	100	5.65
Lint index (g)	40	2.26
2.5% Span length (mm)	22	1.24
Micronaire (10 ⁻⁶ g/in)	26	1.47
Bundle strength (g/tex)	29	1.64
Uniformity ratio	2	0.11
Fibre elongation (%)	158	8.93
Seed cotton yield plant ⁻¹ (g)	94	5.31

Table -18: Clustering of 60 genotypes of cotton (*Gossypium hirsutum* L.) by Tocher's method.

Cluster No.	No. of genotypes	Name of genotype(s)
I	15	NDLH-152, NDLH-1906, NDLH-1905, H-1236/08, NDLH-849, Female-223/08, NH-615, NA-1325, L-801, NDLH-779, NH-545, ARBH-225, GBHV-156, H-1098-1/08, Male-223/08
II	13	Tidewater5-3, SIVANAMELI, IH-07, CPD-478, TCH-1705, NH-630, Female-287/08, NARASIMHA, H-1226/08, HS-6/08, CSH-3129, CPS-141, KH-121
III	12	H-1098/08, Male-2097/08, CPD-1050, F-2170, NDLH-575, NDLH-1938, P-21-15, NDL-770, NH-452, CPD-821, PH-348, CNDJS-55
IV	1	H1-1117/08
V	11	IC-356932, A-7262, L-614, NH-577, WGP-8, GSHY-01/1338, TXORHY-1-78, ADB-28, TSH-333, NDLH-7122, NA-777
VI	1	AKH-9331
VII	1	G-204-13
VIII	1	NDLH-1101
IX	5	KDCAKD, CCH-18, L-713, TxLama, GJHV-01/35

Table -19: Average intra-and inter-cluster D² values among 9 clusters in 60 genotypes of cotton (*Gossypium hirsutum* L.).

Cluster No	I	II	III	IV	V	VI	VII	VIII	IX
I	14.935 (3.86)	28.94 (5.38)	28.07 (5.29)	24.93 (4.99)	42.18 (6.49)	65.99 (8.12)	91.36 (9.56)	41.05 (6.41)	94.17 (9.70)
II		23.44 (4.84)	39.78 (6.31)	36.82 (6.07)	55.03 (7.42)	38.13 (6.17)	57.23 (7.56)	40.01 (6.32)	68.18 (8.26)
III			37.36 (6.11)	50.35 (7.09)	62.65 (7.91)	79.84 (8.93)	98.78 (9.94)	53.01 (7.28)	105.32 (10.26)
IV				0.00 (0.0)	37.08 (6.09)	68.19 (8.26)	111.91 (10.58)	51.75 (7.19)	112.56 (10.61)
V					47.97 (6.93)	87.97 (9.38)	128.82 (11.35)	70.71 (8.40)	125.35 (11.19)
VI						0.00 (0.0)	19.27 (4.39)	50.34 (7.09)	37.74 (6.14)
VII							0.00 (0.00)	84.38 (9.18)	31.82 (5.65)
VIII								0.00 (0.0)	112.413 (10.60)
IX									48.25 (6.94)

Bold and diagonal values indicate intra-cluster distance; figures in parentheses are D values

Table -20: The nearest and the farthest cluster from each cluster based on D² values in 60 genotypes of cotton (*Gossypium hirsutum* L.)

Cluster No.	Nearest cluster with D² values	Farthest cluster with D² values
I	IV (24.93)	IX (94.17)
II	I (28.94)	IX (68.18)
III	I (28.07)	IX (105.32)
IV	I (24.93)	IX (112.56)
V	IV (37.08)	VII (128.82)
VI	VII (19.27)	V (87.97)
VII	IX (31.82)	V (128.82)
VIII	II (40.02)	IX (112.41)
IX	VII (31.82)	V (125.35)

Values in parentheses indicate D² values

Table -21: Mean values of nine clusters for 15 characters estimated from 60 genotypes of cotton (*Gossypium hirsutum* L.)

Cluster N o.	Days to 50% flowering	Plant height (cm)	No. of monopodia plant ⁻¹	No. of sympodia plant ⁻¹	No. of bolls plant ⁻¹	Boll weight (g)	Ginning outturn (%)	Seed index (g)	Lint index (g)	2.5% Span length (mm)	Micron aire (10 ⁻⁶ g/In)	Bundle strength (g/tex)	Uniformity ratio	Elongation (%)	Seed cotton yield Plant ⁻¹
I	54.556	115.061	0.878	15.202	33.325	3.884	33.541	9.594	4.824	27.954	4.622	21.177	49.576	5.447	104.868
II	57.179	93.433	1.215	14.877	31.704	4.418	34.757	9.812	5.236	27.889	4.441	21.889	48.550	5.474	119.108
III	56.500	125.687	0.955	16.089	29.945	4.364	33.230	9.714	4.869	27.248	4.326	21.893	48.850	5.469	111.721
IV	55.667	82.947	0.600	15.100	34.057	3.400	33.840	9.910	5.067	28.373	4.673	20.600	51.000	5.300	92.713
V	54.697	82.021	0.588	13.741	35.076	3.494	36.032	8.183	4.661	26.583	4.122	20.860	47.870	5.502	96.827
VI	56.000	73.053	1.817	12.467	34.453	4.567	39.937	9.200	6.133	27.043	3.877	19.400	47.300	5.433	130.920
VII	54.333	86.370	2.210	15.600	28.723	4.367	39.083	9.533	6.133	25.360	4.200	21.200	48.600	5.533	114.940
VIII	53.000	108.633	1.050	15.833	42.840	4.967	40.120	9.663	6.467	25.530	4.987	20.667	53.433	5.400	179.020
IX	56.800	85.018	2.160	12.296	32.561	3.927	34.920	8.833	4.727	27.471	3.897	20.813	46.733	5.500	104.889

Bold figures are minimum and maximum values

Table -22: Eigen values, proportion of the total variance represented by first eight principal components, cumulative per cent variance and component loading of different characters in cotton (*Gossypium hirsutum* L.).

	PC ₁	PC ₂	PC ₃	PC ₄	PC ₅	PC ₆	PC ₇	PC ₈
Eigene value (Root)	3.212	2.203	1.823	1.725	1.410	1.079	1.010	0.727
% variance explained	21.415	14.688	12.154	11.501	9.401	7.191	6.730	4.849
Cum. variance explained	21.415	36.103	48.257	59.758	69.159	76.349	83.080	87.928
Days to 50% flowering	0.087	0.213	0.016	0.319	0.118	0.619	0.095	0.499
Plant height (cm)	-0.191	0.395	-0.436	-0.032	-0.211	-0.143	0.081	-0.020
No.of monopodia plant ⁻¹	0.419	-0.072	-0.250	0.012	-0.303	0.116	-0.006	0.191
No. of sympodia plant ⁻¹	-0.296	0.396	-0.185	-0.168	0.055	-0.302	-0.088	0.154
No. of bolls plant ⁻¹	-0.318	-0.248	0.194	-0.345	-0.054	0.076	-0.256	0.422
Boll weight (g)	0.106	0.486	0.263	-0.125	-0.237	0.166	-0.038	-0.352
Ginning outturn (%)	0.352	-0.159	0.075	-0.325	-0.342	-0.064	0.042	0.066
Seed index (g)	0.298	0.256	0.242	0.053	-0.016	-0.307	0.275	0.108
Lint index (g)	0.223	0.068	0.336	0.062	0.169	-0.514	-0.140	0.422
2.5% Span length (mm)	-0.317	0.104	0.406	0.263	0.233	0.030	0.098	-0.110
Micronaire (10 ⁻⁶ g/In)	0.046	0.251	-0.303	-0.396	0.390	0.096	-0.064	0.243
Bundle strength (g/tex)	0.229	0.337	0.041	0.296	-0.086	0.025	-0.526	0.046
Uniformity ratio	0.262	-0.027	0.039	-0.240	0.414	0.123	-0.514	-0.334
Fibre elongation (%)	-0.183	-0.167	-0.201	0.409	-0.262	-0.173	-0.479	0.031
Seed cotton yield plant ⁻¹ (g)	-0.247	0.164	0.359	-0.288	-0.433	0.199	-0.169	0.093

PC= Principal component

Table-24: Clustering of 60 cotton (*Gossypium hirsutum* L.) genotypes by Ward's minimum variance method.

Cluster No	No. of genotypes	Name of genotype(s)
I	6	NH-577,WGP-8,IC-356932,A-7262,L-614,TXORHY-1-78
II	12	NDLH-779, L-801, NA-1325, H-1098-1/08, NH-615, ADB-28, GSHY-01/1338, KH-121, P-21-15, NH-545, TSH-333, CNDJS-55
III	8	NDL-770, NH-452(RENUKA), Male-223/08, F-2170, GBHV-156, ARBH-225, PH-348, CPD-821
IV	8	NDLH-849, NDLH-1905, Female-223/08, H1-1117/08, NDLH-152, NDLH-1906, H-1236/08, NDLH-575
V	8	NDLH-1101, NDLH-1938, Female-287/08, NARASIMHA, HS-6/08, H-1098/08, Male-2097/08, CPD-1050
VI	10	NDLH-7122, CPD-478, H-1226/08, CPS-141, Tidewater-5-3, SIVANAMELI, IH-07, NH-630, TCH-1705, CSH-3129
VII	7	KDCAKD, CCH-18, G-204-13, AKH-9331, TxLama, L-713, NA-777
VIII	1	GJHV-01/35

Table -25: Average intra – and inter- cluster Euclidian² values among the eight clusters in 60 cotton (*Gossypium hirsutum* L.) genotypes

Cluster No	I	II	III	IV	V	VI	VII	VIII
I	90.188	147.958	208.525	119.526	196.935	181.828	344.605	755.558
II		73.908	86.296	94.254	118.334	117.044	227.171	477.956
III			59.247	99.547	122.104	117.668	225.778	410.817
IV				41.688	96.264	96.075	260.522	515.667
V					81.625	105.597	252.667	427.134
VI						69.218	160.023	341.405
VII							114.268	196.525
VIII								0.000

Bold and diagonal values indicate intra-cluster distance

Table -26: Mean values of eight clusters estimated from 60 cotton (*Gossypium hirsutum* L.) genotypes by Ward's method.

Cluster No	Days to 50% flowering	Plant height (cm)	No. of monopodia plant ⁻¹	No. of sympodia Plant ⁻¹	No. of bolls plant ⁻¹	Boll weight (g)	Ginning outturn (%)	Seed index (g)	Lint index (g)	2.5% Span length (mm)	Micro-naire ((10 ⁻⁶ g/In)	Bundle strength (g/tex)	Uniformity ratio	Elon-gation (%)	Seed cotton yield/ plant ⁻¹ (g)
I	55.278	74.510	0.325	12.564	33.920	3.511	35.242	8.172	4.450	27.099	3.877	20.903	46.895	5.504	94.606
II	54.417	113.917	0.971	14.986	37.246	3.616	33.318	9.064	4.541	27.425	4.328	21.620	48.222	5.550	107.983
III	55.292	130.911	1.055	16.929	28.958	3.733	33.330	9.930	4.967	26.519	4.486	21.333	49.621	5.483	88.555
IV	54.917	106.444	0.702	14.879	33.698	4.083	34.504	9.438	4.958	28.207	4.665	20.972	50.737	5.337	113.275
V	57.667	110.299	0.998	16.063	30.346	5.221	35.678	9.432	5.258	27.908	4.463	22.156	49.850	5.446	139.207
VI	56.600	88.912	1.173	14.600	31.109	4.260	34.119	10.231	5.353	27.708	4.513	21.633	48.229	5.450	112.703
VII	55.571	76.898	1.880	12.478	31.923	3.871	36.994	8.686	5.100	27.047	3.937	20.458	46.885	5.510	101.483
VIII	61.667	104.407	2.833	14.600	31.043	4.967	38.147	9.200	5.667	25.747	4.750	20.233	49.367	5.367	140.070

Bold figures are minimum and maximum values

Fig-3: Dendrogram showing relationship of 60 cotton (*Gossypium hirsutum L.*) genotypes in nine clusters

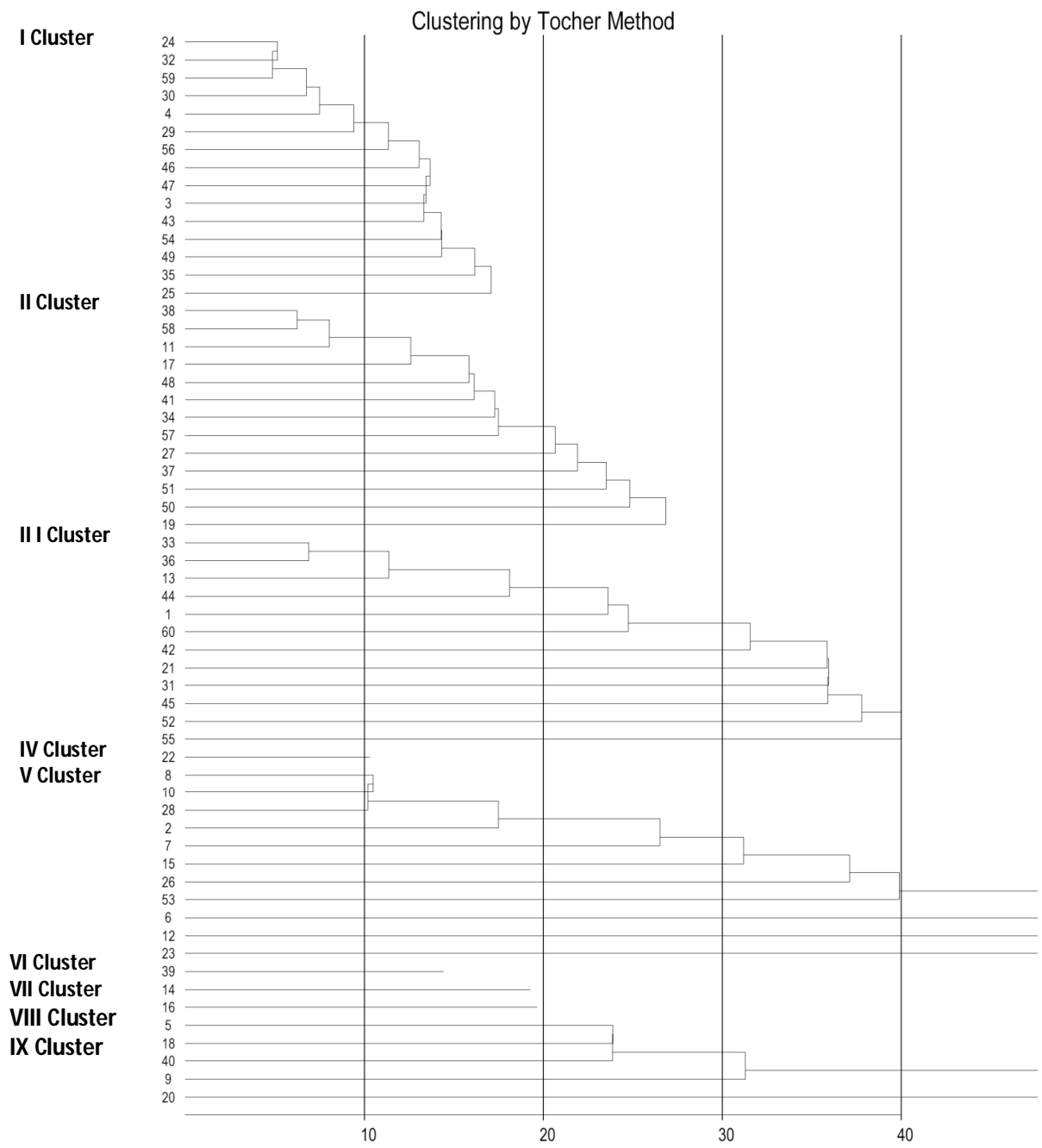


Fig-4: Two dimensional graph showing relative position of 60 cotton (*Gossypium hirsutum* L.) genotypes based on PCA scores.

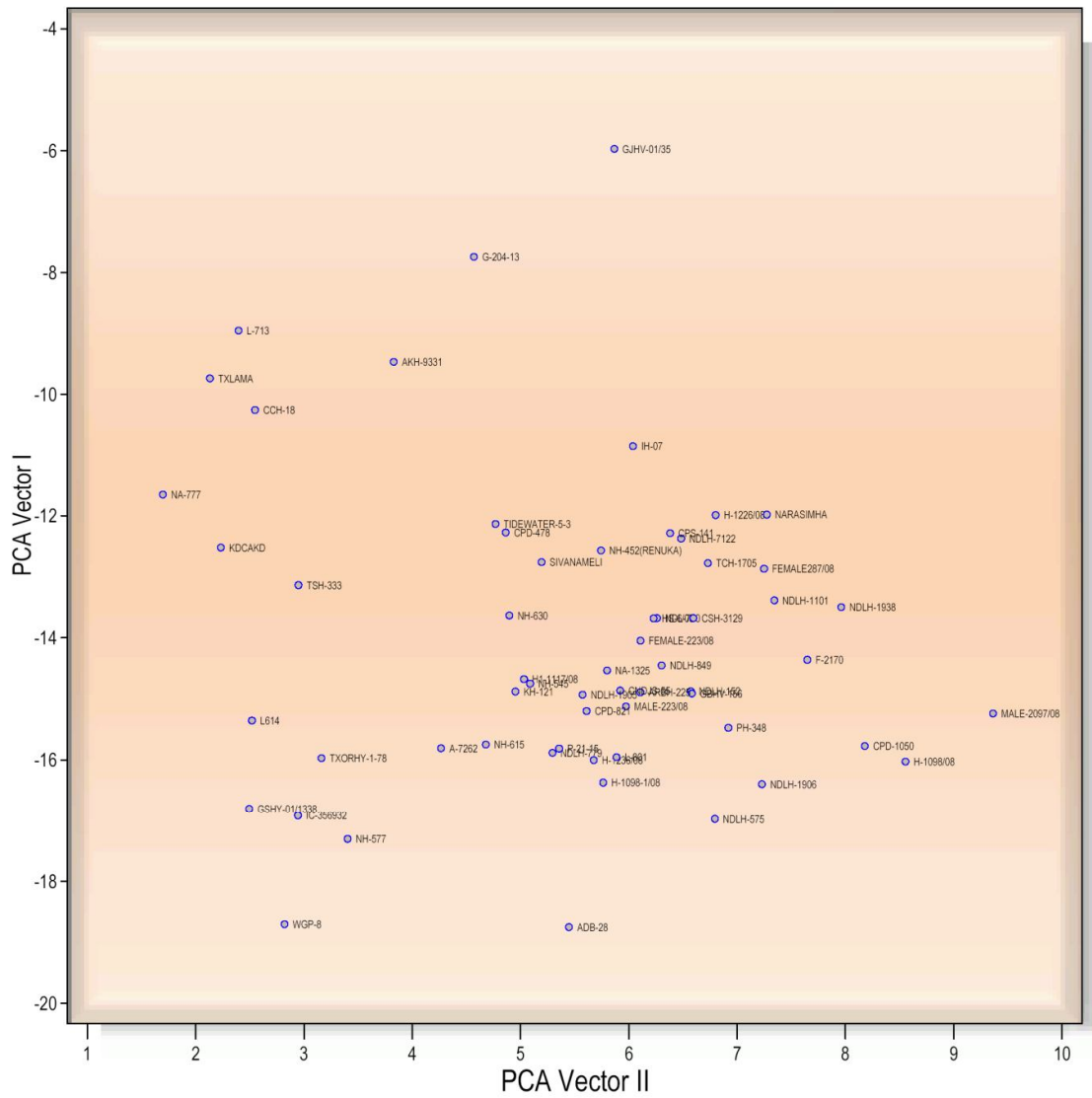


Fig-2: Genotypic path diagram showing cause effect relationship of direct effect with seed cotton yield per plant in cotton (*Gossypium hirsutum* L.)

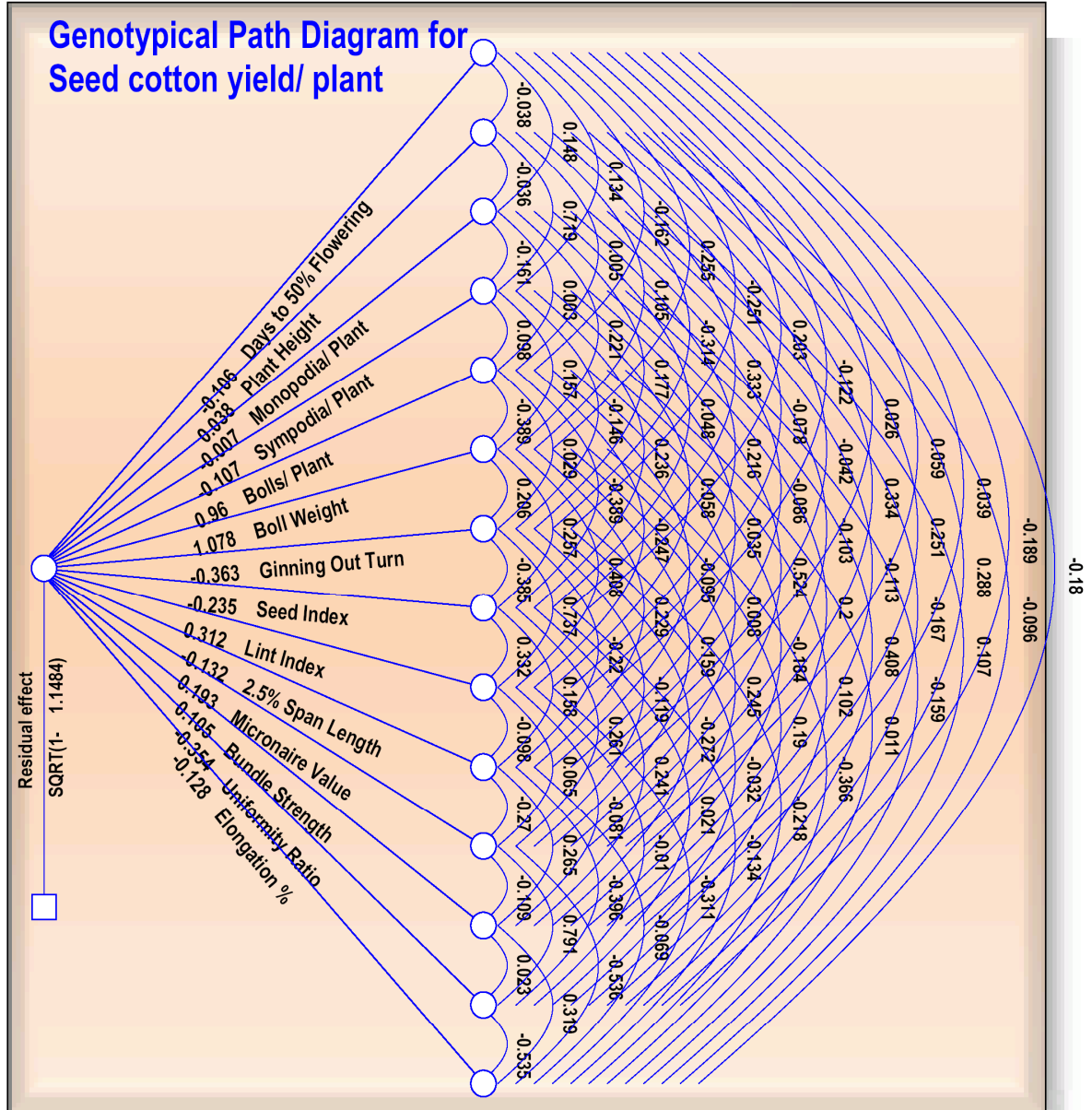
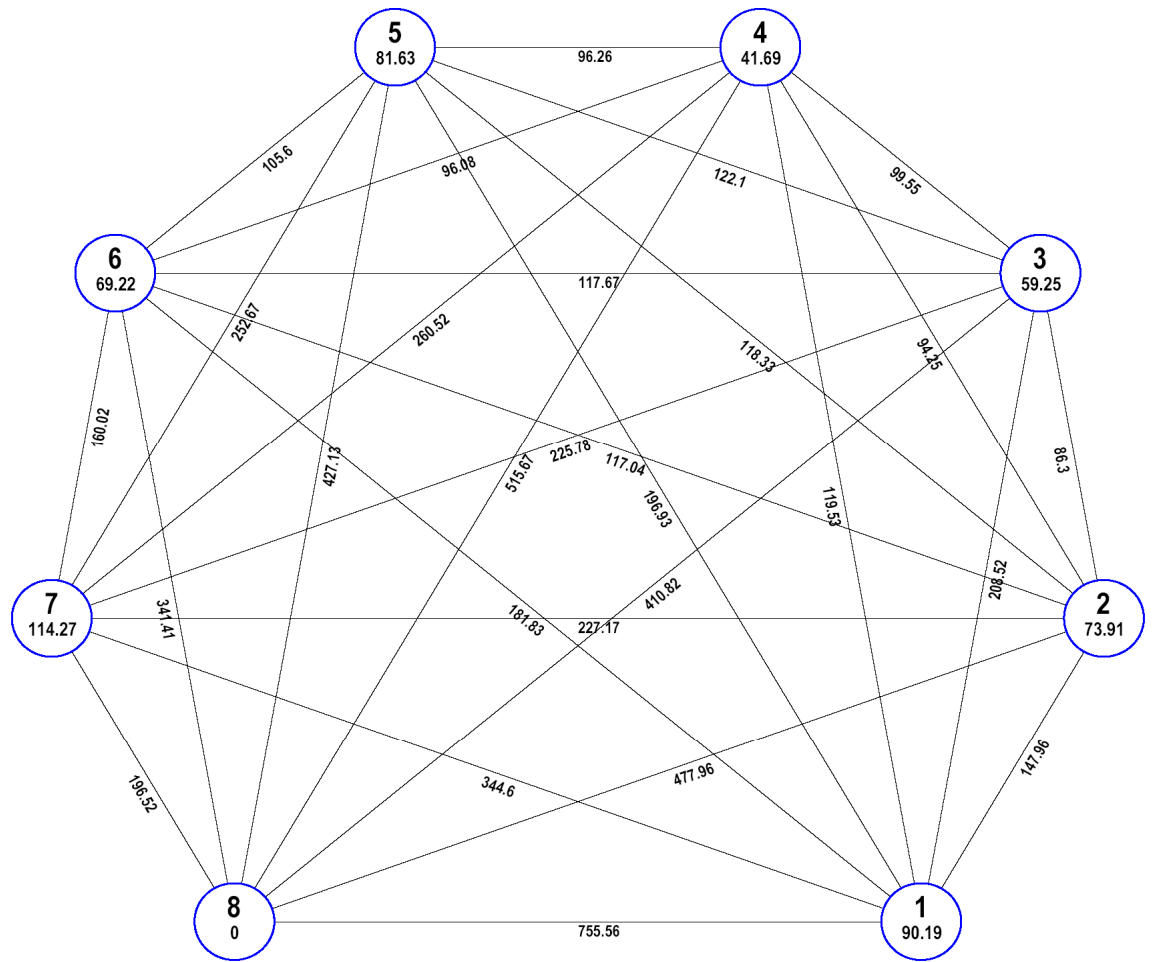
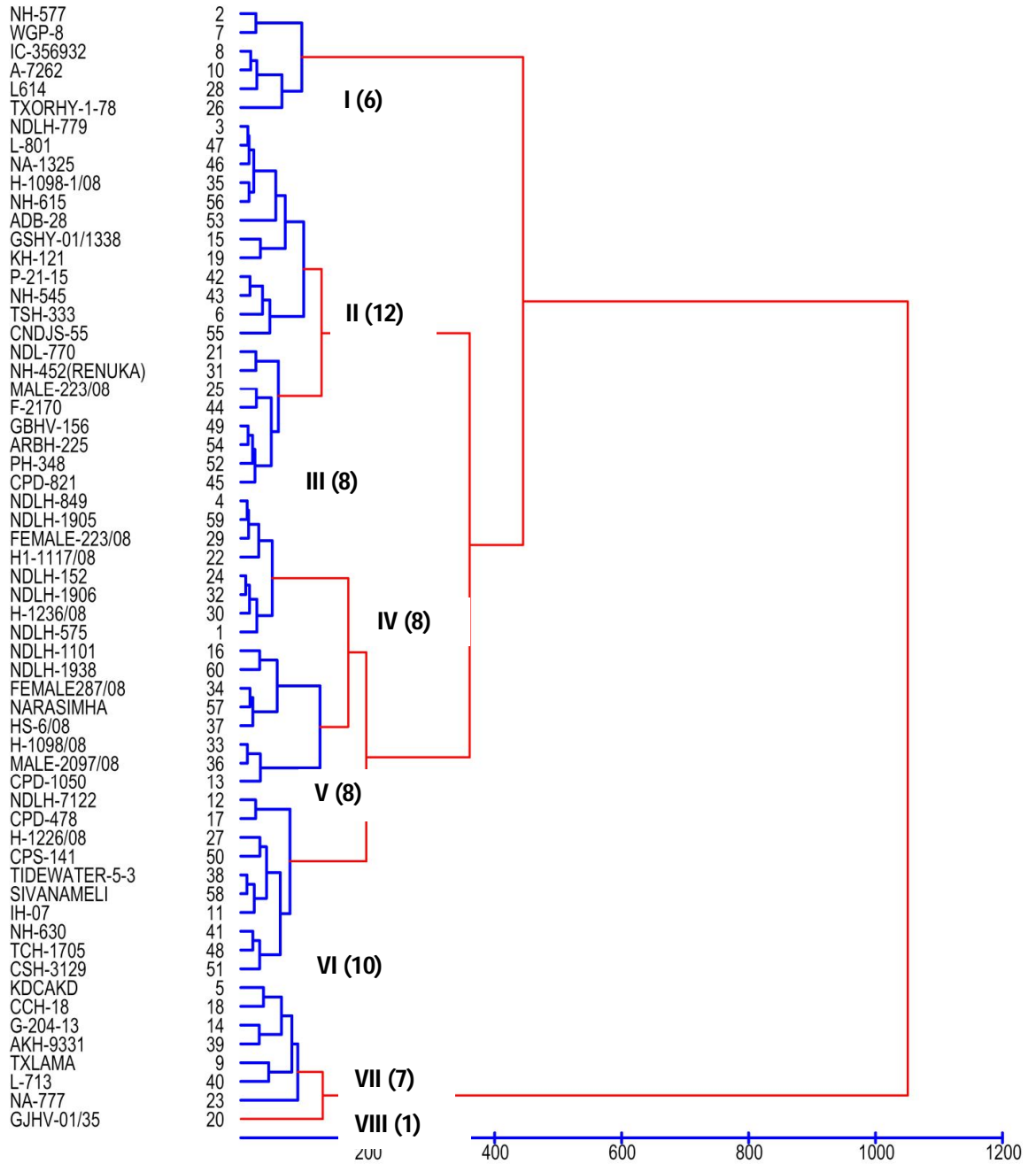


Fig-7: Intra-and inter-cluster distance of 60 cotton (*Gossypium hirsutum* L) in eight clusters based on Euclidean² distance.



Euclidean² Distance (Not to the Scale)

Fig-6: Dendrogram showing relationship of 60 cotton (*Gossypium hirsutum* L.) genotypes in eight clusters



Euclidean² Distance

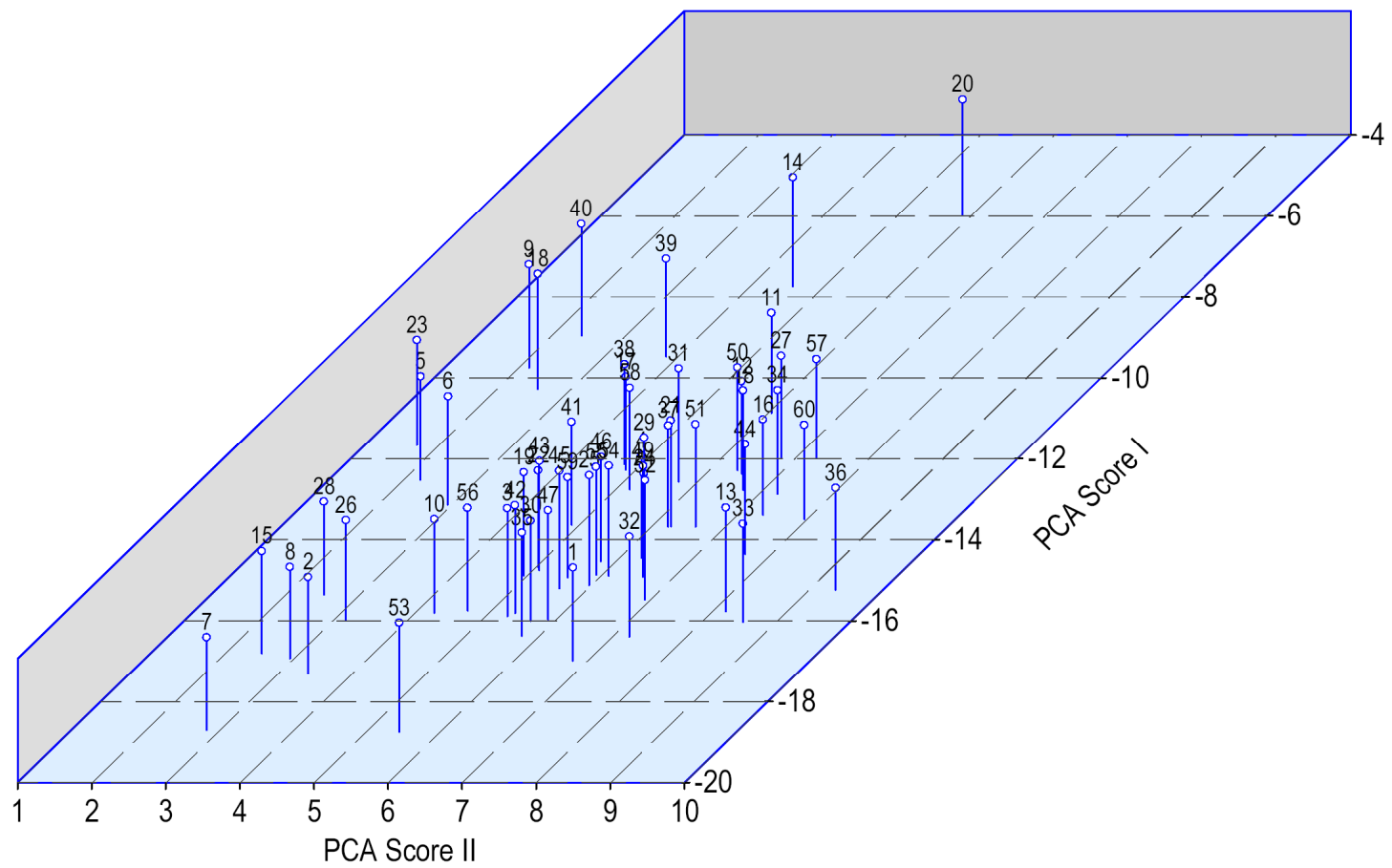


Fig-5: Three dimensional graph showing relative position of 60 cotton (*Gossypium hirsutum* L.) genotypes based on PCA scores. (Genotypes numbers are as per Table no 6).

Table -2: PCA scores of 60 genotypes of cotton (*Gossypium hirsutum* L.)

S.NO	Genotype	PCA1	PCA2	PCA3
		X Vector	Y Vector	Z Vector
1	NDLH-575	-16.977	6.796	-25.496
2	NH-577	-17.307	3.405	-26.521
3	NDLH-779	-15.882	5.296	-29.539
4	NDLH-849	-14.452	6.304	-28.197
5	KDCAKD	-12.526	2.234	-28.533
6	TSH-333	-13.139	2.951	-29.853
7	WGP-8	-18.705	2.821	-25.583
8	IC-356932	-16.920	2.945	-25.030
9	TXLAMA	-9.739	2.133	-28.232
10	A-7262	-15.808	4.267	-25.712
11	IH-07	-10.865	6.039	-27.417
12	NDLH-7122	-12.376	6.484	-25.501
13	CPD-1050	-15.771	8.181	-28.446
14	G-204-13	-7.743	4.571	-30.069
15	GSHY-01/1338	-16.805	2.496	-28.054
16	NDLH-1101	-13.388	7.344	-26.252
17	CPD-478	-12.277	4.865	-25.655
18	CCH-18	-10.274	2.551	-31.503
19	KH-121	-14.883	4.953	-28.355
20	GJHV-01/35	-5.972	5.867	-31.667
21	NDL-770	-13.679	6.262	-29.197
22	H1-1117/08	-14.678	5.034	-26.556
23	NA-777	-11.659	1.699	-28.782
24	NDLH-152	-14.878	6.573	-27.922
25	MALE-223/08	-15.123	5.974	-30.168
26	TXORHY-1-78	-15.970	3.163	-27.266
27	H-1226/08	-11.993	6.803	-28.216
28	L614	-15.354	2.522	-25.451
29	FEMALE-223/08	-14.049	6.109	-28.595
30	H-1236/08	-16.003	5.677	-27.475

Contd.....

S. No	Genotype	PCA1	PCA2	PCA3
		X Vector	Y Vector	Z Vector
31	NH-452(RENUKA)	-12.573	5.744	-31.189
32	NDLH-1906	-16.396	7.231	-27.459
33	H-1098/08	-16.027	8.557	-26.849
34	FEMALE287/08	-12.871	7.250	-28.591
35	H-1098-1/08	-16.371	5.765	-28.308
36	MALE-2097/08	-15.240	9.365	-27.987
37	HS-6/08	-13.684	6.231	-27.910
38	TIDEWATER-5-3	-12.137	4.770	-27.554
39	AKH-9331	-9.469	3.830	-26.795
40	L-713	-8.955	2.397	-30.575
41	NH-630	-13.633	4.898	-28.252
42	P-21-15	-15.814	5.358	-29.605
43	NH-545	-14.751	5.090	-29.946
44	F-2170	-14.361	7.650	-30.259
45	CPD-821	-15.198	5.611	-32.189
46	NA-1325	-14.536	5.801	-28.701
47	L-801	-15.958	5.888	-29.823
48	TCH-1705	-12.779	6.732	-27.425
49	GBHV-156	-14.914	6.583	-30.400
50	CPS-141	-12.290	6.381	-28.321
51	CSH-3129	-13.680	6.598	-28.146
52	PH-348	-15.474	6.921	-32.709
53	ADB-28	-18.754	5.450	-30.120
54	ARBH-225	-14.894	6.108	-30.187
55	CNDJS-55	-14.865	5.920	-29.627
56	NH-615	-15.749	4.681	-28.137
57	NARASIMHA	-11.985	7.276	-27.208
58	SIVANAMELI	-12.764	5.195	-28.013
59	NDLH-1905	-14.932	5.574	-27.501
60	NDLH-1938	-13.500	7.963	-26.052

CHAPTER - V

DISCUSSION

The knowledge of genetic variability present in the given crop species is important for a successful breeding programme. Yield being a complex character is dependent on many quantitatively inherited component characters. It is necessary to have a thorough knowledge on variability present in the available germplasm and the extent of association existing between the yield and yield contributing characters. The correlation and path coefficient analysis further help in establishing the extent of association between yield and yield contributing characters, so that these yield components form additional selection criteria (Sivaprasad, 2003).

In the present investigation, 60 cotton (*Gossypium hirsutum* L.) genotypes were evaluated for morphological characters (descriptors) and 15 quantitative characters and the results of the study are discussed under the following headings.

5.1 Morphological characterization using IBPGR Descriptors

5.2 Genetic variability parameters

5.3 Character association

5.4 Path coefficient analysis

5.5 Genetic divergence

5.1 MORPHOLOGICAL CHARACTERIZATION USING IBPGR DESCRIPTORS

Constant evaluation and characterization of the existent, yet uncharacterized germplasm is useful, and it is many times the cornerstone for the development of new and better varieties. In the present study, the germplasm lines showed variation for most of the morphological traits. The frequency and descriptor values of the sixty cotton germplasm lines are mentioned in Table 27 and no plant among the germplasm lines evaluated showed a deviation to characteristic mentioned in the list. Jimmy Xavier Zumba (2004) and Padmavathi *et al.* (2009) also studied descriptors in cotton and reported the value of the lines in the breeding programmes.

Stem pigmentation was observed in only one line (Tx Lama). Stem hairiness was sparse in 7 lines and medium in 53 lines. A hairy stemmed plant is common cotton plant characteristic and most cotton breeders would rather prefer smooth plants in their breeding programmes as absence for hairiness reduces the egg laying as much as 50% by making the plant unattractive as an oviposition site for the bollworm (Ledge *et al.*, 1992).

Among the leaf characteristics, variation was observed for leaf colour, leaf pubescence, leaf lobes and leaf shape. No variation was observed for leaf size (Large type), leaf appearance (Flat), leaf gossypol glands and leaf nectaries. Large leaf size is helpful to bring optimum plant growth with high dry matter accumulation. Presence of leaf gossypol glands is good for the plant as it had antibiosis effect on insects like *Spodoptera exigua* (army worm), *Helicoverpa zea* (Bollworm) and black flea hopper or at least inhibits the growth of these insects (Bottger *et al.*, 1964). Nectariless cottons help in controlling the pink bollworm damage and also reduction in attack of tarnished plant bugs but no line is showing this character (Mc Carty *et al.*, 1983).

Hairiness on the leaves and modified leaves are common cotton characteristic and among sixty lines, two lines showed strong pubescence and 58 lines were medium in pubescence. Green leaf colour is a common characteristic and 59 lines showed the green leaf character and only one line (Tx Lama) showed the red colour leaf. Leaf lobes are five in 21 lines and three in remaining 39 lines. Leaf shape is okra in only four lines and super okra in three lines and the remaining lines had normal palmate leaf shape which is conducive for the egg laying by bollworms.

Bract is normal and the number of serrations on the bract is many in all the lines. Sepal pigmentation is absent in 59 lines and only one line had red pigmentation (Tx Lama). The cream color is a common petal characteristic of upland cotton and petal colour is cream in 55 lines and yellow in 4 lines and bicolour in one line (Tx Lama). Petal spot is present four lines out of 60 lines which is a distinguishing character of Acala and Pima cottons and can be used as character for the parental or varietal identification. Stigma was exerted in most of the lines (47) and embedded in 13 lines. Filament coloration was absent in all the lines except in three lines. Anther colour was cream in 43 lines and yellow in 16 lines and purple in one line (Tx Lama).

Boll bearing habit was solitary and boll size was medium in all the lines except in six lines. Boll colour is green in 59 lines and red in one line. Boll shape was round in 10 lines and elliptic in 6 lines and ovate in remaining lines. Boll prominence at tip was blunt in eight and pointed in remaining 52 lines. Boll opening was open in all the lines. Plant habit was erect type and boll surface was smooth in all the lines and is the common character in cotton.

The characterization of the germplasm using IBPGR descriptors is helpful for varietal identification and protection. The sixty lines are reservoirs for different parameters and they can be exploited for different breeding programmes and the character stem hairiness can be exploited for breeding pest resistance.

5.2 GENETIC VARIABILITY

The knowledge of genetic variability present in any crop species plays an important role in planning any breeding programme. The genotypic coefficient of variation gives the range of variability available in a crop species and enables the comparison of variability present among different characters. A wider spectrum of variability will enhance the chances of selecting a desired genotype. Besides genetic variability, knowledge on heritability and genetic advance measures the relative degree to which a character is transmitted to progeny, thereby helps the breeder to employ a suitable breeding strategy to achieve the objective quickly. Therefore, for successful improvement of any crop, it is necessary to have a thorough knowledge on the variability present in the available breeding material.

Burton (1952) 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 was the most important aspect of genetic contribution of the breeding material, which has close relationship on its response to selection (Panse, 1957).

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

5.2.1 Days to 50% flowering

The phenotypic coefficient of variation and genotypic coefficient of variation were low for days to 50% flowering. Similar results were reported by Reddy (2001), Neelam and Potdukhe (2002), Altaher and Singh (2003b), Karunakar Raju (2005), Leela Pratap (2006), Vijayalaxmi (2008), Neelima and Chenga Reddy (2008) and Srinivasulu (2009).

High heritability coupled with low genetic advance as per cent of mean was observed for this trait indicating the operation of non additive gene action and further improvement of these characters would be easier through heterosis breeding rather than simple selection. These results are in agreement with the findings of Sangeetha (1998), Reddy (2001), Ravikumar (2004), Muraleedhar (2005), Padmavathi (2008) and Srinivasulu (2009).

5.2.2 Plant height

The estimates of PCV and GCV were high for plant height. Patnaik *et al.* (2004), Tuteja *et al.* (2006) and Kalpande *et al.* (2008) also reported similar results for this character.

High heritability coupled with high genetic advance as per cent of mean was observed for this trait indicating the presence of additive gene action, and offers best possibility of improvement of this trait through simple selection. These findings are in agreement with the results of Sangeetha (1998), Neelam and Potdukhe (2002), Padmavathi (2008) and Srinivasulu (2009).

5.2.3 Number of monopodia plant⁻¹

The PCV and GCV values were high for number of monopodia per plant. Similar findings were reported by Neelam and Potdukhe (2002), Altaher and Singh (2003b), Kaushik *et al.* (2003), Sivaprasad *et al.* (2004b), Ravikumar (2004), Vijayalaxmi (2008) and Srinivasulu (2009).

High heritability coupled with high genetic advance as per cent of mean was observed for this trait indicating the role of additive gene action in the inheritance of this trait and simple selection will be highly rewarding for improving number of monopodia per plant. Similar findings were reported by Girase and Mehetre (2002), Kaushik *et al.* (2003), Karunakar Raju (2005), Leela Pratap (2006), Vijayalaxmi (2008) and Padmavathi (2008).

5.2.4 Number of sympodia plant⁻¹

The estimates of PCV and GCV were moderate for number of sympodia per plant. Similar results are reported by Sumathi and Nadarajan (1996), Valarmathi and Jehangir (1998), Altaher and Singh (2003b), Kiran (2003), Ravikumar (2004) and Padmavathi (2008).

Moderate heritability coupled with moderate genetic advance as per cent of mean was observed for this trait indicating the presence of non-additive gene action in the inheritance of this trait and further improvement of this character would be possible through heterosis breeding rather than simple selection. Neelam and Potdukhe (2002), Girase and Mehetre (2002), Kaushik *et al.* (2003), Ravikumar (2004) and Padmavathi (2008) reported high heritability coupled with high genetic advance, while Rao and Reddy (2001), Sivaprasad *et al.* (2004a) and Kumari and Chamundeswari (2005) reported low heritability coupled with low genetic advance.

5.2.5 Number of bolls plant⁻¹

High estimates of PCV and moderate estimates GCV were observed for number of bolls per plant and these are in accordance with the results of Laxman and Ganesh (2003), Gururajan and Sundar (2004), Narisireddy and Ratnakumari (2004), Ravikumar (2004), Sivaprasad *et al.* (2004 b), Neelima *et al.* (2005), Tuteja *et al.* (2006), Leela Pratap (2006) and Neelima and Chenga Reddy (2008) reported wider genetic variability, while Girase and Mehetre (2002) and Vijayalakshmi (2008) reported narrow genetic variability.

High heritability along with high genetic advance was observed for this character indicating the preponderance of additive gene action, which in turn denotes the feasibility of simple selection procedure for improving this trait. These findings are in accordance with the results obtained by Reddy (2001), Girase and Mehetre (2002), Neelam and Potdukhe (2002), Sivaprasad *et al.* (2004 a), Leela Pratap (2006), Vijayalaxmi (2008) and Padmavathi (2008).

5.2.6 Boll weight

The estimates of PCV and GCV were moderate for boll weight and the findings are in accordance with Rokadia *et al.* (1996), Sumathi and Nadarajan (1996), Jagtap and Mehetre (1998), Sangeetha (1998), Rao and Reddy (2001), Kiran (2003), Prasad (2003), Ravikumar (2004) and Padmavathi (2008).

High heritability coupled with high genetic advance was observed for boll weight indicating the role of additive gene action in the inheritance. This suggests that improvement of boll weight could be possible through simple selection. The studies conducted by Neelam and Potdukhe (2002), Neelima (2002), Kaushik *et al.* (2003),

Narisireddy and Ratnakumari (2004), Karunakar Raju (2005), Verma *et al.* (2006), Vijayalaxmi (2008) and Padmavathi (2008) also supported the findings of the present study.

5.2.7 Ginning outturn

The estimate of PCV was moderate and GCV was low for ginning outturn. These results are in accordance with Ravikumar (2004) and Neelima and Chenga Reddy (2008).

High heritability coupled with moderate genetic advance as per cent of mean was observed for this trait indicating the operation of both additive and non-additive genes and offers the best possibility of improvement through mass selection, progeny selection or any modified selection procedure aiming to exploit the additive gene effects. Prasad (2003), Sivaprasad *et al.* (2004a) and Srinivasulu (2009) reported low heritability coupled with low genetic advance, while Valarmathi and Jehangir (1998) and Gururajan and Sundar (2004) reported high heritability coupled with high genetic advance for this character.

5.2.8 Seed index

The phenotypic coefficient of variation and genotypic coefficient of variation were moderate for seed index. These results are in agreement with the findings of Jagtap and Mehetre (1998), Ravikumar (2004), Leela Pratap (2006), Vijayalaxmi (2008) and Padmavathi (2008).

High heritability coupled with moderate genetic advance as per cent of mean was observed indicating the presence of both additive and non-additive type of gene action and offers the best possibility of improvement through mass selection, progeny

selection or any modified selection procedure aiming to exploit the additive gene effects effectively. Rao and Reddy (2001), Ravikumar (2004), Karunakar Raju (2005), Vijayalaxmi (2008) and Padmavathi (2008) reported high heritability coupled with high genetic advance, while Reddy (2001), Gururajan and Sundar (2004) and Srinivasulu (2009) reported the high heritability coupled with low genetic advance.

5.2.9 Lint index

Moderate estimates of PCV and GCV were observed for lint index in the present study and these findings are in accordance with the results of Sumathi and Nadarajan (1996), Kiran (2003), Ravikumar (2004) and Padmavathi (2008).

High heritability coupled with high genetic advance was observed for this character suggesting the role of additive type of gene action in governing the inheritance of this trait. Thus, direct selection is effective for this trait. Similar results were reported by Reddy (2001), Neelima (2002), Karunakar Raju (2005), Sambamurthy *et al.* (2006), Vijayalaxmi (2008) and Padmavathi (2008).

5.2.10 2.5% Span length

The genotypic coefficient of variation and phenotypic coefficient of variation were low for 2.5% span length. Similar results were reported by Tuteja *et al.* (2006), Leela Pratap (2006), Verma *et al.* (2006), Vijayalaxmi (2008), Padmavathi (2008) and Srinivasulu (2009).

Moderate heritability coupled with low genetic advance as per cent of mean was recorded for this character indicating that this trait is controlled by non-additive genes and further improvement of this character would be possible through heterosis breeding rather than simple selection. Kiran (2003), Verma *et al.* (2006) and

Srinivasulu (2009) reported the high heritability coupled with low genetic advance, while Singh *et al.* (1987) and Prasad (2003) reported the low heritability coupled with low genetic advance for this trait.

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

The estimate of PCV was moderate and GCV was low for micronaire in the present study and these findings are in agreement with the results of Prasad (2003), Eswararao (2008), Vijayalaxmi (2008) and Srinivasulu (2009).

High heritability coupled with moderate genetic advance as per cent of mean was observed for this trait indicating the operation of both additive and non-additive gene action and offers the best possibility of improvement through mass selection, progeny selection or any modified selection procedure aiming to exploit the additive gene effects effectively. Rao and Reddy (2001) and Do Thi Ha An *et al.* (2008) reported high heritability with high genetic advance while, Reddy (2001) and Vijayalakshmi (2008) reported high heritability with low genetic advance.

5.2.12 Bundle strength

Low estimates of PCV and GCV were recorded for bundle strength and similar results are reported by Altaher and Singh (2003b), Karunakar Raju (2005), Leela Pratap (2006), Vijayalaxmi (2008) and Padmavathi (2008).

Moderate heritability coupled with low genetic advance as per cent of mean was recorded for this character indicating that this trait is controlled by non-additive genes and further improvement of this character would be possible through heterosis breeding rather than simple selection. Rao and Reddy (2001) and Kiran (2003) recorded high heritability and low genetic advance for this trait. While, Gururajan and

Sundar (2004), Sivaprasad *et al.* (2004a), Muraleedhar (2005), Vijayalaxmi (2008) and Padmavathi (2008) reported low heritability and low genetic advance for this character.

5.2.13 Uniformity ratio

The estimates of PCV and GCV were low for uniformity ratio. Similar findings were reported by Muraleedhar (2005), Karunakar Raju (2005), Leela Pratap (2006), Vijayalaxmi (2008), Neelima and Chenga Reddy (2008) and Srinivasulu (2009).

Moderate heritability coupled with low genetic advance as per cent of mean was noted for this character indicating that this trait is controlled by non-additive genes and further improvement of this character would be possible through heterosis breeding rather than simple selection. Sangeetha (1989), Kiran (2003) and Karunakar Raju (2005) reported high heritability and low genetic advance while, Muraleedhar (2005), Vijayalakshmi (2008) and Srinivasulu (2009) reported low heritability and low genetic advance.

5.2.14 Fibre elongation (%)

The estimates of PCV and GCV were low for fibre elongation. Similar findings were reported by Valarmathi and Jehangir (1998), Ravi Kumar (2004), Muraleedhar (2005), Vijayalaxmi (2008), Padmavathi (2008) and Srinivasulu (2009).

Presence of high heritability coupled with low genetic advance as per cent of mean indicates that this trait is controlled by both additive and non-additive genes and further improvement of this character would be easier through heterosis breeding rather than simple selection and these results are in agreement with the findings of Vijayalaxmi (2008) and Srinivasulu (2009).

5.2.15 Seed cotton yield plant⁻¹

High estimates of PCV and moderate GCV were observed for seed cotton yield per plant. This was in line with the findings of Narisireddy and Ratnakumari (2004), Neelima *et al.* (2005), Karunakar Raju (2005), Leela Pratap (2006), Verma *et al.* (2006), Vijayalaxmi (2008), Padmavathi (2008) and Srinivasulu (2009).

High heritability coupled with high genetic advance as per cent of mean recorded for this trait indicating the operation of additive genes in the inheritance of seed cotton yield and directional selection for this trait in genetically diverse material could be effective for desired genetic improvement. This finding is in conformity with the results obtained by Girase and Mehetre (2002), Kaushik *et al.* (2003), Sivaprasad *et al.* (2004 a), Karunakar Raju (2005), Tuteja *et al.* (2006), Vijayalaxmi (2008), Padmavathi (2008) and Srinivasulu (2009).

In the present study, wide variability in terms of PCV and GCV was recorded for the characters plant height, number of monopodia per plant, number of bolls per plant and seed cotton yield per plant (kg/ha); variability was moderate for number of sympodia per plant, boll weight, ginning outturn, seed index, lint index and micronaire and low variability was recorded for days to 50% flowering, 2.5% span length, bundle strength, uniformity ratio and fibre elongation. 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). High heritability coupled with high genetic advance indicates operation of additive genes as in the case of plant height, number of monopodia per plant, number of bolls per plant, boll weight, lint index and seed cotton yield per plant and directional selection for these traits in genetically diverse material could be effective for desired genetic

improvement. Moderate genetic advance along with high or medium heritability indicates action of both additive and non-additive genes as in the case of number of sympodia per plant, ginning out turn, seed index and micronaire, which offers the best possibility of improvement through mass selection, progeny selection, family selection or any other suitable modified selection procedure aiming to exploit additive gene effects effectively. Low genetic advance irrespective of heritability indicates action of non-additive genes, which indicates that further improvement of these characters may not be possible through selection, but possible through heterosis breeding (Panse, 1957), as seen in the case of days to 50% flowering, 2.5% span length, bundle strength, uniformity ratio and fibre elongation in the present study.

5.3 CHARACTER ASSOCIATION

Seed cotton yield 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 associations among themselves and also with yield. Unfavourable associations between the desirable attributes under selection may limit genetic advance and hence, knowledge of extent of associations between yield and yield components and also among themselves helps in planning a sound selection programme for improvement in yield through indirect selection for component traits.

In the present study, correlation estimates were obtained for 15 characters in 60 genotypes of cotton and the results are discussed here under.

Genotypic correlations in general are higher than phenotypic correlations. This may be due to the relative stability of genotypes as majority of them were subjected to certain amount of selection (Johnson *et al.*, 1955).

5.3.1 Days to 50% flowering

Days to 50% flowering showed significant positive association with number of monopodia per plant, number of sympodia per plant, boll weight, seed index and seed cotton yield per plant at both genotypic and phenotypic levels. Ginning outturn, uniformity ratio and fibre elongation showed significant negative association at both phenotypic and genotypic levels and number of bolls per plant showed significant negative association only at genotypic level, which indicates masking effect of environment on above character. These results indicated that an increase in days to 50% flowering would bring a decrease in seed cotton yield. Hence, simultaneous improvement of seed cotton yield is not possible through days to 50% flowering. These results are in agreement with Reddy (2001), Muraleedhar (2005) Leela Pratap *et al.* (2007) and Padmavathi (2008).

5.3.2 Plant height

At genotypic level, this trait showed significant positive association with number of sympodia per plant, seed index, micronaire, bundle strength and uniformity ratio revealing that the correlation among all these characters may have influence of environment. These results are in conformity with Samanc and Ozkaynak (2000), Muthu *et al.* (2004), Tuteja *et al.* (2006) and Srinivasulu (2009).

5.3.3 Number of monopodia plant⁻¹

Number of monopodia per plant recorded significant positive association with boll weight, lint index and seed cotton yield per plant at phenotypic and genotypic levels, which indicates simultaneous improvement of these traits is possible where as ginning outturn showed significant positive association at genotypic level only which indicates masking effect of environment on these traits. Uniformity ratio and number of sympodia per plant showed significant negative association at genotypic level only. Similar results are reported by Kaushik *et al.* (2003), Altaher and Singh (2003b), Leela Pratap *et al.* (2007), Padmavathi (2008) and Srinivasulu (2009).

5.3.4 Number of sympodia plant⁻¹

At both genotypic and phenotypic levels, this trait showed significant positive association with seed index, micronaire, uniformity ratio and seed cotton yield per plant which indicates simultaneous improvement is possible. While ginning outturn at genotypic level and fibre elongation at both levels showed significant negative association which indicates masking effect of environment on ginning outturn and fibre elongation. These results are in accordance with Neelima (2002), Alather and Singh (2003b), Neelima *et al.* (2005), Tuteja *et al.* (2006), Padmavathi (2008) and Srinivasulu (2009).

5.3.5 Number of bolls plant⁻¹

Both genotypic and phenotypic correlations revealed that number of bolls per plant had strong significant positive association with seed cotton yield per plant indicating this trait is one of the main component selection criteria to improve seed cotton yield. Boll weight, seed index, lint index and bundle strength showed

significant negative association with number of bolls per plant at both levels. This indicates masking effect of environment on these traits. Selection for this trait will lead to antagonistic effect on above characters. These results are in conformity with Rao *et al.* (2001), Karunakar Raju (2005), Leela Pratap *et al.* (2007), Eswararao (2008), Padmavathi (2008), Vijayalaxmi (2008) and Srinivasulu (2009).

5.3.6 Boll weight

At both genotypic and phenotypic levels, this trait showed significant positive association with seed cotton yield per plant. Significant positive association of this trait with seed cotton yield per plant indicates improvement of seed cotton yield per plant may be achieved if this trait is selected as one of the parameter.

It also showed significant positive association with ginning outturn, seed index, lint index, 2.5% span length, micronaire, bundle strength and uniformity ratio which indicates simultaneous improvement of these characters will be possible with boll weight. This trait showed significant negative association with fibre elongation at both phenotypic and genotypic levels. These findings are in accordance with Sivaprasad (2003), Muthu *et al.* (2004), Neelima *et al.* (2005), Karunakar Raju (2005), Murthy *et al.* (2006), Do Thi Ha An *et al.* (2008), Eswararao (2008), Padmavathi (2008), Vijayalaxmi (2008) and Srinivasulu (2009).

5.3.7 Ginning outturn

Ginning outturn recorded significant positive association with lint index and seed cotton yield per plant both at genotypic and phenotypic levels indicating that this trait may be considered if the above traits were to be improved. Simultaneous improvement of seed index and bundle strength with ginning outturn is not possible

since they recorded significant negative association. The results of the present study are in agreement with previous reports of Muthu *et al.* (2004), Karunakar Raju (2005), Leela Pratap *et al.* (2007) and Vijayalaxmi (2008).

5.3.8 Seed index

Both the genotypic and phenotypic correlations revealed that seed index showed significant association with lint index and micronaire. It indicates that it is possible to improve above characters with seed index.

These results are in conformity with reports of Muthuswamy and Vivekanandan (2004), Karunakar Raju (2005), Neelima *et al.* (2005), Leela Pratap *et al.* (2007), Eswararao (2008), Padmavathi (2008), Vijayalaxmi (2008) and Srinivasulu (2009).

5.3.9 Lint index

This trait showed significant positive association with seed cotton yield per plant at genotypic and phenotypic levels. At both levels, it showed significant negative association with fibre elongation. Since they recorded significant positive association, improvement in this trait will result in increased seed cotton yield per plant. Similar results are reported by Sambamurthy *et al.* (2006), Leela Pratap *et al.* (2007) and Padmavathi (2008).

5.3.10 2.5% Span length

At both genotypic and phenotypic levels, this trait showed significant positive association with bundle strength and showed significant negative association with uniformity ratio. As significant negative association of 2.5% span length existed with

micronaire, greater care is required in selection programme for improvement of this character simultaneously. However, bundle strength could be improved simultaneously as it showed positive association. These results are in agreement with reports of Muraleedhar (2005), Karunakar Raju (2005), Tuteja *et al.* (2005b) and Padmavathi (2008).

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

Micronaire showed significant positive association with uniformity ratio, so simultaneous improvement of micronaire is possible through uniformity ratio. It showed significant negative association with fibre elongation at both levels. This may be due to masking effect of environment. Karunakar Raju (2005) and Padmavathi (2008) reported similar association between micronaire and uniformity ratio.

5.3.12 Bundle strength (g/tex)

At both genotypic and phenotypic levels, this trait showed significant positive association with fibre elongation. Ravikumar (2004), Muraleedhar (2005) and Padmavathi (2008) reported similar results for bundle strength and fibre elongation.

5.3.13 Uniformity ratio

At both genotypic and phenotypic levels, this trait showed significant positive association with seed cotton yield per plant. This trait showed significant negative association with fibre elongation at both phenotypic and genotypic levels indicating simultaneous improvement is not possible and economic balance has to be made among these traits. These findings are in accordance with Muraleedhar (2005) and Srinivasulu (2009).

5.3.14 Fibre elongation (%)

Fibre elongation showed significant negative association with seed cotton yield per plant at both phenotypic and genotypic levels.

5.3.15 Seed cotton yield plant⁻¹

The character association studies indicated that number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, ginning outturn, lint index and uniformity ratio found to have significant positive association with seed cotton yield plant⁻¹ at both phenotypic and genotypic levels. 2.5% span length showed significant positive association at genotypic level only. Improvement in seed cotton yield may be possible if these characters are considered in selection programme.

The genetic factors responsible for correlated response are linkage and pleiotropy. Magnitude of correlation due to pleiotropy depends upon the direction of their effects. In the present study, two correlated characters were also correlated with yield and these led to inference that association among different characters was mostly due to pleiotropy. In some cases, one character was correlated with yield while other was not correlated with yield which led to the inference that the association among the different characters were mostly due to linkage and not due to pleiotropy which was supported by the fact that the genetic variability parameters for some of the characters correlated with yield were not of same magnitude as that of yield (Mallikarjun *et al.*, 2003).

5.4 PATH COEFFICIENT ANALYSIS

The observed correlation between yield and its component character is the net result of the direct and indirect effects of the component character through other yield attributes. The total correlation coefficient between yield and its component characters may sometimes be misleading, as it may be an over or under estimate of its association with other characters. In these cases, direct selection on the basis of correlated response may not be fruitful. For critical evaluation, the correlation coefficient need to be split into direct and indirect effects using path coefficient analysis since, many characters affect a given trait. Thus, the correlation and path coefficients in combination can give a better insight into cause and effect relationship between different pairs of characters.(Dewey and Lu 1959).

As a guideline for interpretation of the results of path analysis, the following broad points may be kept in view (Singh and Chaudhary, 1977).

- If the correlation coefficient between a causal factor and the effect is almost equal to its direct effect, then correlation explains the true relationship and a direct selection through this trait will be effective.
- If the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effects seem to be the cause of positive correlation. In such situations, the indirect causal factors are to be considered simultaneously for selection.
- Correlation coefficient may be negative but the direct effect is positive and high. Under these circumstances, 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 the direct effect.

- If correlation coefficient is negative and direct effect is also negative, then we have to drop the selection based on that character.

The residual effect determines how best the causal factors account for the variability of the dependent factor. If the residual effect is high, some other factors which have not been considered in the study need to be included in the analysis to account fully for the variation in yield.

Based on the above, the characters subjected to correlations were also subjected to path coefficient analysis for estimating the direct and indirect effects so as to formulate a basis for selection in cotton. The results are discussed character-wise hereunder.

5.4.1 Days to 50% flowering

Days to 50% flowering exhibited negative direct effect (-0.0215) and positive phenotypic correlation with seed cotton yield per plant (0.1038). It had positive indirect effects through plant height (0.0020), number of monopodia per plant (0.0138), number of sympodia per plant (0.0118), boll weight (0.1500), seed index (0.0244), lint index (0.0167), micronaire (0.0006), uniformity ratio (0.0003) and fibre elongation (0.0104).

Hence, direct effect along with indirect positive effects are to be considered to bring about improvement in seed cotton yield. These results are in agreement with Gururajan (2000), Neelima (2002), Altaher and Singh (2003b), Muthu *et al.* (2004) and Anandan (2009).

5.4.2 Plant height

Plant height recorded negative direct effect (-0.0542) and positive phenotypic nonsignificant correlation with seed cotton yield per plant (0.0803). It had negative indirect effects through number of monopodia per plant (-0.0033), ginning outturn (-0.0594) and uniformity ratio (-0.0005) and positive indirect effects through days to 50% flowering (0.0008), number of sympodia per plant (0.0450), number of bolls per plant (0.0150), boll weight (0.0632), seed index (0.0460), lint index (0.0085), micronaire (0.0036), bundle strength (0.0099) and fibre elongation (0.0056).

Though direct effect is negative and low, positive correlation might have resulted due to out weighing positive indirect effects. These results are in conformity with Gururajan (2000), Muthu *et al.* (2004), Vijayalakshmi (2008) and Padmavathi (2008).

5.4.3 Number of monopodia plant⁻¹

Number of monopodia per plant exhibited negative direct effect (0.1057) and positive significant phenotypic correlation with seed cotton yield per plant (0.2428**). It had negative indirect effects through days to 50% flowering (-0.0028), number of sympodia per plant (-0.0096), lint index (-0.0326), 2.5% span length (-0.0001), micronaire (-0.0012), bundle strength (-0.0051) and fibre elongation (-0.0060) which have outweighed by the positive indirect effects of plant height (0.0017), number of bolls per plant (0.0126), boll weight (0.1410), ginning outturn (0.0307), seed index (0.0082) and uniformity ratio (0.0002) resulting in positive correlation.

Hence, greater emphasis in selection should be based on the above traits, which showed high positive indirect effects when number of monopodia per plant is used as one of the selection criteria in seed cotton yield improvement. The results were in accordance with Sivaprasad (2003), Karunakar Raju (2005), Tuteja *et al.* (2006), Verma *et al.* (2006), Eswararao (2008) and Srinivasulu (2009).

5.4.4 Number of sympodia plant⁻¹

Number of sympodia per plant showed positive direct effect (0.0879) and positive significant phenotypic correlation with seed cotton yield per plant (0.1653**). It had positive indirect effects through number of bolls per plant (0.0470), boll weight (0.0583), seed index (0.0342), micronaire (0.0032), bundle strength (0.0070) and fibre elongation (0.0095).

Though correlation is positive and significant, direct effect is low. Hence, indirect positive effects are to be considered to bring about improvement in seed cotton yield. These results are in agreement with Neelima *et al.* (2005), Verma *et al.* (2006), Leela Pratap *et al.* (2007), Padmavathi (2008) and Srinivasulu (2009).

5.4.5 Number of bolls plant⁻¹

Number of bolls per plant exhibited positive direct effect (0.6401) and significant positive phenotypic correlation with seed cotton yield per plant (0.4136**). It had positive indirect effects through days to 50% flowering (0.0020), number of monopodia per plant (0.0021), number of sympodia per plant (0.0065), lint index (0.0391) and fibre elongation (0.0012).

This explains true relationship and a direct selection through number of bolls per plant will be effective for seed cotton yield improvement. Similar results were reported by Karunakar Raju (2005), Neelima *et al.* (2005), Verma *et al.* (2006), Leela Pratap *et al.* (2007), Padmavathi (2008) and Srinivasulu (2009).

5.4.6 Boll weight

Boll weight exhibited positive direct effect (0.7100) and positive significant phenotypic correlation with seed cotton yield per plant (0.5670**). It had positive indirect effects through number of monopodia per plant (0.0210), number of sympodia per plant (0.0072), ginning outturn (0.0382), seed index (0.0300), 2.5% span length (0.0003), micronaire (0.0017), bundle strength (0.0083) and fibre elongation (0.0187).

Direct selection for seed cotton yield through this trait will be rewarding. Similar results were earlier reported by Muthu *et al.* (2004), Gururajan and Sundar (2004), Karunakar Raju (2005), Sakthi *et al.* (2007), Padmavathi (2008) and Srinivasulu (2009).

5.4.7 Ginning outturn

Ginning outturn exhibited positive direct effect (0.2513) and positive significant phenotypic correlation with seed cotton yield per plant (0.1605**). It had positive indirect effects through days to 50% flowering (0.0037), plant height (0.0128), number of monopodia per plant (0.0129), boll weight (0.1080), uniformity ratio (0.0001) and fibre elongation (0.0089). Direct selection for seed cotton yield through this trait will be rewarding. These results are in agreement with Gururajan (2000), Sivaprasad (2003), Tuteja *et al.* (2005a) and Anandan (2009).

5.4.8 Seed index

Seed index showed direct positive effect (0.1610) and nonsignificant negative phenotypic correlation with seed cotton yield per plant (-0.0277). It showed positive indirect effects through number of monopodia per plant (0.0054), number of sympodia per plant (0.0187), boll weight (0.1323), 2.5% span length (0.0002), micronaire (0.0022), bundle strength (0.0063) and fibre elongation (0.0060). Though direct effect is high, correlation was negative and nonsignificant hence indirect effects are to be considered to bring about improvement in seed cotton yield. These results are in accordance with Rao *et al.* (2001), Sivaprasad (2003), Eswararao (2008), Padmavathi (2008) and Anandan (2009).

5.4.9 Lint index

Lint index exhibited negative direct effect (-0.1894) and significant positive phenotypic correlation with seed cotton yield per plant (0.1689**). It had negative indirect effects through number of bolls per plant (-0.1320), 2.5% span length (-0.0001) and bundle strength (-0.0043) which have outweighed by the positive indirect effects of days to 50% flowering (0.0019), plant height (0.0024), number of monopodia per plant (0.0182), number of sympodia per plant (0.0049), boll weight (0.2239), ginning outturn (0.1893), seed index (0.0392), micronaire (0.0011) and fibre elongation (0.0136) resulting in positive correlation.

Hence, greater emphasis in selection should be placed on the above traits, which showed positive indirect effects, when lint index is used as one of the selection criteria in seed cotton yield improvement. These findings are in agreement with Sivaprasad (2003), Muthu *et al.* (2004), Leela Pratap *et al.* (2007) and Padmavathi (2008).

5.4.10 2.5% Span length

2.5% span length exhibited positive direct effect (0.0023) and non significant positive phenotypic correlation with seed cotton yield per plant (0.0861). Negative indirect effects were recorded for the characters number of monopodia per plant (-0.0034), number of bolls per plant (-0.0239), ginning outturn (-0.0203), micronaire (-0.0013), bundle strength (-0.0085) and fibre elongation (-0.0001). As the direct effect is positive but low and correlation is also positive and non significant this character can be considered in seed cotton yield improvement programme. Similar results were reported by Ladole and Meshram (2000), Muthu *et al.* (2004), Vijayalakshmi (2008), Anandan (2009).

5.4.11 Micronaire

Micronaire exhibited positive direct effect (0.0128) and nonsignificant positive phenotypic correlation with seed cotton yield per plant (0.1194). It had positive indirect effects through number of sympodia per plant (0.0222), boll weight (0.0936), seed index (0.0275) and fibre elongation (0.0215). Though direct effect was positive and low, it showed nonsignificant correlation. So, micronaire is of little importance in seed cotton yield improvement. These results are in conformity with Neelima *et al.* (2005), Sambamurthy *et al.* (2006), Leela Pratap *et al.* (2007) and Padmavathi (2008).

5.4.12 Bundle strength

Bundle strength exhibited positive direct effect (0.0546) and positive nonsignificant phenotypic correlation with seed cotton yield per plant (0.0513). Positive indirect effects were recorded for the characters, days to 50% flowering (0.0008), number of sympodia per plant (0.0112), boll weight (0.1075), seed index

(0.0187), lint index (0.0150) and 2.5% span length (0.0003). Though direct effect with seed cotton yield was positive and low, it showed nonsignificant correlation with seed cotton yield. So bundle strength is of little importance in seed cotton yield improvement. Similar results were reported by Sivaprasad (2003), Sambamurthy *et al.* (2006) and Padmavathi (2008).

5.4.13 Uniformity ratio

Uniformity ratio exhibited negative direct effect (-0.0021) and significant positive phenotypic correlation with seed cotton yield per plant (0.2022**). It had positive indirect effects through days to 50% flowering (0.0027), number of sympodia per plant (0.0217), numbers of bolls per plant (0.0779), boll weight (0.1102), seed index (0.0111), lint index (0.0045), micronaire (0.0065) and fibre elongation (0.0193) which over weighed the negative indirect effects of plant height (-0.0124), number of monopodia per plant (-0.0115), ginning outturn (-0.0181), 2.5% span length (-0.0003) and bundle strength (-0.0073). Though correlation was positive and significant, direct effect was low and negative. So, uniformity ratio had little importance in seed cotton yield improvement. Similar results were reported by Muthu *et al.* (2004), Leela Pratap *et al.* (2007) and Padmavathi (2008).

5.4.14 Fibre elongation

Fibre elongation exhibited negative direct effect (-0.0640) and significant negative phenotypic correlation with seed cotton yield per plant (-0.2834**). It showed positive indirect effects through days to 50% flowering (0.0035), plant height (0.0048), number of monopodia per plant (0.0099), lint index (0.0403), bundle strength (0.0083) and uniformity ratio (0.0006) which outweighed the negative indirect effects of number of sympodia per plant (-0.0130), number of bolls per plant

(-0.0124), boll weight (-0.2072), ginning outturn (-0.0348), seed index (-0.0151) and micronaire (-0.0043). Similar results were reported by Muraleedhar (2005) and Padmavathi (2008).

The path analysis indicated that number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, ginning outturn, seed index, micronaire and bundle strength had direct positive effects on seed cotton yield per plant.

In plant breeding, it is very difficult to have complete knowledge of all component traits of yield. The residual effect permits precise explanation about the pattern of interaction of other possible components of yield. In other words, residual effect measures the role of the possible independent variables which were not included in the study on the dependent variable. In the present study, the residual effect observed was 0.5225 at phenotypic and 0.6957 at genotypic levels, which explains the importance of some other characters which were not included in the present study. Based on the results of path analysis, the present study revealed that major emphasis should be laid on selection process with more number of bolls per plant and boll weight and there should be economic balance among these traits to get higher seed cotton yield per plant.

5.5 GENETIC DIVERGENCE

For a successful breeding programme, the diversity of parents is of utmost importance, since the crosses between the parents with maximum genetic divergence would more likely to yield desirable recombinants in the segregating progenies. However, it is desirable to select suitable genetically divergent parents, based on the information about the genetic variability and genetic diversity present in the available germplasm for exploitation of heterosis.

Generally, geographical diversity was considered as a measure of genetic diversity when no scientific tools were available. However, this is an inferential criterion and may not be used for discrimination among the populations occupying ecologically marginal habitats (Arunachalam and Ram, 1967).

The multivariate analysis like Mahalanobis' D^2 statistic and principal component analysis provides useful statistical tool for measuring the genetic diversity in a given population with respect to the characters that were considered together. Further, the problem of selecting diverse parents for hybridization programme can be narrowed, if one can identify the characters responsible for the discriminations between the populations.

The data collected in the present study was subjected to multivariate analysis *i.e.*, Mahalanobis' D^2 statistic, principal component and cluster analysis. The magnitude of values suggested that there was considerable variability in the material studied, which led to genetic diversity.

5.5.1 Mahalanobis' D^2 analysis

In the present investigation, based on the D^2 values for all 1770 pairs of genotypes, 60 genotypes were grouped into nine 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 number of monopodia plant⁻¹ (39.72), plant height (16.55), fibre elongation (8.93), boll weight (7.23), seed index (5.65), seed cotton yield plant⁻¹

(5.31), days to 50% flowering (4.24), number of bolls plant⁻¹ (3.16), lint index (2.26), ginning outturn (2.20), bundle strength (1.64), micronaire (1.47) and 2.5% Span length (1.24).

The distribution of 60 genotypes into nine clusters was at random with maximum number of genotypes in cluster I (15 genotypes) from different locations. Cluster II was the second largest with 13 genotypes followed by cluster III with 12 genotypes, cluster V with 11 genotypes and cluster IX with 5 genotypes which also exhibited similar type of diversity. The clusters IV, VI, VII, and cluster VIII were solitary and 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.

The intra- and inter- cluster distances revealed that inter- cluster distance values were greater than intra-cluster distance values. Cluster IX (48.25) had maximum intra-cluster distance followed by cluster V (47.97), cluster III (37.36), cluster II (23.44) and cluster I (14.94). Four clusters (cluster IV, VI, VII and VIII) which were solitary had no intra-cluster distances. The high intra-cluster distance in cluster IX indicates the presence of wide genetic diversity among the genotypes present within this cluster.

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). Therefore, it would be desirable to attempt crosses between genotypes belonging to distant clusters for getting highly heterotic crosses which are likely to yield a wide range of segregants on which selection can be practiced.

In the present study, inter-cluster distances were worked out considering 15 characters and these distances ranged from 19.27 (between clusters VII and VI) to 128.82 (between clusters V and VII).

The inter-cluster distance was maximum between cluster V and VII (128.82) followed by cluster V and IX (125.35), cluster IV and IX (112.56), cluster VIII and IX (112.41), cluster IV and VII (111.91), cluster III and IX (105.32), III and VII (98.78), I and IX (94.17) and I and VII (91.36). This suggested that there is wide genetic diversity between these clusters. Based on these studies crosses can be made between genotypes of these clusters to obtain desirable transgressive segregants.

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

Cluster VIII (NDLH-1101) recorded high mean values for number of bolls per plant (42.84), boll weight (4.96), ginning outturn (40.12), lint index (6.46), micronaire (4.98), uniformity ratio (53.43) and seed cotton yield per plant (179.02) and it was farthest from cluster IX (112.41) (KDCAKD, CCH-18, L-713, Tx Lama and GJHV-01/35) followed by cluster VII (84.38) (G-204-13). Therefore, crosses can be made among the desirable genotypes of these clusters to obtain desirable segregants for the important economic attributes.

The success and usefulness of Mahalanobis' D^2 analysis in quantifying genetic divergence has been studied by Rajarathinam *et al.* (1994), Sumathi and Nadarajan (1995), Kalsy and Garg (1995), Murthy *et al.* (1995a,b), Kumar *et al.* (2000), Jain and Yadav (2001), Gururajan and Manickam (2002), Altaher and Singh (2003b), Kiran

(2003), Ravikumar (2004), Pushpam *et al.* (2004), Muraleedhar (2005), Eswararao (2008), Padmavathi (2008), Vijayalaxmi (2008), Gopinath *et al.* (2009) and Srinivasulu (2009).

5.5.2 Principal Component Analysis

Results obtained from principal component analysis on the correlation matrix of the traits reduce the dimensionality of the data set by creating seven 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 eight principal components with eigen value more than one contributed 87.928 per cent of the variability amongst 60 genotypes evaluated for 15 traits. Other principal components had eigen values less than one, which were considered as nonsignificant and were ignored as they are unlikely to have any practical significance (Legendre and Legendre, 1984).

These results are in accordance with the reports of Altaher and Singh (2003a) where eight principal components were formed to describe the maximum variance of the data set.

First principal component (PC_1) described maximum variability (21.415%). Characters *viz.*, number of monopodia per plant (0.419), ginning outturn (0.352), seed index (0.298), uniformity ratio (0.262), bundle strength (0.229) and lint index (0.223) explained maximum variance in first principal component.

The second principal component (PC₂) described 14.688 per cent of total variance and it reflected significant loading of boll weight (0.486), number of sympodia per plant (0.396), plant height (0.395), bundle strength (0.337), seed index (0.256) and micronaire (0.251).

The third principal component (PC₃) was characterized by 12.154 per cent contribution towards the total variability. Characters *viz.*, 2.5% span length (0.406), seed cotton yield per plant (0.359), lint index (0.336), boll weight (0.263) and seed index (0.242) showed the maximum variance in this principal component.

The fourth principal component (PC₄) was characterized by conspicuously high loading of fibre elongation (0.409), micronaire (-0.396), number of bolls per plant (-0.345), ginning outturn (-0.325) and days to 50% flowering (0.319). Contribution of this principal component towards the total variability was 11.501 per cent.

Similarly fifth principal component (PC₅) contributed 9.401 per cent and towards total variability of the study material. High loading value of seed cotton yield per plant (-0.433), uniformity ratio (0.414), micronaire (0.390), ginning outturn (-0.342), number of monopodia per plant (-0.303), boll weight (-0.237) and 2.5% span length (0.233) in PC₅ was observed.

PC₆ was characterized by high loading value of days to 50% flowering (0.619), lint index (-0.514), seed index (-0.307) and number of sympodia per plant (-0.302). Contribution of this component was 7.191 per cent towards total variability.

Similarly, principal components seventh (PC₇) and eighth (PC₈) contributed 6.730 per cent and 4.849 per cent, respectively towards total variability of the study material. High loading value of bundle strength (-0.526), uniformity ratio (-0.514), fibre elongation (-0.479), and number of bolls per plant (-0.256) in PC₇ was observed whereas, PC₈ had high loading value of days to 50% flowering (0.499), number of bolls per plant (0.422), lint index (0.422), boll weight (-0.352), uniformity ratio (-0.334) and micronaire (0.243).

The analysis thus identified the maximum contributing variables *i.e.*, number of bolls per plant, seed index, micronaire, uniformity ratio, boll weight, lint index, 2.5% span length, bundle strength, days to 50% flowering, plant height, number of monopodia per plant, number of sympodia per plant, ginning outturn and fibre elongation in principal component analysis. It is important for studying the variance as the relative contributions are more important than the signs (indicative of direction) in principal component analysis.

The PCA scores for 60 cotton genotypes were plotted in graph to get the 2 D and 3D scattered diagram. These graphs showed wide divergence between the genotypes, ADB-28 and WGP-8 from GJHV-01/35 and G-204-13 signifying their usefulness in cotton breeding.

The success and usefulness of principal component analysis was carried out in cotton earlier by Altaher and Singh (2003a), Karunakar Raju *et al.* (2005), Muraleedhar *et al.* (2005), Vijayalakshmi (2008), Padmavathi (2008) and Srinivasulu (2009).

5.5.3 Hierarchical cluster analysis

The cluster analysis using Euclidean² distance provides a useful statistical tool for measuring the genetic diversity in germplasm collections with respect to the characters considered together.

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 Euclidean² distance (dissimilarity coefficients). 60 genotypes were grouped into eight clusters and distributions of various genotypes into various clusters were at random indicating the geographical diversity and genetic diversity were not related. Among all the clusters, cluster II was the largest one containing 12 genotypes followed by cluster VI with 10 genotypes, clusters III, IV and V with 8 genotypes, cluster VII with 7 genotypes each, cluster I with 6 genotypes and cluster VIII with 1 genotype.

Of the eight clusters formed, the maximum inter-cluster distance was observed between cluster I (NH-577, WGP-8, IC-356932, A-7262, L-614 and TXORHY-1-78) and cluster VIII (GJHV-01/35) (755.56) followed by cluster IV (NDLH-849, NDLH-1905, Female-287/08, NARASIMHA, HS-6/08, H-1098/08, Male-2097/08 and CPD-1050) and cluster VIII (GJHV-01/35) (515.67) and cluster II (NDLH-779, L-801, NA-1325, H-1098-1/08, NH-615, ADB-28, GSHY-01/1338, KH-121, P-21-15, NH-545, TSH-333 and CNDJS-55) and cluster VIII (GJHV-01/35) (477.96). This suggested that there is 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 principal component analysis on a visual aid in delineating clusters in the 2 D and 3 D scattered diagrams. The genotypes falling in same cluster were present closer to each other in scattered diagram.

Brown (1991), Altaher and Singh (2003a), Karunakar Raju *et al.* (2005), Muraleedhar *et al.* (2005), Padmavathi (2008) and Srinivasulu (2009) also studied the utilization of principal component analysis combined with clustering of Ward's method in genetic divergence studies in cotton.

Among eight clusters, cluster VIII recorded high mean value for days to 50% flowering (61.66), number of monopodia plant⁻¹ (2.83) ginning outturn (38.15), lint index (5.67), micronaire (4.75) and seed cotton yield plant⁻¹ (140.07). Whereas cluster I recorded, low mean value for number of monopodia plant⁻¹ (0.32), lint index (4.45) and micronaire (3.87). So, the genotypes from these clusters can be used for cotton yield improvement. Among the quality attributes, high mean values for 2.5% span length (28.20) and uniformity ratio (50.73) were recorded in cluster IV. So, the genotypes in these clusters can be used for cotton fibre improvement. Cluster VIII recorded low mean value for 2.5% span length (25.74). So, the crosses between these two distant clusters (cluster IV and VIII) may produce transgressive segregants for 2.5% span length. As far as uniformity ratio is concerned, cluster IV and cluster VII recorded high and low mean values for this character. For bundle strength improvement crosses can be made between cluster V and VIII.

5.5.4 Comparative study of both D² analysis, principal component analysis and cluster analysis

The grouping or clustering pattern using the D² analysis, principal component analysis and cluster analysis was compared and the implications are discussed here.

All the three methods of grouping revealed a single concept of non correspondence of genetic divergence and geographic diversity. In D² analysis, the intra-and inter-cluster distances are low while in the cluster analysis the distances are high. This is same with the utilization of correlation matrix in principal component analysis derived from covariance matrix. This standardization made the principal component analysis to support the cluster analysis.

Mahalanobis' D² statistic and Jackson's principal component analysis both are the tools for analyzing multivariate data. The advantage of PCA over D² 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 15 attributes. The contribution of the main characters for variance easily identified by the characters loaded on the PC₁ with high loading values. PCA facilitates the in depth analysis for genetic diversity. In D² analysis, number of monopodia per plant followed by plant height, fibre elongation, boll weight, seed index, seed cotton yield per plant and days to 50% flowering contributed maximum for the divergence. While in PCA the characters *viz.*, number of monopodia per plant,

ginning outturn, number of bolls per plant, 2.5% Span length, seed index, number of sympodia per plant, uniformity ratio, seed cotton yield per plant, bundle strength and lint index were significantly loaded in PC₁ and contributed more towards variability. It can be concluded that the characters which contributed more towards divergence in D² analysis were loaded in PC₁.

D² analysis grouped the 60 cotton genotypes into 9 clusters, where as Ward's method grouped them into 8 clusters. In D² analysis, cluster I is the largest with 15 genotypes followed by cluster II, cluster III and cluster V, where as in Ward's method, the cluster II is the largest comprising of 12 genotypes followed by cluster VI (10 genotypes), cluster III, IV and V (8 genotypes each).

The pattern of distribution of genotypes into different clusters was at random. Furthermore, the two clustering methods grouped differently and clustering pattern for genotypes are not same. In both the cases, solitary clusters were formed but number of solitary clusters was three (VI, VII and VIII) in D² analysis and only one solitary cluster (VIII) was present in Ward's minimum variance method. Genetic diversity was the outcome of several factors along with geographic diversity. Hence, the selection for hybridization should be more based on generic diversity rather than geographic diversity.

Ward's minimum variance dendrogram (cluster analysis) created sub-groups within a cluster, so relative position of the genotypes within the cluster can be determined by seeing the dendrogram distance. In case of D² analysis, the intra-cluster distance but not the genotypes relative position in the respective cluster is known.

FUTURE LINE OF WORK

The sixty germplasm lines showed variability for many of the morphological characters and can be used for varietal identification and IPR protection. The correlation and path coefficient analyses together indicated that number of bolls plant⁻¹, boll weight and ginning outturn had significant positive association with seed cotton yield per plant.

The genotypes showed NH-577, WGP-8, IC-356932, A-7262, L-614 and TXORHY-1-78 showed maximum inter-cluster distance in all the three divergence methods. So they can be exploited for the development of heterotic hybrids after testing their combining ability.

CHAPTER VI

SUMMARY

The present investigation was carried out during *kharif* 2009-10 at Agricultural College Farm, Bapatla, with 60 genotypes of cotton (*Gossypium hirsutum* L.).

A systematic effort was made to study the genetic variability, divergence, character association and path analyses of yield components with seed cotton yield in sixty cotton germplasm lines and also to characterize the lines using IBPGR descriptors. The data were collected on morphological characters of stem, leaf, flower and boll along with fifteen quantitative characters *viz.*, days to 50% flowering, plant height (cm), number of monopodia plant⁻¹, number of sympodia plant⁻¹, number of bolls plant⁻¹, boll weight (g), ginning out-turn (%), seed index (g), lint index (g), 2.5% Span length (mm), micronaire (10⁻⁶g/in), bundle strength (g/tex), uniformity ratio (%), fibre elongation (%) and seed cotton yield plant⁻¹ (g).

Variability was observed for seventeen parameters out of twenty seven IBPGR descriptors studied and these are helpful in varietal identification and protection and some of the characters like medium stem hairiness can be exploited for breeding pest resistant genotypes.

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating the data generated from the material will yield reliable information. The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the masking effects of the environment.

The characters *viz.*, plant height, number of monopodia plant⁻¹, number of sympodia plant⁻¹, number of bolls plant⁻¹, boll weight, ginning outturn, seed index, lint index, micronaire and seed cotton yield plant⁻¹ exhibited moderate to high variability. High heritability coupled with high genetic advance was noted in the case of plant height, number of monopodia plant⁻¹, number of bolls plant⁻¹, boll weight, lint index and seed cotton yield plant⁻¹. This indicates the predominance of additive gene action and hence, direct selection may be effective to some extent. High heritability coupled with moderate genetic advance was observed in case of number of sympodia plant⁻¹, ginning outturn, seed index and micronaire revealing the role of additive and non additive gene action. The other traits *viz.*, days to 50% flowering, 2.5% Span length, bundle strength, uniformity ratio and fibre elongation (%) showed moderate to high heritability and moderate to 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 study indicated that number of monopodia plant⁻¹, number of sympodia plant⁻¹, number of bolls plant⁻¹, boll weight, ginning out turn, lint index, and uniformity ratio had significant positive association with seed cotton yield plant⁻¹. The path analysis further indicated that number of monopodia plant⁻¹, number of bolls plant⁻¹, boll weight, ginning outturn and seed index had direct positive effects on seed cotton yield plant⁻¹.

The results of multivariate analysis revealed that the distribution of 60 cotton genotypes into nine clusters in case of D² analysis and into eight clusters in case of agglomerative cluster analysis was at random indicating that the genetic diversity and geographical diversity were not related.

On the basis of D² analysis the maximum inter cluster distance was observed between cluster V and VII (128.82), followed by cluster V and IX (125.35), cluster IV and IX (112.56), cluster VIII and IX (112.41) and cluster IV and VII (111.91). The characters, number of monopodia plant⁻¹, 2.5% Span length, plant height, micronaire, ginning out turn, bundle strength, lint index, number of bolls plant⁻¹, boll weight and number of sympodia plant⁻¹ contributed maximum towards genetic divergence.

Based on the inter- cluster distances among the groups, suggestions were made to attempt crosses after confirming their general combining ability between cluster VII (G-204-13) and cluster V (IC-356932, A-7262, L-614, NH-577, WGP-8, GSHY-01/1338, TXORHY-1-78, ADB-28, TSH-333, NDLH-7122 and NA-777) to obtain better and desirable segregants.

In the principal component method, first 8 principal components altogether explained 87.928 of the variability. The first component explained 21.415% of total variability and remaining ones accounted for progressive lesser and lesser amount of variation. The population with high PC₁ values were characterized by high loading values of number of monopodia plant⁻¹, ginning outturn, seed index, uniformity ratio, bundle strength and lint index, whereas, population with high PC₂ values were characterized by boll weight, number of sympodia plant⁻¹, plant height, bundle strength, seed index and micronaire which showed maximum weightage in this principal components.

Agglomerative cluster analysis revealed that wide genetic distance exists between cluster I and VIII (755.55) followed by cluster IV (GJHV-01/35) and VIII (515.66). Agglomerative cluster analysis revealed crosses can be attempted between clusters I (NH-577, WGP-8, IC-356932, A-7262, L-614, and TXORHY-1-78) and cluster VIII (GJHV-01/35).

The genotypes showed NH-577, WGP-8, IC-356932, A-7262, L-614 and TXORHY-1-78 showed maximum inter-cluster distance in all the three divergence methods. So they can be exploited for the development of heterotic hybrids after testing their combining ability.

LITERATURE CITED

- Ahuja S L, Monga D, Tuteja O P, Verma S K, Dhayal L S and Yagna Dutt 2004 Association and path analysis in the selections made from colored linted *Gossypium hirsutum* cotton germplasm. Journal of Cotton Research and Development 18 (2): 137-140.
- Ahuja S L and Tuteja O P 2000 Variability and association analysis for chemical components imparting resistance to cotton *Gossypium hirsutum* L. 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 2003b Yield component analysis in upland cotton (*Gossypium hirsutum* L.). Journal of the Indian Society for Cotton Improvement 28 (3): 151-157.
- *Anderberg M R 1993 Cluster Analysis for Application. Academic Press, New York.
- Anandan A 2009 Studies on choice of characters for breeding for seed cotton yield and fibre quality traits in cotton. Crop Improvement 36(1):35-37.
- 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 Simulation 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.
- Bottger G T, Sheehan E T and Lukefahr M J 1964 Relation of gossypol content of cotton plants to insect resistance. Journal of Economic Entomology 57 (2): 283-285.
- 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 Grassland Congress pp. 277-283.
- Cochran G W and Cox M G 1950 Experimental Designs. John Wiley and Sons Inc., New York pp. 45-67.
- Chopra V L 2001 Breeding Field Crops Oxford and IBH Publishing Co.Pvt.Ltd. Cotton pp.531-575.
- Dedaniya A D and Pethani K V 1994 Genetic variability, correlation and path analysis in desi cotton (*Gossypium arboreum* L.). Indian Journal of Genetics and Plant Breeding 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.
- Doss D K and Kadambavanasundaram M 1993 Genetic variability, heritability and Genetic advance in tetraploid species of cotton. *Indian Journal of Genetics and Plant Breeding* 53: 55-59.
- Do Thi Ha An, Ravikesavan R and Iyanar K 2008 Genetic advance and heritability as a selection index for improvement of yield and quality in cotton. *Journal of Cotton Research and Development* 22 (1): 14-18.
- Ehrenberg A S C 1985 *Data Reduction Analysis and Interpreting Statistical Data*. John Wiley and Sons Inc., New York.
- Eswararao G 2008 Genetic divergence in cotton (*Gossypium hirsutum* L.). M.Sc. (Ag) thesis, Acharya N.G. Ranga Agricultural University, Rajendranagar, 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*. Oliver and Boyd, Edinburgh, London pp. 312-324.
- Fisher R A and Yates F 1963 *Statistical Tables for Biological, Agricultural and Medical Research*. Oliver and Boyd, Edinburgh, 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.

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 variability studies in F₂ population 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.

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

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

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.

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.

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

- Jagtop and Mehetre S S 1998 Genetic variability in Inter-varietal crosses of upland cotton (*Gossypium hirsutum* L.). Annals of Agricultural Research 19: 130-132.
- Jain D K, Mor B R and Nehra S S 1984 Studies on heritability and genetic advance in upland cotton. Journal of the Indian Society for Cotton Improvement 9:1-4.
- Jain P P 1986 Studies on quantitative dynamics and characterization of genetic variation in upland cotton. Ph.D thesis, Haryana Agricultural University, Hissar.
- 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.
- Jimmy Xavier Zumba 2004 Evaluation of the USDA Shafter cotton (*Gossypium* spp.) collection for agronomic and fiber traits. M.Sc. (Ag) Thesis, Louisiana State University, USA.
- Johnson H W, Robinson H F and Comstock R E 1955 Estimates of genetic and environmental variability in soybean. Agronomy Journal 47: 314-318.
- Kamal M M, Ragab M T, Mahgoub M A and Elmalek M R A 2002 Quality valuation of Egyptian cotton varieties. Egyptian Journal of Agricultural Research 80 (3): 1231-1246.
- 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, Bhale S D, Kale U V, Deshmukh J D, Gite V K and Kakde S S 2008 Genetic variability and correlation studies in F₃ generation of cotton (*Gossypium hirsutum* L.). International Journal of Plant Sciences 3 (1): 94-97.

- 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 2003 Studies on genetic divergence in upland cotton (*Gossypium hirsutum* L.). M.Sc. (Ag) thesis, Acharya N.G. Ranga Agricultural University, Rajendranagar, Hyderabad.
- Kowsalya R and Raveendran T S 1996 Correlation and path coefficient analysis in cotton. *Madras Agricultural Journal* 83 (11): 705-707.
- Kumari S R and Chamundeswari N 2005 Studies on genetic variability, heritability and genetic advance in cotton (*Gossypium hirsutum* L.). *Research on Crops* 6 (1): 98-99.
- 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.
- 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.

Ledge K E, Smith C W and Cothen J T 1992 Genotypic and cultural effects on condensed tannin concentration of cotton leaves. *Crop Science* 4: 1024-1028.

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*. Presses de l'Université du Québec. Xv + 260p, viii+335 p.

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

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.

*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.

Mc Carty J C, Meredith W R, Jenkins J N, Parrot W L and Bailey J C 1983 Genotype X Environmental interaction of cottons varying in insect resistance. *Crop Science* 23 (5): 970-973.

Ministry of Commerce, Kolkata 2008-09 <http://www.Agricoop.nic.in>

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.

Murthy J S V S 1999 Character association and component analysis in upland cotton. Madras Agricultural Journal 86 (1-3): 39-42.

Murthy J S V S, Gopinath M and Mukundan S 1994 Association of characters and path coefficient analysis in upland cotton. Madras Agricultural Journal 81:308-311.

Murthy J S V S, Reddy D M and Reddy K H G 1995a Studies on the nature of genetic divergence in upland cotton (*Gossypium hirsutum* L.). Annals of Agricultural Research 16 (3): 307-310.

Murthy J S V S, Reddy D M and Reddy K H G 1995b Genetic divergence for lint characters in upland cotton (*Gossypium hirsutum* L.). Annals of Agricultural Research 16 (3): 357-359.

Murthy J S V S, 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.

- 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.
- Padmavathi A, 2008 Characterization of cotton germplasm (*Gossypium hirsutum* L.). M.Sc. (Ag) thesis, Acharya N.G. Ranga Agricultural University, Rajendranagar, Hyderabad.
- Padmavathi A Lal Ahamed M Rama Kumar P V and Anil Kumar A, 2009 Characterization of Cotton Germplasm using IBPGR Descriptors. The Andhra Agricultural Journal 56(2):186-191.
- Pandey S K, Prakash Singh and Pandey S B 2002 Genetic variability in upland cotton (*Gossypium hirsutum* L.). Society for Recent Development in Agriculture. 2 (2): 178-179.
- 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 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. Indian Council of Agricultural Research, New Delhi pp 103-108.
- 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.

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

Prasad U S, Reddy V C and Reddy A N 2005 Studies on genetic variability in American cotton (*Gossypium hirsutum* L.). *Karnataka Journal of Agricultural Sciences* 18 (4): 1095-1098.

Preetha S and Raveendran T S 2007 Genetic variability and association analysis in three different morphological groups of cotton (*Gossypium hirsutum* 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.

- Rajarathinam S and Nadarajan N 1993 Multivariate analysis of genetic divergence in upland cotton (*Gossypium hirsutum* L.). Journal of the Indian Society for Cotton Improvement 18(1):107-112.
- Rajarathinam S, Natarajan M and Sukanya Subramanian 1993 Genetic variability and association analysis in cotton. Journal of the Indian Society for Cotton Improvement 18:54-59.
- Rajarathinam S, Subramanian S and Nadarajan 1994 Genetic divergence in upland cotton (*Gossypium hirsutum* L.). Madras Agricultural Journal 84(6): 471-473.
- Rao C R 1952 Advanced Statistical Methods in Biometrical Research. John Wiley and Sons Inc., 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.
- Reddy Y R and Reddy C V V M 2007 Genetic variability for yield components and fibre characters in cotton. Plant Archives 7 (2): 759-761.

Roy A 2006 Genetic variability in indigenous cotton (*Gossypium arboreum*) of north eastern region. *Annals of Agriculture Research New Series* 27(2): 200-202.

Saeed Rauf, Khan T M, Sadaqat H A and Khan A I 2004 Correlation and path analysis of yield components in cotton (*Gossypium hirsutum* L.). *International Journal of Agriculture and Biology* 6 (4): 686-688.

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.

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.

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 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 2004b 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.

*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.

Srinivasulu P 2009 Genetic divergence in upland cotton (*Gossypium hirsutum* L.). M.Sc. (Ag) thesis, Acharya N.G. Ranga Agricultural University, Rajendranagar, Hyderabad.

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

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, 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, 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, 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 1994a 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.
- Tyagi A P 1994 b Correlation coefficients and selection indices in upland cotton (*Gossypium hirsutum* L.). Indian Journal of Agricultural Research 28 (3):189-196.
- Valarmathi M and Jehangir K S 1998 Studies on genetic parameters for yield and fibre quality traits in intra-varietal crosses of cotton (*Gossypium hirsutum* L.). Journal of the Indian Society for Cotton Improvement 23(1): 103-109.
- 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.

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

Original not seen

Note : The pattern of Literature Cited presented above is in accordance with the guidelines for thesis presentation, Acharya N. G. Ranga Agricultural University, Hyderabad.