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

By
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B.Sc. (Ag.)

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

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2011

CERTIFICATE

Ms. J. TULASI has satisfactorily prosecuted the course of research and that thesis entitled **"GENETIC DIVERSITY 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 neither the thesis nor its part thereof has not been previously submitted by her for a degree of any university.

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This is to certify that thesis entitled **“GENETIC DIVERSITY IN COTTON (*Gossypium hirsutum* L.)”** submitted in partial fulfilment of the requirements for the degree of Master of Science in Agriculture of the Acharya N. G. Ranga Agricultural University, Hyderabad, is a record of the bonafide original research work carried out by **Ms. J. TULASI** under our guidance and supervision.

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

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DECLARATION

I, **Ms. J. TULASI,** hereby declare that the thesis entitled **"GENETIC DIVERSITY IN COTTON (***Gossypium hirsutum* **L.)"** submitted to **Acharya N. G. Ranga Agricultural University** for the degree of **Master of Science in Agriculture** is the result of original research work done by me. I also declare that no material contained in the thesis has not been published earlier in any manner.

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LIST OF SYMBOLS AND ABBREVIATIONS

AICCIP	All India Coordinated Cotton Improvement Project
ANOVA	Analysis of Variance
ARS	Agricultural Research Station
CICR	Central Institute for Cotton Research
CV	Coefficient of Variation
GA	Genetic Advance
GAM	Genetic Advance as Per cent of Mean
GAU	Gujarat Agricultural University
GCV	Genotypic Coefficient of Variation
IBPGR	International Bureau of Plant Genetic resources
IPR	Intellectual Property Rights
JNKV	Jawarharlal Nehru Krishi Vidyalaya
mm	Millimeter
NS	Non-significant
PCV	Phenotypic Coefficient of Variation
RARS	Regional Agricultural Research Station
S	Significant
TNAU	Tamilnadu Agricultural University
UAS	University of Agricultural Sciences
%	Per cent
^{0}C	Degree Centigrade
Df	Degrees of freedom
et al.,	and coworkers
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
viz.,	Namely
2D	Two dimensional
3D	Three dimensional

ABSTRACT

Name of the Author	: **J. TULASI**
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The present investigation was carried out during *kharif* 2010-11 at Agricultural College Farm, Bapatla, with 40 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 lines using IBPGR descriptors. The data were recorded on 27 morphological characters, *viz.*, 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, type of bract, number of serrations of bract, sepal pigmentation, petal colour, petal spot, position of stigma, filament colouration, anther colour, boll bearing habit, boll size, boll colour, boll shape, boll surface, boll prominence of tip, boll opening and plant habit, and 15 quantitative characters viz., days to 50% flowering, plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), ginning out-turn (%), seed index (g), lint index (g), 2.5% span length (mm), micronaire (10^{-6} g/in), bundle strength (g/tex), uniformity ratio, fibre elongation (%) and seed cotton yield per plant (g).

IBPGR descriptors data revealed that variability was present for thirteen characters out of twenty seven descriptors studied and they can be exploited for varietal identification and IPR protection along with crop improvement programmes.

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., number of sympodia plant^{-1}, number of bolls per plant, boll weight and seed cotton yield per plant exhibited moderate phenotypic coefficient of variation. Moderate heritability coupled with moderate genetic advance was noted for number of sympodia plant^{-1}, number of bolls per plant and seed cotton yield per plant. This indicates the presence of non-additive gene action and further improvement of these traits would be possible through heterosis breeding rather than simple selection.

The correlation and path coefficient analyses together indicated that plant height, number of sympodia plant^{-1}, number of bolls plant^{-1} and seed index had significant positive and positive direct effects on seed cotton yield per plant indicating the existence of true relationship between these characters and their exploitation in selection programmes.

The results of multivariate analysis revealed that the distribution of 40 genotypes into seven clusters in case of D^2 analysis and agglomerative cluster analysis. The distribution of genotypes into these clusters was at random indicating genetic diversity and geographical diversity were not related.

Mahalanobis' D^2 statistic indicated that the characters, fibre elongation, seed index, number of monopodia plant^{-1}, boll weight, lint index, micronaire, ginning out-turn, 2.5% span length, seed cotton yield per plant and uniformity ratio contributed maximum towards genetic divergence.

Based on the inter- cluster distances among the groups suggestions were made to attempt crosses after confirming the general combining ability of the genotypes from the clusters IV (KH-11, RAH-101) and VII (COP-420) which had maximum inter-cluster distance (276.846) to obtain better heterotic and desirable segregants.

In the principal component method, first 5 principal components explained 78.35% of the variability. The first component was characterized by the high loading values of plant height, boll weight, days to 50% flowering, seed cotton yield per plant, number of bolls per plant, ginning out-turn and fiber elongation in assessing the genetic diversity. Agglomerative cluster analysis revealed crosses can be attempted between the clusters III (KH-11, RAH-101) and VII (COP-420) which had maximum inter cluster distance to obtain desirable segregants.

The genotypes KH-11 and RAH-101, and COP-420 showed maximum inter-cluster distance and wide genetic distance in multivariate analysis. These genotypes can be exploited in hybridization programme for identification of desirable segregants.

Chapter I

INTRODUCTION

Cotton (*Gossypium* spp.) is an important cash crop and the second largest source of textile fibre and edible oil throughout the world. It plays a key role in the national economy in terms of contribution in trade, industrial activities, employment and foreign exchange earnings in India (Gite *et al*., 2006).

Cotton being the king of fibres in preparing human apparel has played a key role in the development of civilization. Due to its importance in agriculture as well as industrial economy, it is also known as **"white gold"**. Cotton is the main economic and industrial crop of our country serving prime raw material for textile mills.

The genus *Gossypium* has the basic chromosome number of 13 and contains 50 species (Poehlman and Sleper, 1995) out of which four species are cultivated, including two tetraploid *G. hirsutum* and *G. barbadense* (2n = 4x = 52), and two diploid *G.arboreum* and *G. herbaceum* (2n = 2x = 26) species. *Gossypium* genomes are designated A to G and K. The agriculturally superior New world AD-genome species, *G. hirsutum* and G. *barbadense* have largely supplanted the old world A-genome species, G. *herbaceum* and G. *arboreum* and 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, upland cotton (*G. hirsutum*) is known for its production potential, as demonstrated by the release of number of stable varieties and hybrids.

In India, cotton is being grown over an area of 110 lakh hectares with an annual production of 325 lakh bales (1 bale =170 kg) with a productivity of 503 kg lint/ha (Anonymous, 2010). In Andhra Pradesh, cotton is a crop of great economic value and playing significant role in the socio-economic status of the farmers. It occupies an area of about 17.1 lakh hectares with an annual production of 65.68 lakh bales (170 kg each) and productivity of 653 kg lint/ha (Anonymous, 2010).

The latest technological innovations coupled with global demand for a quality textile product offers a great challenge to the plant breeders for working on different aspects of cotton. At the same time, changing national and international textile scenario availability of quality cotton with better fibre properties assumes great importance. At present, the research efforts are aimed at not only for augmenting the production and productivity, but also to meet the technological requirements in respect of fibre quality as well.

Before actual breeding programme is taken up to accomplish these objectives, it is desirable to elicit information on the extent of genetic variability present in the material (Swarup and Chaugle, 1962). The extent of heritability of the selected traits and the magnitude of genetic advance are equally important. Genetic divergence is of considerable practical interest in crop improvement, since quantification of the degree of divergence present in the population is of immense value in identifying diverse genotypes for recombination breeding programmes. The crosses involving genotypes with wider genetic base are likely to generate desirable recombinants in the progeny. The Mahalanobis' D^2 statistic 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.

Keeping this in view, a systematic effort was made to characterize the cotton germplasm using International Bureau of Plant Genetic Resources (IBPGR) descriptors along with the following objectives.

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

Chapter II

REVIEW OF LITERATURE

Cotton (*Gossypium hirsutum* L.) is an important commercial crop of India. 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.

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.

Manjunath Reddy *et al.* (2007) studied the characterization of two interspecific (DCH-32 and DHB-105) and one intraspecific cotton hybrids (DHH-11) along with their parents for various morphological characters and observed variation for leaf characters *viz.*, leaf size, leaf shape, leaf colour, leaf incision and leaf hairiness. Whereas plant characters such as growth habit, stem pigmentation, stem hairiness and plant height and flower characters such as days to 50% flowering, petal colour, petal spot, anther colour, position of stigma, boll shape, bract type and number of serrations on bract can be used efficiently for differentiation of genotypes one another. Padmavathi (2008) and Sarada (2010) evaluated cotton germplasm lines and observed variation for most of the IBPGR descriptors.

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-2.1.

2.3. HERITABILITY ($H^2_{(b)}$) AND GENETIC ADVANCE (GA) AS PER CENT OF MEAN

Heritability indicates the degree of correspondence between phenotypic value and breeding value. The knowledge of heritability helps the plant breeder to predict the behaviour of succeeding generations, making desirable selection and assessing the magnitude of genetic improvement through selection (Hafiz Munir Ahmed *et al.*, 2006).

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

2.4. CHARACTER ASSOCIATION

Correlation coefficient is the measure of mutual relationships between two variables. The study of correlations between two different characters may help the plant breeder to know the improvement of one character will bring simultaneous changes in other character(s).

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-2.3.

2.4.2 Association among the yield component characters

The available literature on the associations among the yield component characters is presented in Table -2.4.

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).

Correlation studies in conjunction with path coefficient analysis will give a better picture of the cause and effect relationship existing between pairs of characters

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-2.5.

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.

Rajarathinam 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.

Rajarathinam *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 maximum 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 and grouped the genotypes 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 this, 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.

Sarada (2010) reported maximum contribution of number of monopodia plant^{1}, plant height, fibre elongation, boll weight, seed index, seed cotton yield^{-1}, days to 50% flowering, number of bolls plant^{-1}, lint index, ginning outturn, bundle strength, micronaire and 2.5% span length towards genetic divergence in the study involving sixty genotypes.

2.5.2 Principal component analysis and cluster analysis

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

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

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

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

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

Vijayalaxmi (2008) used cluster analysis and PCA to estimate genetic divergence in 72 genotypes of upland cotton. PCA identified seven principle components which contributed 87.47% of cumulative variance. The population with high PC_1values were characterized by high number of bolls per plant, where as population with high PC_2 values were characterized by high boll weight.

Eswararao *et al.* (2009b) by using cluster analysis grouped 60 genotypes into VII clusters by Ward's minimum variance method. Maximum intra cluster distance was observed in cluster VI and inter-cluster distance between cluster VIII and X. The first six principal components with eigen values more than one contributed 78.21% towards total variability in the population studied.

Rajamani and Mallikarjuna Rao (2009) using PCA and cluster analyses assessed 63 genotypes of upland cotton. Based on Ward's minimum variance method, cluster III was largest comprising of 17 genotypes. The genotypes of clusters V and II can be utilized in the breeding programme to develop heterotic hybrids as the inter-cluster distance was maximum. All the five principal components showed eigen values more than 1 and they altogether explained 93.91% of the variability.

Sarada (2010) used cluster analysis and PCA to estimate genetic divergence in 60 genotypes of upland cotton. PCA identified eight principle components which contributed 87.92% of cumulative variance. The population with high PC_1 values were characterized by high number of monopodia per plant, where as population with high PC_2 values were characterized by high boll weight.

Srinivasulu *et al.* (2010a) carried out genetic divergence analysis with 60 genotypes of upland cotton using cluster analysis and principal component analysis. PCA identified 6 principal components which explained 83.89% variability in upland cotton. The multivariate analysis revealed maximum divergence signifying their role in exploitation of heterosis.

Venkateswarlu *et al.* (2010) collected 50 genotypes of upland cotton from different research centers across the country and carried out PCA and cluster analysis based on 16 characters. PCA identified 6 principal components which explained 77.41% variability in upland cotton. The clustering pattern based on Ward's minimum variance method revealed cluster III was the largest with 13 genotypes where as maximum inter-cluster distance was observed between clusters VII and VIII followed by VI and VIII revealing maximum divergence for the characters considered.

Kulkarni *et al.* (2011b) studied genetic diversity in 29 upland cotton genotypes for 19 yield attributes and quality characters. The pattern of grouping of genotypes into clusters revealed that the genetic diversity was not fully related to geographical diversity. They further reported that hybridization programme with the selected genotypes based on inter-cluster distances may produce high magnitude of heterosis/desirable segregants which would be helpful in improvement of yield and quality attributes in cotton.

Table-2.1: 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 *et al*. (2005) Leela Pratap (2006) Eswararao (2008) Neelima *et al*. (2008) Padmavathi (2008) Vijayalaxmi (2008) Srinivasulu (2009) Sarada (2010)
2.	Plant height (cm)	Neelam and Potdukhe (2002) Laxman and Ganesh (2003) Patnaik *et al.* (2004) Kale *et al.* (2006) Tuteja *et al.* (2006) Kalpande *et al.* (2008)	Sangeetha (1998) Deshpande and Baig (2003) Leela Pratap (2006) Eswararao (2008) Neelima *et al.* (2008) Vijayalaxmi (2008) Sarada (2010)
3.	No.of monopodia per plant	Neelam and Potdukhe (2002) Altaher and Singh (2003b) Kaushik *et al.* (2003) Ravikumar (2004) Sivaprasad *et al.* (2004 b) Karunakar Raju (2005) Prasad *et al.* (2005) Kumari and Chamundeswari (2005) Tuteja *et al.* (2006) Verma *et al.* (2006) Gitte *et al.* (2007) Eswararao (2008) Kalpande *et al.* (2008) Neelima *et al*. (2008) Padmavathi (2008) Vijayalaxmi (2008) Srinivasulu (2009) Sarada (2010)	Ahuja and Tuteja (2000) Gururajan (2000) Girase and Mehetre (2002)

Table 2.1 (Cont.)

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 *et al.* (2003) Tuteja *et al.* (2006) Gitte *et al.* (2007) Kalpande *et al.* (2008) Neelima *et al*. (2008)	Girase and Mehetre (2002) Laxman and Ganesh (2003) Prasad *et al.* (2005) Eswararao (2008) Vijayalaxmi (2008) Saidu Bazi (2011)
5.	No. of bolls per plant	Laxman and Ganesh (2003) Gururajan and Sundar (2004) Narisireddy and Ratnakumari (2004) Sivaprasad *et al.* (2004 b) Kale *et al.* (2006) Leela Pratap (2006) Tuteja *et al.* (2006) Gitte *et al.* (2007) Reddy and Reddy (2007) Padmavathi (2008) Sarada (2010) Saidu Bazi (2011)	Girase and Mehetre (2002) Vijayalaxmi (2008)
6.	Boll weight (g)	Kaushik *et al.* (2003) Laxman and Ganesh (2003) Muthuswamy *et al.* (2003) Gururajan and Sundar (2004) Sivaprasad *et al.* (2004 b) Kale *et al.* (2006) Tuteja *et al.* (2006) Gitte *et al.* (2007) Reddy and Reddy (2007) Kalpande *et al.* (2008)	Reddy (2001) Altaher and Singh (2003b) Eswararao (2008) Neelima *et al*. (2008) Vijayalaxmi (2008)
7.	Ginning out- turn (%)	Laxman and Ganesh (2003) Muthuswamy *et al.* (2003) Tuteja *et al.* (2003) Patnaik *et al.* (2004) Tuteja *et al.* (2006) Srinivasulu (2009)	Rao and Reddy (2001) Reddy (2001) Muraleedhar (2005) Prasad *et al.* (2005) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008) Saidu Bazi (2011)
8.	Seed index (g)	Muthuswamy *et al.* (2003) Gururajan and Sundar (2004) Patnaik *et al.* (2004) Ravikumar (2004) Sivaprasad *et al.* (2004 b)	Rao and Reddy (2001) Reddy (2001) Neelam and Potdukhe (2002) Altaher and Singh (2003b)

Table 2.1 (Cont.)

S.No.	Character	Wider genetic variability	Narrow genetic variability
			Laxman and Ganesh (2003) Neelima *et al*. (2008) Vijayalaxmi (2008) Srinivasulu (2009)
9.	Lint index (g)	Laxman and Ganesh (2003) Muthuswamy *et al.* (2003) Patnaik *et al.* (2004) Gururajan and Sundar (2004) Sivaprasad *et al.* (2004 b)	Rao and Reddy (2001) Altaher and Singh (2003b) Vijayalaxmi (2008)
10.	2.5% span length (mm)	Muthuswamy *et al.* (2003) Gururajan and Sundar (2004) Naphade *et al.* (2004) Patnaik *et al.*(2004)	Reddy (2001) Neelam and Potdukhe (2002) Altaher and Singh (2003b) Prasad *et al.* (2005) Leela Pratap (2006) Tuteja *et al.* (2006) Verma *et al.* (2006) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008) Srinivasulu (2009) Sarada (2010)
11.	Micronaire value (10^{-6} g/in)	Rao and Reddy (2001) Neelam and Potdukhe (2002) Muthuswamy *et al.* (2003) Naphade *et al.* (2004) Patnaik *et al.* (2004)	Reddy (2001) Altaher and Singh (2003b) Prasad *et al.* (2005) Eswararao (2008) Vijayalaxmi (2008) Srinivasulu (2009)
12.	Bundle strength (g/tex)	Muthuswamy *et al.* (2003) Gururajan and Sundar (2004) Naphade *et al.* (2004) Patnaik *et al.* (2004) Neelima *et al.* (2005)	Reddy (2001) Rao and Reddy (2001) Neelam and Potdukhe (2002) Girase and Mehetre (2002) Altaher and Singh (2003b) Karunakar Raju (2005) Prasad *et al*. (2005) Leela Pratap (2006) Eswararao (2008) Neelima *et al*. (2008) Padmavathi (2008) Vijayalaxmi (2008) Srinivasulu (2009) Sarada (2010) Saidu Bazi (2011)

Table 2.1 (Cont.)

S.No.	Character	Wider genetic variability	Narrow genetic variability
13.	Uniformity ratio	Patnaik *et al.* (2004)	Altaher and Singh (2003b) Karunakar Raju (2005) Muraleedhar (2005) Prasad *et al.* (2005) Leela Pratap (2006) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008) Srinivasulu (2009) Sarada (2010) Saidu Bazi (2011)
14.	Fibre elongation (%)	—	Valarmathi and Jehangir (1998) Ravikumar (2004) Muraleedhar (2005) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008) Srinivasulu (2009) Sarada (2010) Saidu Bazi (2011)
15.	Seed cotton yield per plant (g)	Rao and Reddy (2001) Reddy (2001) Neelam and Potdukhe (2002) Kaushik *et al.* (2003) Laxman and Ganesh (2003) Muthuswamy *et al.* (2003) Tuteja *et al.* (2003) Sivaprasad *et al.* (2004 b) Gururajan and Sundar (2004) Narisireddy and Ratnakumari (2004) Karunakar Raju (2005) Kumari and Chamundeswari (2005) Leela Pratap (2006) Verma *et al.* (2006) Gitte *et al.* (2007) Reddy and Reddy (2007) Padmavathi (2008) Vijayalaxmi (2008) Srinivasulu (2009) Saidu Bazi (2011)	

Table- 2.2 : 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 *et al.* (2008) Padmavathi (2008) Srinivasulu (2009) Sarada (2010)	Vijayalaxmi (2008)	Neelima (2002) Sivaprasad *et al.* (2004a) Karunakar Raju (2005)
2.	Plant height (cm)	Sangeetha (1998) Neelam and Potdukhe (2002) Pandey *et al.*(2002) Kale *et al.*(2006) Roy (2006) Preetha and Raveendran (2007) Sakthi *et al.*(2007) Do Thi Ha An *et al.* (2008) Padmavathi (2008) Srinivasulu (2009) Sarada (2010)	Verma *et al.* (2006) Vijayalaxmi (2008)	-	Kumari and Chamundeswari (2005) Eswararao (2008)

Table 2.2 (Cont.)

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 *et al.* (2003) Karunakar Raju (2005) Leela Pratap (2006) Verma *et al.* (2006) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008) Sarada (2010)	Reddy (2001) Kumari and Chamundeswari (2005) Srinivasulu (2009)	Neelima (2002) Sivaprasad *et al.*(2004a)	Rao and Reddy (2001)
4.	No. of sympodia per plant	Neelam and Potdukhe (2002) Girase and Mehetre (2002) Kaushik *et al.* (2003) Ravikumar (2004) Verma *et al.* (2006) Preetha and Raveendran (2007) Sakthi *et al.* (2007) Do Thi Ha An *et al.* (2008) Padmavathi (2008) Sarada (2010)	Gururajan (2000) Reddy (2001) Kiran (2003) Vijayalaxmi (2008) Srinivasulu (2009)	-	Rao and Reddy (2001) Sivaprasad *et al.* (2004a) Kumari and Chamundeswari (2005)

Table 2.2 (Cont.)

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 *et al.* (2003) Ravikumar (2004) Sivaprasad *et al.* (2004a) Kale *et al.* (2006) Leela Pratap (2006) Roy (2006) Preetha and Raveendran (2007) Reddy and Reddy (2007) Sakthi *et al.* (2007) Do Thi Ha An *et al.* (2008) Padmavathi (2008) Vijayalaxmi (2008) Sarada (2010) Saidu Bazi (2011)	Murthy *et al.* (1994) Gururajan and Sundar (2004) Srinivasulu (2009)	-	-

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**
6.	Boll weight (g)	Neelam and Potdukhe (2002) Neelima (2002) Kaushik *et al.* (2003) Narisireddy and Ratnakumari (2004) Karunakar Raju (2005) Kale *et al.* (2006) Verma *et al.* (2006) Roy (2006) Preetha and Raveendran (2007) Sakthi *et al.* (2007) Do Thi Ha An *et al.* (2008) Padmavathi (2008) Vijayalaxmi (2008) Sarada (2010) Saidu Bazi (2011)	Gururajan (2000) Gururajan and Sundar (2004) Srinivasulu (2009)	Sivaprasad *et al.* (2004a)	Kiran (2003) Kumari and Chamundeswari (2005)
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 *et al.*(2006) Vijayalaxmi (2008) Do Thi Ha An *et al.* (2008)	-	Prasad (2003) Sivaprasad *et al.* (2004a) Srinivasulu (2009)

Table 2.2 (Cont.)

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 *et al.* (2008) Padmavathi (2008) Vijayalaxmi (2008) Saidu Bazi (2011)	Gururajan (2000) Neelam and Potdukhe (2002) Sivaprasad *et al.* (2004a)	**-**	Reddy (2001) Gururajan and Sundar (2004) Srinivasulu (2009)
9.	Lint index (g)	Reddy (2001) Neelima (2002) Karunakar Raju (2005) Murthy *et al.*(2006) Do Thi Ha An *et al.* (2008) Padmavathi (2008) Vijayalaxmi (2008) Sarada (2010) Saidu Bazi (2011)	Rao and Reddy (2001) Neelam and Potdukhe (2002) Sivaprasad *et al.* (2004a)	**-**	Prasad (2003) Srinivasulu (2009)

Table 2.2 (Cont.)

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) Saidu Bazi (2011)	Kiran (2003) Tuteja *et al.* (2005a) Verma *et al.* (2006) Do Thi Ha An *et al.* (2008) Srinivasulu (2009)	-	Singh and Gill (1984) Prasad (2003)
11.	Micronaire value (10^{-6}g/in)	Rao and Reddy (2001) Do Thi Ha An *et al.* (2008) Saidu Bazi (2011)	Reddy (2001) Vijayalaxmi (2008)	-	Prasad (2003) Sivaprasad *et al.* (2004a) Srinivasulu (2009)
12.	Bundle strength (g/tex)	Reddy (2001) Murthy *et al.* (2006) Do Thi Ha An *et al.* (2008)	Rao and Reddy (2001) Kiran (2003)	-	Gururajan and Sundar (2004) Sivaprasad *et al.* (2004a) Muraleedhar (2005) Eswararao (2008) Vijayalaxmi (2008) Srinivasulu (2009)
13.	Uniformity ratio	-	Sangeetha (1998) Neelima (2002) Kiran (2003) Karunakar Raju (2005)	-	Sivaprasad *et al.* (2004a) Muraleedhar (2005) Vijayalaxmi (2008) Srinivasulu (2009)

Table 2.2 (Cont.)

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) Sarada (2010) Saidu Bazi (2011)	-	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 *et al.*(2002) Kaushik *et al.* (2003) Sivaprasad *et al.* (2004a) Karunakar Raju (2005) Kumari and Chamundeswari (2005) Kale *et al.* (2006) Leela Pratap (2006) Tuteja *et al.* (2006) Verma *et al.*(2006) Murthy *et al.* (2006) Roy (2006) Preetha and Raveendran (2007) Reddy and Reddy (2007) Padmavathi (2008) Vijayalaxmi (2008) Srinivasulu (2009) Sarada (2010) Saidu Bazi (2011)	Gururajan and Sundar (2004)	-	Jain *et al.* (1984) Jain (1986)

Table 2.3: 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) Ashok Kumar and Ravikesavan (2010))
			NS	Murthy (1997) Ravikumar (2004) Sarada (2010)
		Negative	S	Reddy (2001) Leela Pratap *et al.* (2007)
			NS	Ladole and Meshram (2000) Altaher and Singh (2003b) Kaushik *et al.* (2003) Karunakar Raju (2005) Vijayalaxmi (2008) Srinivasulu (2009)
2.	Plant height (cm)	Positive	S	Samanc and Ozkaynak (2000) Tuteja *et al.* (2006) Kalpande *et al.* (2008) Padmavathi (2008) Anandan (2009) Srinivasulu (2009) Sarada (2010)
			NS	Sumathi and Nadarajan(1995)
		Negative	S	Neelima *et al.* (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 *et al.* (2003) Padmavathi (2008) Srinivasulu (2009)
			NS	Neelam and Potdukhe (2002) Altaher and Singh (2003b) Pradeep and Sumalini (2005) Vijayalaxmi (2008)

Table 2.3 (Cont.)

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 *et al.* (2004) Ravikumar (2004) Saeed *et al.* (2004) Neelima *et al.* (2005) Tuteja *et al.* (2006) Leela Pratap *et al.* (2007) Kalpande *et al.*(2008) Padmavathi (2008) Vijayalaxmi (2008) Anandan (2009) Srinivasulu (2009) Shazia Salahuddin *et al.* (2010)
			NS	Ladole and Meshram(2000) Neelam and Potdukhe (2002) Karunakar Raju (2005) Pradeep and Sumalini (2005)
5.	No. of bolls/plant	Positive	S	Sivaprasad (2003) Muthu *et al.* (2004) Gururajan and Sundar (2004) Saeed *et al.*(2004) Neelima *et al.* (2005) Karunakar Raju (2005) Tuteja *et al.* (2006) Verma *et al.* (2006) Leela Pratap *et al.* (2007) Kalpande *et al.*(2008) Do Thi Ha An *et al.*(2008) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008) Anandan (2009) Srinivasulu (2009) Batool *et al.*(2010) Shazia Salahuddin *et al.* (2010)
			NS	Pradeep and Sumalini (2005)

Table 2.3 (Cont.)

S. No.	**Character**	**Association**	**S/NS**	**Reference**
		Negative	S	Patil *et al.* (1991)
6.	Boll weight (g)	Positive	S	Altaher and Singh (2003b) Sivaprasad (2003) Gururajan and Sundar (2004) Muthu *et al.* (2004) Neelima *et al.* (2005) Karunakar Raju (2005) Murthy *et al.* (2006) Do Thi Ha An *et al.*(2008) Eswararao (2008) Padmavathi (2008) Anandan (2009) Srinivasulu (2009) Khadijah Makhdoom *et al.* (2010) Shazia Salahuddin *et al.* (2010)
			NS	Ladole and Meshram (2000) Reddy (2001) Kaushik *et al.* (2003) Vijayalaxmi (2008)
		Negative	S	Gururajan (2000) Rao *et al.* (2001)
			NS	Pradeep and Sumalini (2005) Ravikumar (2004)
7.	Ginning out -turn (%)	Positive	S	Ganapathy (2001) Reddy (2001) Sivaprasad (2003) Tuteja *et al.* (2005a) Anandan (2009) Naqib Ullah *et al.* (2010)
			NS	Rao *et al.* (2001) Neelam and Potdukhe (2002)
		Negative	S	Mandloi *et al.* (2003) Muthuswamy and Vivekanandan (2004) Srinivasulu (2009)
			NS	Karunakar Raju (2005) Vijayalaxmi (2008)
8.	Seed index (g)	Positive	S	Sivaprasad (2003) Gururajan and Sundar (2004) Muthu *et al.* (2004) Neelima *et al.* (2005) Murthy *et al.* (2006)

Table 2.3 (Cont.)

S. No.	Character	Association	S/NS	Reference
				Do Thi Ha An *et al.*(2008) Padmavathi (2008) Anandan (2009) Srinivasulu (2009)
		Negative	S	Tyagi (1994b) Gururajan and Sundar (2004)
			NS	Neelam and Potdukhe (2002) Pankaj Rathore *et al.* (2004) Ravikumar (2004) Karunakar Raju (2005) Tuteja *et al.* (2005a) Vijayalaxmi (2008) Padmavathi (2008)
9.	Lint index (g)	Positive	S	Reddy (2001) Neelima (2002) Neelam and Potdukhe (2002) Sivaprasad (2003) Muthu *et al.* (2004) Karunakar Raju (2005) Neelima *et al.* (2005) Murthy *et al.* (2006) Naqib Ullah *et al.* (2010)
			NS	Rao *et al.* (2001) Ravikumar (2004) Vijayalaxmi (2008)
		Negative	NS	Ladole and Meshram (2000) Mandloi *et al.* (2003)
10.	2.5% span length (mm)	Positive	S	Rajarathinam *et al.* (1993) Kiran (2003)
			NS	Rao *et al.* (2001) Reddy (2001) Neelima (2002) Mandloi *et al.* (2003)
		Negative	S	Tyagi (1994b) Gururajan and Sundar (2004)
			NS	Neelam and Potdukhe (2002) Ravikumar (2004) Pankaj Rathore *et al.* (2004)

Table 2.3 (Cont.)

S. No.	**Character**	**Association**	**S/NS**	**Reference**
				Tuteja *et al.* (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 *et al.* (2005) Murthy *et al.* (2006) Srinivasulu (2009)
			NS	Rao *et al.*(2001) Neelam and Potdukhe (2002) Mandloi *et al.* (2003) Pankaj Rathore *et al.* (2004) Ravikumar (2004) Tuteja *et al.* (2005a) Vijayalaxmi (2008) Padmavathi (2008)
12.	Bundle strength (g/tex)	Positive	S	Rao *et al.* (2001)
			NS	Neelima (2002) Neelam and Potdukhe (2002) Mandloi *et al.* (2003) Padmavathi (2008) Anandan (2009)
		Negative	S	Sangeetha (1998) Rao *et al.* (2001) Sivaprasad (2003)
			NS	Pankaj Rathore *et al.* (2004) Ravikumar (2004) Karunakar Raju (2005) Vijayalaxmi (2008) Srinivasulu (2009)

Table 2.3 (Cont.)

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

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

Table-2.4: Review of literature on association among the yield component characters 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) Ashok Kumar and Ravikesavan (2010)
			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) Ashok Kumar and Ravikesavan (2010)
			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)

Table 2.4 (Cont.)

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)
5.	Boll weight (g)	Positive	S	Altaher and Singh (2003b) Sivaprasad (2003)
		Negative	S	Karunakar Raju (2005) Muraleedhar (2005) Leela Pratap *et al.* (2007) Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000) Neelima (2002) Anandan (2009) Srinivasulu (2009)
6.	Ginning out-turn (%)	Positive	S	Neelam and Potdukhe (2002) Karunakar Raju (2005) Ashok Kumar and Ravikesavan (2010)
			NS	Murthy (1997) Vijayalaxmi (2008)
		Negative	S	Leela Pratap *et al.* (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 *et al.* (2007)
		Negative	S	Ladole and Meshram (2000) Neelima (2002) Muraleedhar (2005) Vijayalaxmi (2008)

Table 2.4 (Cont.)

S. No.	Character	Association	S/NS	Reference
			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 *et al.* (2007)
			NS	Vijayalaxmi (2008) Srinivasulu (2009)
9.	2.5% span length (mm)	Positive	S	Muraleedhar (2005) Ashok Kumar and Ravikesavan (2010)
			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 *et al.* (2007)
			NS	Sangeetha (1998)
		Negative	S	Altaher and Singh (2003b) Muraleedhar (2005) Vijayalaxmi (2008)
			NS	Reddy (2001) Neelam and Potdukhe (2002) Neelima (2002), Anandan (2009), Srinivasulu (2009)
11.	Bundle strength (g/tex)	Positive	S	Sivaprasad (2003) Vijayalaxmi (2008) Ashok Kumar and Ravikesavan (2010)

Table 2.4 (Cont.)

S. No.	Character	Association	S/NS	Reference
			NS	Neelam and Potdukhe (2002) Srinivasulu (2009)
		Negative	S	Altaher and Singh (2003b) Karunakar Raju (2005) Sabir Hussain *et al*. (2010)
			NS	Reddy (2001) Neelima (2002)
12.	Uniformity ratio	Positive	S	Neelima (2002) Neelima *et al.* (2005)
			NS	Sangeetha (1998)
		Negative	NS	Karunakar Raju (2005) Vijayalaxmi (2008)
13.	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 *et al.* (2004) Tuteja *et al.* (2006) Verma *et al.* (2006) Joshi *et al.* (2006) Leela Pratap *et al.* (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 *et al.* (2004) Tuteja *et al.* (2006) Padmavathi (2008) Vijayalaxmi (2008)

Table 2.4 (Cont.)

S. No.	Character	Association	S/NS	Reference
			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 out-turn (%)	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 *et al.* (2004) Padmavathi (2008)
			NS	Sumathi and Nadarajan (1995) Sangeetha (1998) Padmavathi (2008) Vijayalaxmi (2008) Anandan (2009)
		Negative	NS	Tyagi (1994a) Srinivasulu (2009)
			S	Leela Pratap *et al.* (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 *et al.* (2004) Verma *et al.* (2006)
			NS	Sumathi and Nadarajan (1995) Vijayalaxmi (2008) Anandan (2009)
		Negative	NS	Sangeetha (1998) Srinivasulu (2009)

Table 2.4 (Cont.)

S. No.	Character	Association	S/NS	Reference
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)
11.	Uniformity ratio	Positive	NS	Dedaniya and Pethani (1994) Sangeetha (1998) Srinivasulu (2009)
		Negative	S	Padmavathi (2008) Vijayalaxmi (2008)
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 *et al.* (2007) Padmavathi (2008)
			NS	Ladole and Meshram (2000) Reddy (2001) Neelima (2002) Kaushik *et al.* (2003) Srinivasulu (2009)
		Negative	S	Verma *et al.* (2006) Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002) Pradeep and Sumalini (2005)

Table 2.4 (Cont.)

S. No.	Character	Association	S/NS	Reference
2.	No.of bolls/plant	Positive	S	Ladole and Meshram (2000) Kaushik *et al.* (2003) Verma *et al.* (2006) Leela Pratap *et al.* (2007) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Neelima (2002) Neelam and Potdukhe (2002) Srinivasulu (2009)
		Negative	NS	Reddy (2001)
3.	Boll weight (g)	Positive	S	Basha (1997)
			NS	Ladole and Meshram (2000) Reddy (2001), Neelima (2002)
		Negative	NS	Murthy (1997) Sangeetha (1998) Kaushik *et al.* (2003) Pradeep and Sumalini (2005) Vijayalaxmi (2008) Srinivasulu (2009)
			S	Leela Pratap *et al.* (2007)
4.	Ginning out-turn (%)	Positive	S	Gururajan (2000) Muthu *et al.* (2004) Leela Pratap *et al.* (2007) Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000), Reddy (2001), Neelima (2002), 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)

Table 2.4 (Cont.)

S. No.	Character	Association	S/NS	Reference
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)
7.	2.5% span length (mm)	Positive	S	Reddy (2001) Sivaprasad (2003)
			NS	Ladole and Meshram (2000) Neelam and Potdukhe (2002) Srinivasulu (2009)
			S	Verma *et al.* (2006)
		Negative	NS	Neelima (2002) Vijayalaxmi (2008)
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)

Table 2.4 (Cont.)

S. No.	Character	Association	S/NS	Reference
IV. Association of number of sympodia per plant with				
1.	Number of bolls/plant	Positive	S	Altaher and Singh (2003b), Sivaprasad (2003) Muthu *et al.* (2004) Muthuswamy and Vivekanandan (2004) Neelima *et al.* (2005) Tuteja *et al.* (2006) Eswararao (2008) Padmavathi (2008) Ashok Kumar and Ravikesavan (2010)
		Positive	NS	Ladole and Meshram (2000) Ganapathy (2001) Kaushik *et al.* (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) Ashok Kumar and Ravikesavan (2010)
			NS	Neelima *et al.* (2005) Vijayalaxmi (2008) Srinivasulu (2009)
		Negative	S	Rao *et al.* (2001) Leela Pratap *et al.* (2007)
			NS	Pradeep and Sumalini (2005) Anandan (2009)
3.	Ginning out-turn (%)	Positive	S	Muthu *et al.* (2004) Muthuswamy and Vivekanandan (2004) Neelima *et al.* (2005) Padmavathi (2008) Ashok Kumar and Ravikesavan (2010)
			NS	Reddy (2001) Vijayalaxmi (2008) Anandan (2009)
		Negative	S	Altaher and Singh (2003b)
			NS	Basha (1997) Murthy (1997) Vijayalaxmi (2008)

Table 2.4 (Cont.)

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 *et al.* (2004) Neelima *et al.* (2005)
			NS	Reddy (2001) Neelima (2002) Vijayalaxmi (2008) Anandan (2009)
		Negative	S	Rao *et al.* (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 *et al.* (2004) Neelima *et al.* (2005) Karunakar Raju (2005) Padmavathi (2008)
			NS	Reddy (2001) Vijayalaxmi (2008) Anandan (2009)
		Negative	NS	Rao *et al.* (2001) Srinivasulu (2009)
			S	Muraleedhar (2005)
6.	2.5% span length (mm)	Positive	NS	Reddy (2001) Neelam and Potdukhe (2002)
			S	Verma *et al.* (2006) Ashok Kumar and Ravikesavan (2010)
		Negative	NS	Ladole and Meshram (2000) Rao *et al.* (2001)

Table 2.4 (Cont.)

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 *et al*. (2001)
				Reddy (2001) Neelima (2002) Neelam and Potdukhe (2002)
		Negative	NS	Srinivasulu (2009)
8.	Bundle strength (g/tex)	Positive	S	Rao *et al*. (2001) Altaher and Singh (2003b) Muthu *et al*. (2004) Ashok Kumar and Ravikesavan (2010)
			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)

Table 2.4 (Cont.)

S. No.	Character	Association	S/NS	Reference
		Negative	S	Muthu *et al.* (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 *et al* .(2005) Ashok Kumar and Ravikesavan (2010)
		Negative	S	Rao *et al.* (2001) Karunakar Raju (2005) Padmavathi (2008) Vijayalaxmi (2008) Anandan (2009)
			NS	Ladole and Meshram (2000) Reddy (2001) Kaushik *et al.* (2003) Pradeep and Sumalini (2005) Srinivasulu (2009)
2.	Ginning out-turn (%)	Positive	S	Ganapathy (2001) Muthu *et al.* (2004) Leela Pratap *et al.* (2007) Anandan (2009) Ashok Kumar and Ravikesavan (2010)
			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 *et al.* (2004) Neelima *et al.* (2005) Anandan (2009) Ashok Kumar and Ravikesavan (2010)
			NS	Reddy (2001) Srinivasulu (2009)
		Negative	S	Rao *et al.* (2001) Muraleedhar (2005) Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000)

Table 2.4 (Cont.)

S. No.	Character	Association	S/NS	Reference
4.	Lint index (g)	Positive	S	Neelima (2002) Neelam and Potdukhe (2002) Muthu *et al.* (2004) Neelima *et al.* (2005) Anandan (2009) Ashok Kumar and Ravikesavan (2010)
			NS	Reddy (2001) Srinivasulu (2009)
		Negative	S	Murthy (1997) Karunakar Raju *et al.* (2005) Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000) Rao *et al.* (2001) Neelam and Potdukhe (2002) Neelima (2002)
5.	2.5% span length (mm)	Positive	NS	Ladole and Meshram (2000) Rao *et al.* (2001) Reddy (2001) Neelam and Potdukhe (2002) Sakthi *et al.*(2007) Srinivasulu (2009) Ashok Kumar and Ravikesavan (2010)
		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 *et al.* (2004) Karunakar Raju (2005) Sakthi *et al.*(2007) Eswararao (2008) Anandan (2009) Ashok Kumar and Ravikesavan (2010)

Table 2.4 (Cont.)

S. No.	Character	Association	S/NS	Reference
			NS	Rao *et al.* (2001) Neelam and Potdukhe (2002)
		Negative	S	Leela Pratap *et al.* (2007) Vijayalaxmi (2008)
7.	Bundle strength (g/tex)	Positive	S	Rao *et al.* (2001) Altaher and Singh (2003b) Muthu *et al.* (2004) Ashok Kumar and Ravikesavan (2010)
			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 *et al.* (2004)
			NS	Srinivasulu (2009)
		Negative	S	Vijayalaxmi (2008)
			NS	Sangeetha (1998) Neelima (2002) Anandan (2009)
9.	Fibre elongation (%)	Negative	S	Muthu *et al.* (2004) Vijayalaxmi (2008)
			NS	Muraleedhar (2005) Anandan (2009)
		Positive	NS	Srinivasulu (2009)
VI. Association of boll weight (g) with				
1.	Ginning out-turn (%)	Positive	S	Reddy (2001) Muthuswamy and Vivekanandan (2004) Karunakar Raju (2005) Ashok Kumar and Ravikesavan (2010)
			NS	Neelima (2002) Srinivasulu (2009)
		Negative	NS	Murthy (1997) Ladole and Meshram (2000) Vijayalaxmi (2008) Anandan (2009)

Table 2.4 (Cont.)

S. No.	Character	Association	S/NS	Reference
2.	Seed index (g)	Positive	S	Ladole and Meshram (2000) Altaher and Singh (2003b) Sivaprasad (2003) Muthu *et al.* (2004) Karunakar Raju (2005) Neelima *et al.* (2005) Padmavathi (2008) Vijayalaxmi (2008) Ashok Kumar and Ravikesavan (2010)
			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 *et al.* (2005) Karunakar Raju (2005) Padmavathi (2008) Vijayalaxmi (2008) Ashok Kumar and Ravikesavan (2010)
		Negative	NS	Anandan (2009) Srinivasulu (2009)
4.	2.5% span length (mm)	Positive	NS	Rao *et al.* (2001) Reddy (2001) Anandan (2009) Srinivasulu (2009)
			S	Sivaprasad (2003) Verma *et al.* (2006) Vijayalaxmi (2008) Ashok Kumar and Ravikesavan (2010)
		Negative	NS	Neelima (2002)
5.	Micronaire value (10^{-6} g/in)	Negative	S	Rao *et al.* (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) Ashok Kumar and Ravikesavan (2010)

Table 2.4 (Cont.)

S. No.	Character	Association	S/NS	Reference
			S	Muraleedhar (2005)
		Negative	S	Rao *et al.* (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 out-turn with				
1	Seed index (g)	Positive	NS	Reddy (2001) Neelima (2002) Mandloi *et al.* (2003) Altaher and Singh (2003b) Leela Pratap *et al.* (2007) Padmavathi (2008) Anandan (2009) Srinivasulu (2009)
			S	Sabir Hussain *et al.* (2010)
		Negative	S	Vijayalaxmi (2008)
			NS	Ladole and Meshram (2000) Rao *et al.* (2001) Neelam and Potdukhe (2002)
2.	Lint index (g)	Positive	S	Reddy (2001) Neelima (2002) Altaher and Singh (2003b) Mandloi *et al.* (2003) Muthu *et al.* (2004) Karunakar Raju (2005) Leela Pratap *et al.* (2007) Padmavathi (2008) Vijayalaxmi (2008) Ashok Kumar and Ravikesavan (2010)
			NS	Rao *et al.* (2001) Neelam and Potdukhe (2002) Anandan (2009)
		Negative	NS	Srinivasulu (2009)

Table 2.4 (Cont.)

S. No.	Character	Association	S/NS	Reference
3.	2.5% span length (mm)	Positive	S	Sivaprasad (2003)
			NS	Ladole and Meshram (2000) Rao *et al.* (2001) Reddy (2001) Neelima (2002)
		Negative	S	Muthu *et al.* (2004) Padmavathi (2008)
			NS	Neelam and Potdukhe (2002) Mandloi *et al.* (2003) Vijayalaxmi (2008) Anandan (2009) Srinivasulu (2009)
4.	Micronaire value (10^{-6} g/in)	Positive	S	Rao *et al.* (2001) Muthu *et al.* (2004) Padmavathi (2008)
			NS	Reddy (2001) Neelam and Potdukhe (2002) Neelima (2002)
		Negative	S	Vijayalaxmi (2008)
			NS	Mandloi *et al.* (2003) Karunakar Raju (2005) Anandan (2009) Srinivasulu (2009)
5.	Bundle strength (g/tex)	Positive	S	Mandloi *et al.* (2003) Murthy *et al.(*2006)
			NS	Rao *et al.* (2001) Reddy (2001) Neelima (2002) Vijayalaxmi (2008) Srinivasulu (2009)
		Negative	S	Neelam and Potdukhe (2002) Padmavathi (2008)
			NS	Neelam and Potdukhe (2002) Anandan (2009)
6.	Uniformity ratio	Positive	S	Muthu *et al.* (2004) Karunakar Raju (2005) Padmavathi (2008) Ashok Kumar and Ravikesavan (2010)
			NS	Sangeetha (1998)

Table 2.4 (Cont.)

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 *et al.* (2003) Altaher and Singh (2003b) Muthu *et al.* (2004) Karunakar Raju (2005) Neelima *et al.* (2005) Leela Pratap *et al.* (2007) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002) Anandan (2009)
		Negative	NS	Srinivasulu (2009)
2.	2.5% span length (mm)	Positive	S	Rao *et al.* (2001) Karunakar Raju (2005) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002) Anandan (2009) Srinivasulu (2009)
		Negative	NS	Ladole and Meshram (2000) Neelima (2002) Mandloi *et al.* (2003)
3.	Micronaire value (10^{-6} g/in)	Positive	S	Sivaprasad (2003) Eswararao (2008) Vijayalaxmi (2008)
			NS	Reddy (2001) Neelam and Potdukhe (2002) Neelima (2002)

Table 2.4 (Cont.)

S. No.	Character	Association	S/NS	Reference
		Negative	NS	Rao *et al.* (2001) Mandloi *et al.* (2003) Anandan (2009) Srinivasulu (2009)
4.	Bundle strength (g/tex)	Positive	S	Muthu *et al.* (2004) Padmavathi (2008)
			NS	Sangeetha (1998) Neelima (2002) Neelam and Potdukhe (2002) Altaher and Singh (2003b) Anandan (2009)
		Negative	S	Rao *et al.* (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 *et al.* (2004)
			NS	Muraleedhar (2005) Anandan (2009) Srinivasulu (2009)
IX. Association of lint index (g) with				
1.	2.5% span length (mm)	Positive	S	Muthu *et al.* (2004) Murthy *et al. (*2006) Vijayalaxmi (2008) Ashok Kumar and Ravikesavan (2010)
			NS	Reddy (2001)
		Negative	NS	Ladole and Meshram (2000) Neelam and Potdukhe (2002) Neelima (2002) Mandloi *et al.* (2003) Anandan (2009) Srinivasulu (2009)
2.	Micronaire value (10^{-6} g/in)	Positive	S	Reddy (2001) Neelima (2002) Neelam and Potdukhe (2002) Eswararao (2008)

Table 2.4 (Cont.)

S. No.	Character	Association	S/NS	Reference
			NS	Karunakar Raju (2005) Vijayalaxmi (2008) Anandan (2009)
		Negative	NS	Rao *et al.* (2001) Srinivasulu (2009)
			S	Mandloi *et al.* (2003)
3.	Bundle strength (g/tex)	Positive	S	Muthu *et al.* (2004) Murthy *et al.* (2006)
			NS	Neelima (2002) Vijayalaxmi (2008) Anandan (2009)
		Negative	NS	Reddy (2001) Neelam and Potdukhe (2002) Mandloi *et al.* (2003) Karunakar Raju (2005) Srinivasulu (2009)
4.	Uniformity ratio	Positive	NS	Karunakar Raju (2005) Vijayalaxmi (2008) Anandan (2009) Srinivasulu (2009)
		Negative	S	Muthu *et al.* (2004)
			NS	Sangeetha (1998) Neelima (2002)
5.	Fibre elongation (%)	Positive	S	Vijayalaxmi (2008)
			NS	Muraleedhar (2005) Srinivasulu (2009)
		Negative	S	Muthu *et al.* (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 *et al.* (2007) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Neelima (2002)
		Positive	S	Mandloi *et al.* (2003) Muthuswamy and Vivekanandan (2004)

Table 2.4 (Cont.)

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 *et al.* (2003) Muthuswamy and Vivekanandan (2004) Muthu *et al.* (2004) Pankaj Rathore *et al.* (2004) Karunakar Raju (2005) Tuteja *et al.* (2005 b) Padmavathi (2008) Vijayalaxmi (2008) Anandan (2009)
		Negative	NS	Rao *et al.* (2001) Reddy (2001) Neelima (2002) Srinivasulu (2009)
			S	Rao *et al.* (2001)
3.	Uniformity ratio	Positive	NS	Neelima (2002)
			S	Sivaprasad (2003)
		Negative	S	Altaher and Singh (2003b) Karunakar Raju (2005) Leela Pratap *et al.* (2007) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Muthu *et al.* (2004) Tuteja *et al.* (2005b) Anandan,(2009) Srinivasulu (2009)
XI. Association of micronaire value with				
1.	Bundle strength (g/tex)	Positive	S	Neelima (2002)
			NS	Rao *et al.* (2001) Reddy (2001) Mandloi *et al.* (2003) Srinivasulu (2009)

Table 2.4 (Cont.)

S. No.	Character	Association	S/NS	Reference
		Negative	S	Karunakar Raju (2005) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Neelam and Potdukhe (2002) Tuteja *et al.* (2005 b) Anandan (2009)
2.	Uniformity ratio	Positive	S	Altaher and Singh (2003b) Pankaj Rathore *et al.* (2004) Karunakar Raju (2005) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Muthu *et al.* (2004) Srinivasulu (2009)
		Negative	S	Tuteja *et al.* (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 *et al.* (2005a) Leela Pratap *et al.*(2007) Padmavathi (2008) Vijayalaxmi (2008) Srinivasulu (2009)
			NS	Neelima (2002)
2.	Fibre elongation (%)	Positive	S	Kamal *et al.* (2002) Muthuswamy and Vivekanandan (2004) Ravi kumar (2004) Muraleedhar (2005) Padmavathi (2008) Vijayalaxmi (2008)
			NS	Anandan (2009)

Table 2.4 (Cont.)

S. No.	Character	Association	S/NS	Reference
		Negative	S	Muthu *et al.* (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-2.5: 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 *et al.* (2006) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008)	Gururajan (2000) Muthu *et al.* (2004) Anandan (2009) Sarada (2010)
2.	Plant height (cm)	Reddy (2001) Altaher and Singh (2003b) Sivaprasad (2003) Ahuja *et al.*(2004) Muthu *et al.* (2004) Eswararao (2008) Anandan (2009) Srinivasulu (2009)	Ladole and Meshram (2000) Karunakar Raju (2005) Verma *et al.* (2006) Padmavathi (2008) Vijayalaxmi (2008) Sarada (2010)
3.	No. of monopodia per plant	Gururajan (2000) Reddy (2001) Kaushik *et al.* (2003) Altaher and Singh (2003a) Muthu *et al.* (2004) Eswararao (2008) Srinivasulu (2009) Remzi Ekinci *et al*. (2010)	Ladole and Meshram (2000) Sivaprasad (2003) Karunakar Raju (2005) Tuteja *et al.* (2006) Verma *et al*. (2006) Padmavathi (2008) Vijayalaxmi (2008) Sarada (2010)
4.	No. of sympodia per plant	Ladole and Meshram (2000) Rao *et al.* (2001) Kaushik *et al.* (2003) Neelima *et al.* (2005) Verma *et al*. (2006) Leela Pratap *et al.* (2007) Padmavathi (2008) Vijayalaxmi (2008) Anandan (2009) Srinivasulu (2009) Sarada (2010) Remzi Ekinci *et al*. (2010)	Sumathi and Nadarajan (1995) Gururajan (2000) Reddy(2001) Sivaprasad (2003) Muthu *et al.* (2004) Karunakar Raju (2005) Tuteja *et al.* (2006) Eswararao (2008)

Table 2.5 (Cont.)

S. No.	**Character**	**Positive Direct effect**	**Negative Direct effect**
5.	No. of bolls/plant	Altaher and Singh (2003b) Sivaprasad (2003) Ahuja *et al.*(2004) Muthu *et al.* (2004) Gururajan and Sundar (2004) Saeed *et al.*(2004) Karunakar Raju (2005) Neelima *et al.* (2005) Verma *et al*. (2006) Leela Pratap *et al.* (2007) Sakthi *et al.*(2007) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008) Anandan (2009) Srinivasulu (2009) Sarada (2010) Remzi Ekinci *et al*.(2010) Shazia Salahuddin *et al.* (2010)	Kaushik *et al.* (2003) Tuteja *et al.* (2006)
6.	Boll weight (g)	Neelima (2002) Altaher and Singh (2003b) Kaushik *et al.* (2003) Muthu *et al.* (2004) Gururajan and Sundar (2004) Karunakar Raju (2005) Sakthi *et al.*(2007) Padmavathi (2008) Anandan (2009) Srinivasulu (2009) Sarada(2010) Shazia Salahuddin *et al.* (2010)	Ladole and Meshram (2000) Verma *et al*. (2006) Eswararao (2008) Vijayalaxmi (2008)
7.	Ginning out-turn (%)	Gururajan (2000) Reddy (2001) Muthu *et al.* (2004) Tuteja *et al.* (2006) Verma *et al*. (2006) Leela Pratap *et al.* (2007) Vijayalaxmi (2008) Anandan (2009) Sarada (2010)	Ladole and Meshram (2000) Altaher and Singh (2003b) Sivaprasad (2003) Gururajan and Sundar (2004) Karunakar Raju (2005) Eswararao (2008) Padmavathi (2008) Srinivasulu (2009) Shazia Salahuddin *et al.* (2010)

Table 2.5 (Cont.)

S. No.	Character	Positive Direct effect	Negative Direct effect
8.	Seed index (g)	Gururajan (2000) Rao *et al.* (2001) Reddy (2001) Sivaprasad (2003) Murthy *et al.*(2006) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008) Anandan (2009) Srinivasulu (2009) Sarada (2010)	Ladole and Meshram (2000) Neelima (2002) Altaher and Singh (2003a) Gururajan and Sundar (2004) Karunakar Raju (2005)
9.	Lint index (g)	Reddy (2001) Altaher and Singh (2003b) Gururajan and Sundar (2004) Neelima *et al.*(2005) Karunakar Raju (2005) Sakthi *et al.*(2007) Eswararao (2008) Vijayalaxmi (2008) Anandan (2009)	Sivaprasad (2003) Muthu *et al.* (2004) Leela Pratap *et al.* (2007) Padmavathi (2008) Sarada (2010)
10.	2.5% span length (mm)	Ladole and Meshram (2000) Muthu *et al.* (2004) Karunakar Raju (2005) Tuteja *et al.* (2006) Vijayalaxmi (2008) Sarada (2010)	Reddy (2001) Neelima (2002) Sivaprasad (2003) Gururajan and Sundar (2004) Verma *et al*. (2006) Eswararao (2008) Padmavathi (2008)
11.	Micronaire value (10^{-6} g/in)	Rao *et al.* (2001) Reddy (2001) Sivaprasad (2003) Muthu *et al.* (2004) Neelima *et al.* (2005) Murthy *et al.* (2006) Leela Pratap *et al.* (2007) Padmavathi (2008) Vijayalaxmi (2008) Srinivasulu (2009) Sarada (2010)	Dedaniya and Pethani (1994) Karunakar Raju (2005) Eswararao (2008) Anandan (2009)

Table 2.5 (Cont.)

S. No.	Character	Positive Direct effect	Negative Direct effect
12.	Bundle strength (g/tex)	Sivaprasad (2003) Murthy *et al.*(2006) Padmavathi (2008) Sarada (2010)	Muthu *et al.* (2004) Gururajan and Sundar (2004) Karunakar Raju (2005) Eswararao (2008) Vijayalaxmi (2008)
13.	Uniformity ratio	Sivaprasad (2003) Karunakar Raju (2005) Murthy *et al.*(2006) Eswararao (2008) Vijayalaxmi (2008)	Muthu *et al.* (2004) Leela Pratap *et al.* (2007) Padmavathi (2008) Anandan (2009) Sarada (2010)
14.	Fibre elongation (%)	Muthu *et al.* (2004)	Muraleedhar (2005) Eswararao (2008) Padmavathi (2008) Vijayalaxmi (2008) Anandan (2009) Srinivasulu (2009) Sarada (2010)

Chapter III

MATERIAL AND METHODS

The present investigation entitled as "Genetic diversity in cotton (*Gossypium hirsutum* L.)" was taken up during *kharif* 2010-11 at Agricultural College Farm, Bapatla, Andhra Pradesh. The site of the experiment is situated at 15^{0}54' North and 80^{0}3' 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 MATERIAL

The experimental material used in the present study comprised of 40 cotton lines obtained from all over India. The source of origin of these genotypes is presented in Table-3.1. International Bureau of Plant Genetic Resources (IBPGR) descriptor list of morphological traits was used to characterize the given germplasm and presented in Table-3.2.

3.2 METHODS

3.2.1 Experimental Technique

The detailed experimental technique for the present investigation is furnished in Table-3.3.

Table 3.3 : Experimental details of the present investigation

Location	:	Agricultural College Farm, Bapatla
Season	:	*Kharif*, 2010-11
Entries	:	40
Design	:	Randomized complete block design (RCBD)
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_2O_5: 45 K_2O kg ha^{-1}
Plant protection	:	Need based

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 harvest.

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 were 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 quantitative traits data were recorded on 10 randomly selected competitive plants per entry per replication and labeled for recording observations on quantitative traits.

The quantitative characters recorded for the present study are days to 50% flowering, plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), ginning out-turn (%), seed index (g), lint index (g), micronaire (10^{-6}g/in), bundle strength (g/tex), uniformity ratio, elongation (%) and seed cotton yield per plant (g). The mean of the ten plants was used for statistical analysis. However, the data on days to 50% flowering, ginning out- turn (%), 2.5% span length (mm), micronaire (10^{-6}g/inch), bundle strength (g/tex) and uniformity ratio were recorded on plot basis. To estimate fibre quality parameters composite sample of 300g 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)

Plant height 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 out-turn (%)

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

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

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)

The distance from the clamp on a fibre board to a point up to which only 2.5% of the fibres extends. It is expressed as span length in (mm) and was estimated by premier HFT 9000 V 2.1.5 SP high volume instrument.

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

A physical property indicating the cross-sectional thickness of fibre, which determines the spinning value of a variety. The fibre fineness was estimated by premier HFT 9000 V 2.1.5 SP high volume instrument**.**

3.2.2.12 Bundle strength (g/tex)

A measure of the tensile strength of fibre using the principal of constant rate of loading. This was measured by using premier HFT 9000 V 2.1.5 SP high volume instrument at 1/8th gauge length.

3.2.2.13 Uniformity ratio

The ratio between 2 span lengths (2.5% and 50%) expressed as a percentage and was estimated by using premier HFT 9000 V 2.1.5 SP high volume instrument.

3.2.2.14 Fibre elongation (%)

It is fibre extensibility measured with the help of HFT 9000V 2.1.5 SP High volume instrument.

3.2.2.15 Seed cotton yield per plant (g)

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

3.3 STATISTICAL ANALYSIS

The data recorded on various characters were subjected to 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 i^{th} block in the j^{th} genotype

μ = general mean

b_i = effect of i^{th} block

t_j = effect of j^{th} genotype

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

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

Source of variation	**d.f**	**SS**	**MSS**	**F ratio**
Replications	r-1	RSS	Mr = σ^2e+ σ^2r	Mr/Me
Treatments (genotypes)	t-1	TrSS	Mt= σ^2e+ σ^2g	Mt/Me
Error	(r-1)(t-1)	ESS	Me= σ^2e	
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^2e = Error variance

σ^2g = Variance due to genotypes

σ^2r = 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).

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

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

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

Low = Less than 10%

Moderate = 10-20%

High = More than 20%

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

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

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

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

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

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

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

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

3.3.3 Correlation Analysis

Analysis of Covariance

Analysis of Covariance was computed by following procedure.

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

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

$X_{ij} - X$ = 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	rxy
Genotypes	(t-1)	TY	TX	TXY	ty	tx	txy
Error	(r-1)(t-1)	EY	EX	EXY	ey	ex	exy

Where,

df = Degrees of freedom

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)

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

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)

$$r(x_{i.}x_j)g = \frac{Cov(\ x_i.x_j\ )g}{\sqrt{V(x_i)g.V(x_j)g}}$$

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 to yield.

Path coefficient analysis permits the separation of coefficient in to direct effects (path coefficients) and indirect effects (effect exerted through other variables). It is a standardized partial regression analysis and deals with a closed system of variable that are linearly related. Such information provides for realistic basis of allocation of appropriate weightage to various yield components (Iqbal *et al.*, 2006).

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

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

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

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

$$r_{ky} = r_{k1} P_{1y} + r_{k2} P_{2y} + r_{k3} P_{3y} + \ldots. + r_{kk} P_{ky}$$

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:

$$\overset{\mathbf{A}}{\begin{pmatrix} r_{1Y} \\ r_{2Y} \\ . \\ . \\ . \\ . \\ r_{iY} \end{pmatrix}} = \overset{\mathbf{C}}{\begin{pmatrix} 1 & r_{12} & r_{1i} \\ r_{21} & 1 & r_{2i} \\ . & . & . \\ . & . & . \\ r_{i1} & r_{i2} & 1 \end{pmatrix}} \overset{\mathbf{B}}{\begin{pmatrix} P_{1Y} \\ P_{2Y} \\ . \\ . \\ . \\ . \\ P_{iY} \end{pmatrix}}$$

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

where,

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

The direct effects were calculated as follows

$$P_{1Y} = \sum_{i=1}^{k} C_{1i} r_{iY}$$

$$P_{2Y} = \sum_{i=1}^{k} C_{2i} r_{iY}$$

$$p_{iy} = \sum_{i=1}^{k} c_{1i} r_{iy}$$

3.3.4.1 Residual effect

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

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

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

Genetic divergence

3.3.5 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

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

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

where,

$\wedge$ = Wilk’s criterion

(E) = Determinant of error matrix and

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

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

where,

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

n = Degrees of freedom for error + varieties

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

P = Number of variables or characters (15)

Q = Number of varieties – 1 (or d.f for population 39)

V (Stat) is distributed as α^2 with PQ (585= 15x39) degrees of freedom.

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.,* d^2_i. Therefore transformation of the correlated variables into uncorrelated ones was done before working out the D^2 values. Transformation was done using pivotal condensation method.

3.3.5.1.2 Computation of D^2 values

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

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

where,

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

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

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

3.3.5.1.3 Testing the significance of D^2 values

The D^2 value obtained for a pair of population is taken as calculated value of X^2 and is tested against the tabulated value of α^2 for P (15) degrees of freedom where P (15) is the number of characters considered.

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.

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

where,

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

M = All possible combinations of number of genotypes considered.

3.3.5.1.5 Grouping of genotypes into various clusters

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

To start with, two populations having the closest distance from each other were considered, to which the third population having the smallest D^2 value from the first two populations was added.

Similarly, the next nearest fourth population was considered and this procedure was continued. At certain stage when it was felt that after adding a particular population there was an abrupt increase in the average D^2, that population was not considered for including in that cluster.

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

3.3.5.1.6 Average intra- cluster distance

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

3.3.5.1.7 Average inter-cluster distance

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

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

where,

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.

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

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

The principal components were identified by following procedure.

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

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

where,

A_{ij} are found such that Y_j is uncorrelated Y_1, $Y_{2,}$……..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) = $\lambda_1+\lambda_2 +\ldots+ \lambda_{p.}$ The importance of the j^{th} principal component is given by

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

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

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

where S_i is the standard deviation of $X_{i.}$

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

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

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

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

3.3.5.2.2 Cluster analysis

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

1. Obtaining data matrix

PCA scores for 40 genotypes were used as input for clustering because principal component analysis provides variable independence and balanced weighting of traits, which leads to an effective contribution of different characters on the basis of respective variation.

2. Standardizing the data matrix

To compare the similarities among the genotypes the data matrix was 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.

$$Z_{ij} = \frac{\overline{X}_{ij} - \overline{X}_j}{s_{ij}}$$

where,

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

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

For

i= genotypes *i.e.,* 40

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

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

3. Computing the resemblance matrix

A resemblance coefficient, which measures the over all resemblance (the degree of similarity or distance) between a pair of genotypes was computed. Here, 40 genotypes were taken in data matrix therefore resemblance coefficient was computed for a total of 780 combinations *i.e.*, ${}^{40}C_2$ 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.*, 40

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

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

4. Execution of the clustering method

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

3.3.5.2.3 Complete linkage diagram

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

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

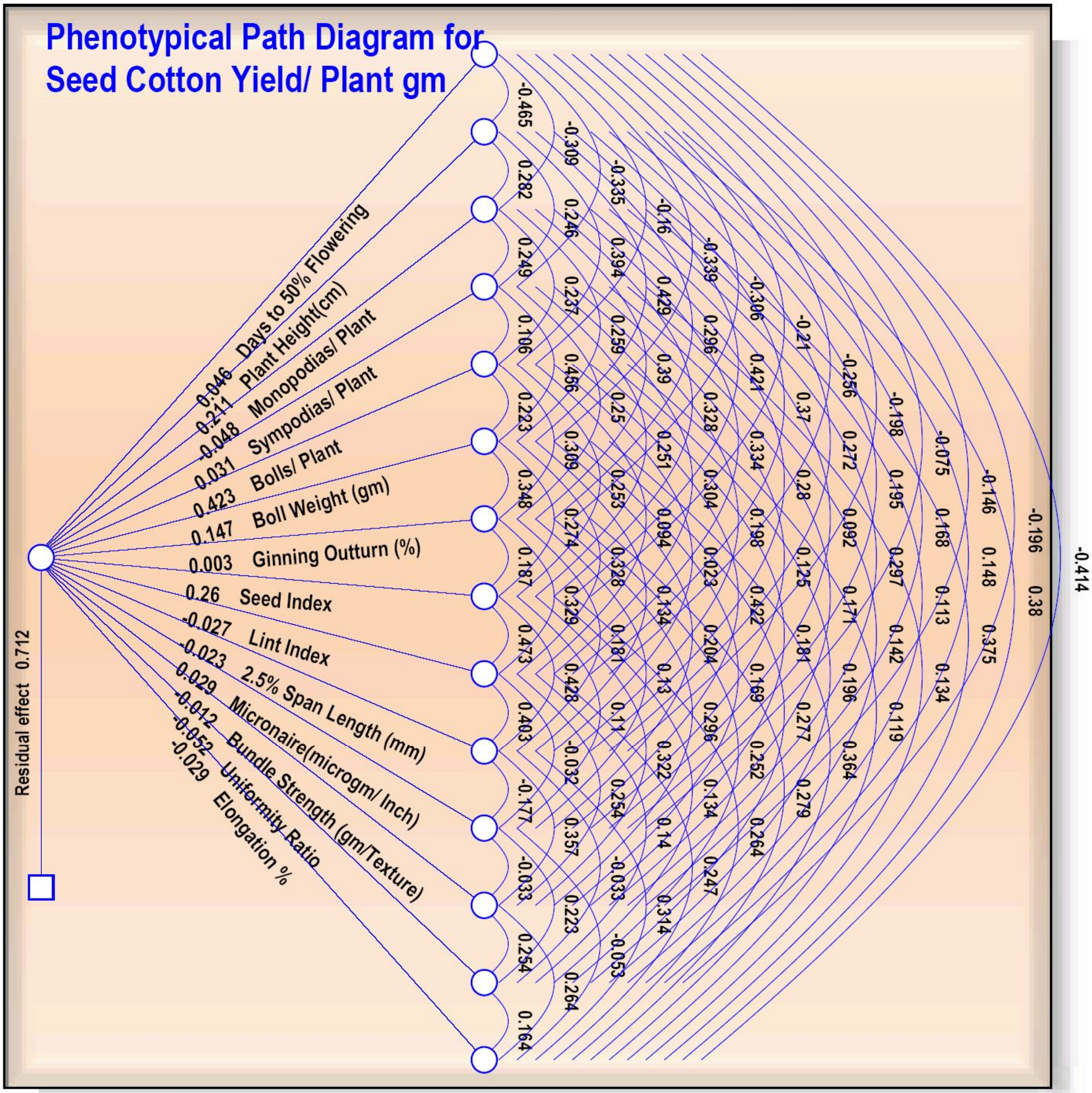


Fig-4.2: Phenotypic path diagram showing cause and effect relationship of yield components with seed cotton yield per plant in cotton (*Gossypium hirsutum* L.)

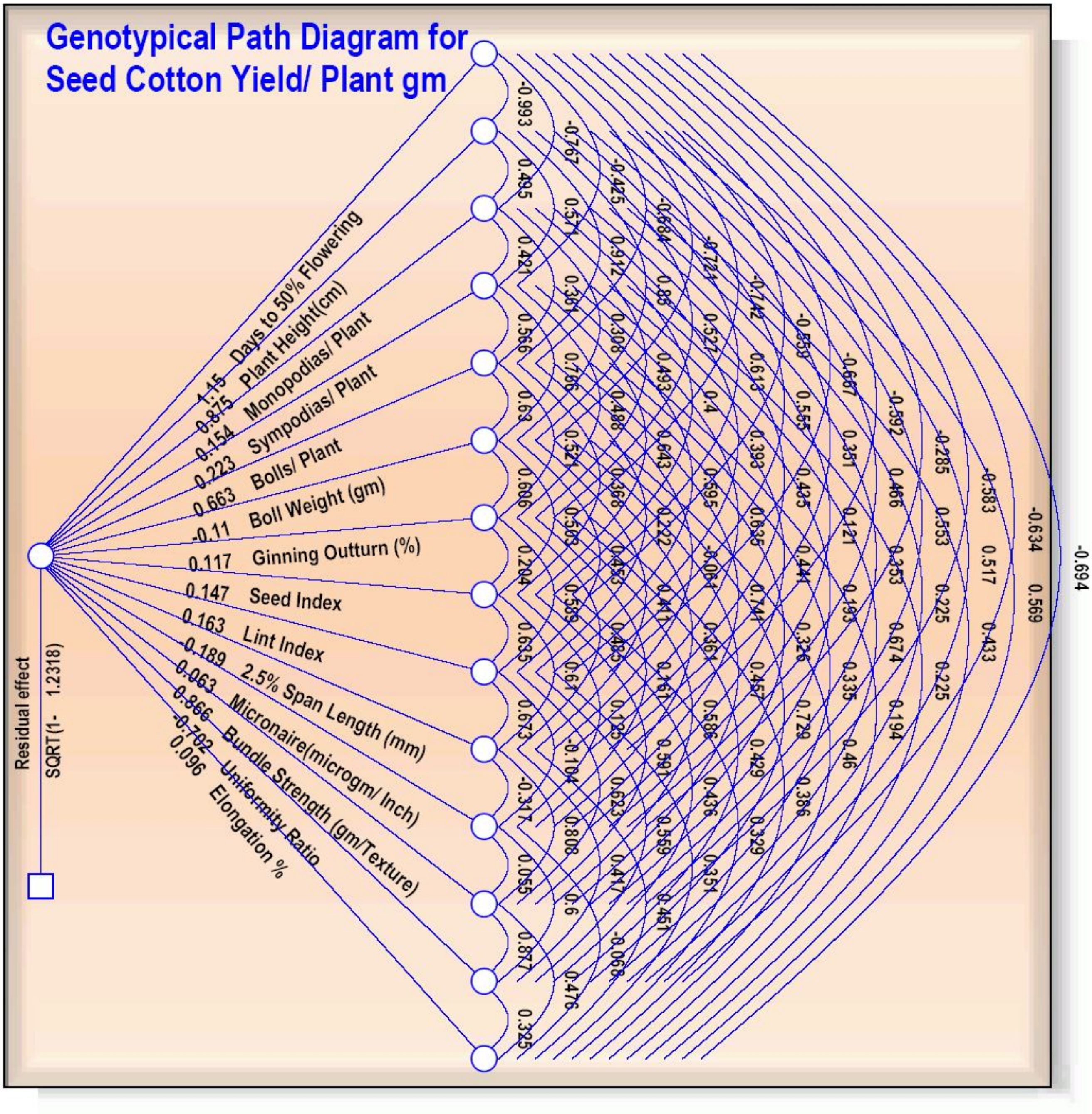


Fig-4.3: Genotypic path diagram showing cause and effect relationship of yield components with seed cotton yield per plant in cotton (*Gossypium hirsutum* L.)

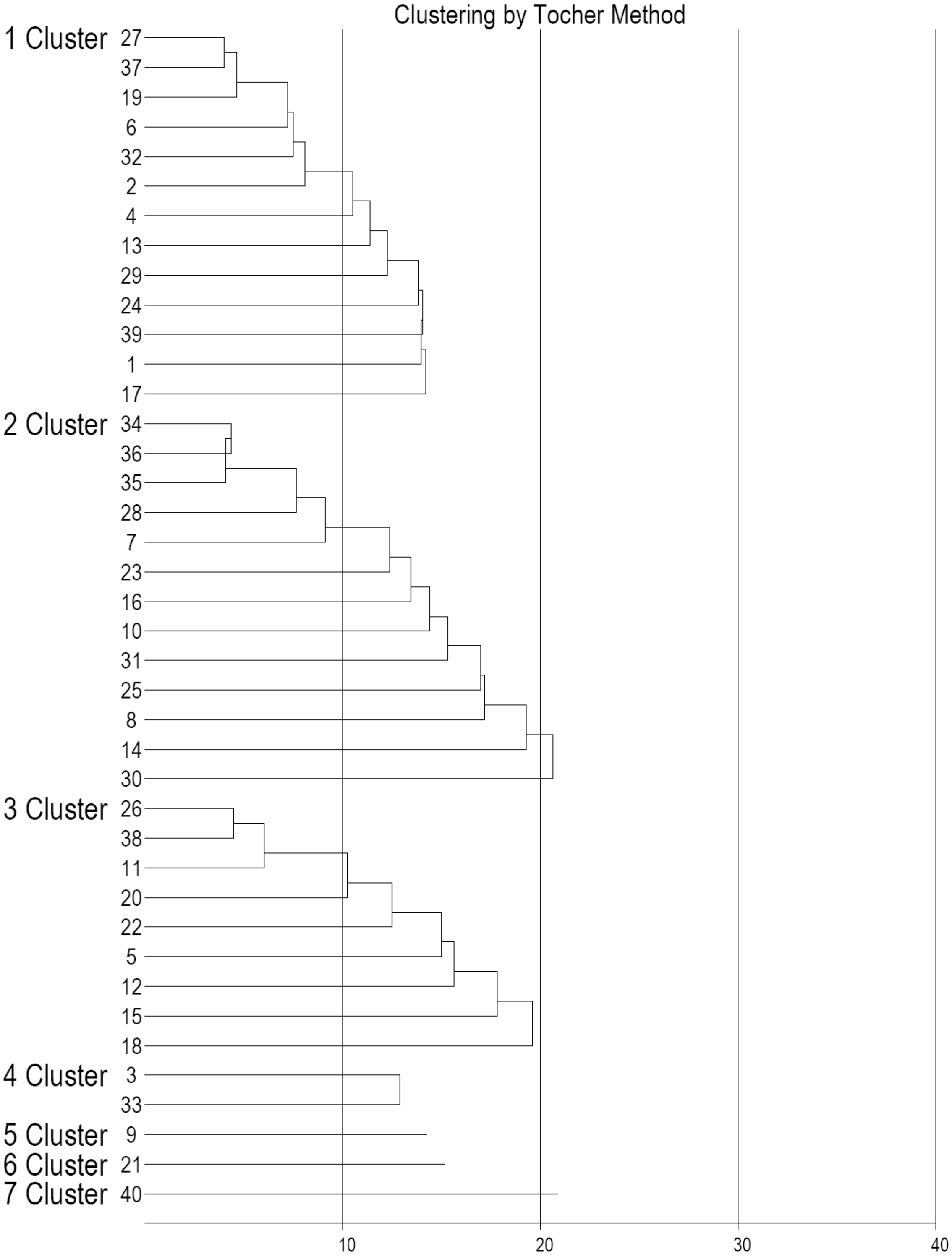


Fig-4.4: **Dendrogram showing relationship of 40 cotton (*Gossypium hirsutum* L.) genotypes in seven clusters using Tocher's method (Genotype numbers are as per Table No. 3.1).**

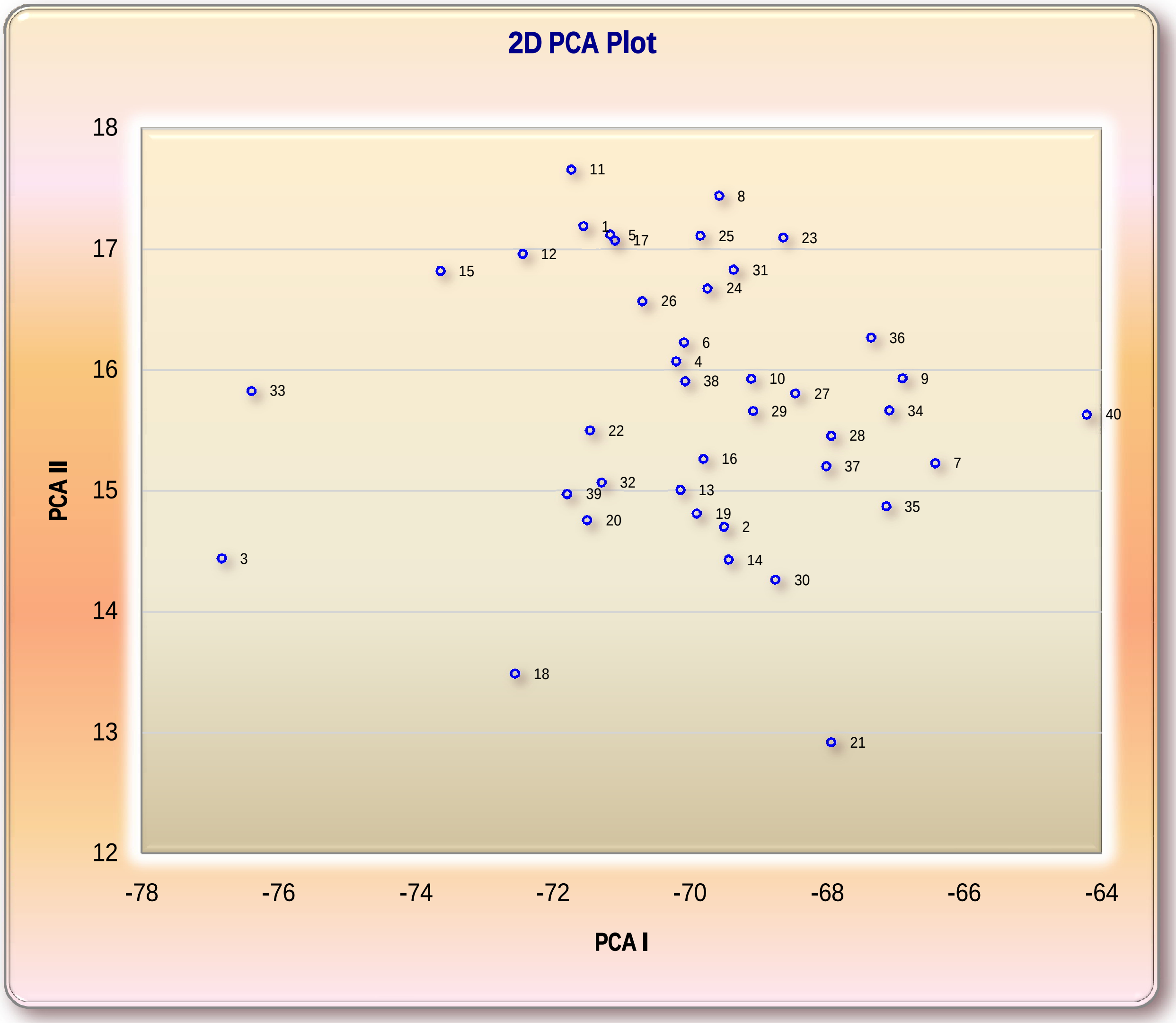


Fig-4.5: Two dimensional graph showing relative position of 40 cotton (*Gossypium hirsutum* L.) genotypes based on PCA scores (Genotype numbers are as per the Table No. 3.1).

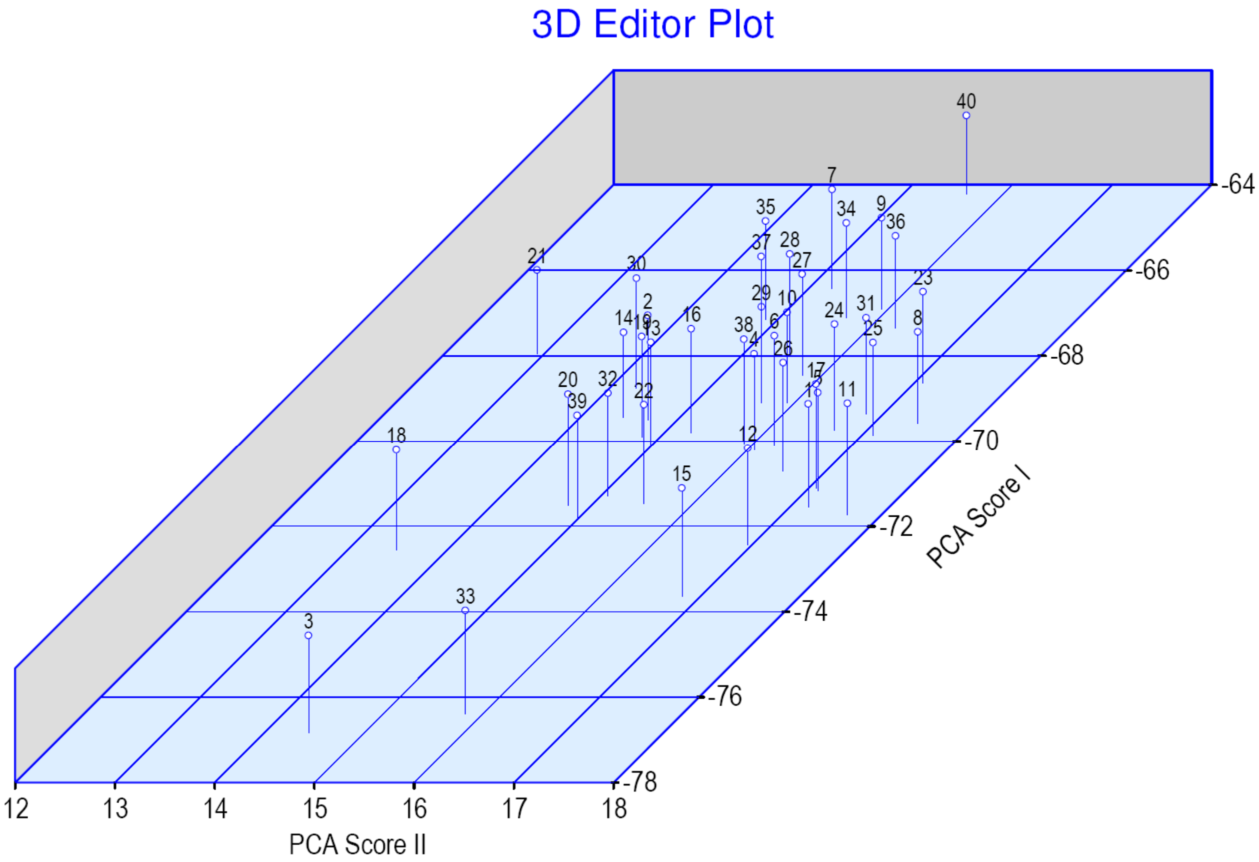


Fig-4.6: Three dimensional graph showing relative position of 40 cotton (*Gossypium hirsutum* L.) genotypes based on PCA scores (Genotype numbers are as per the Table No. 3.1).

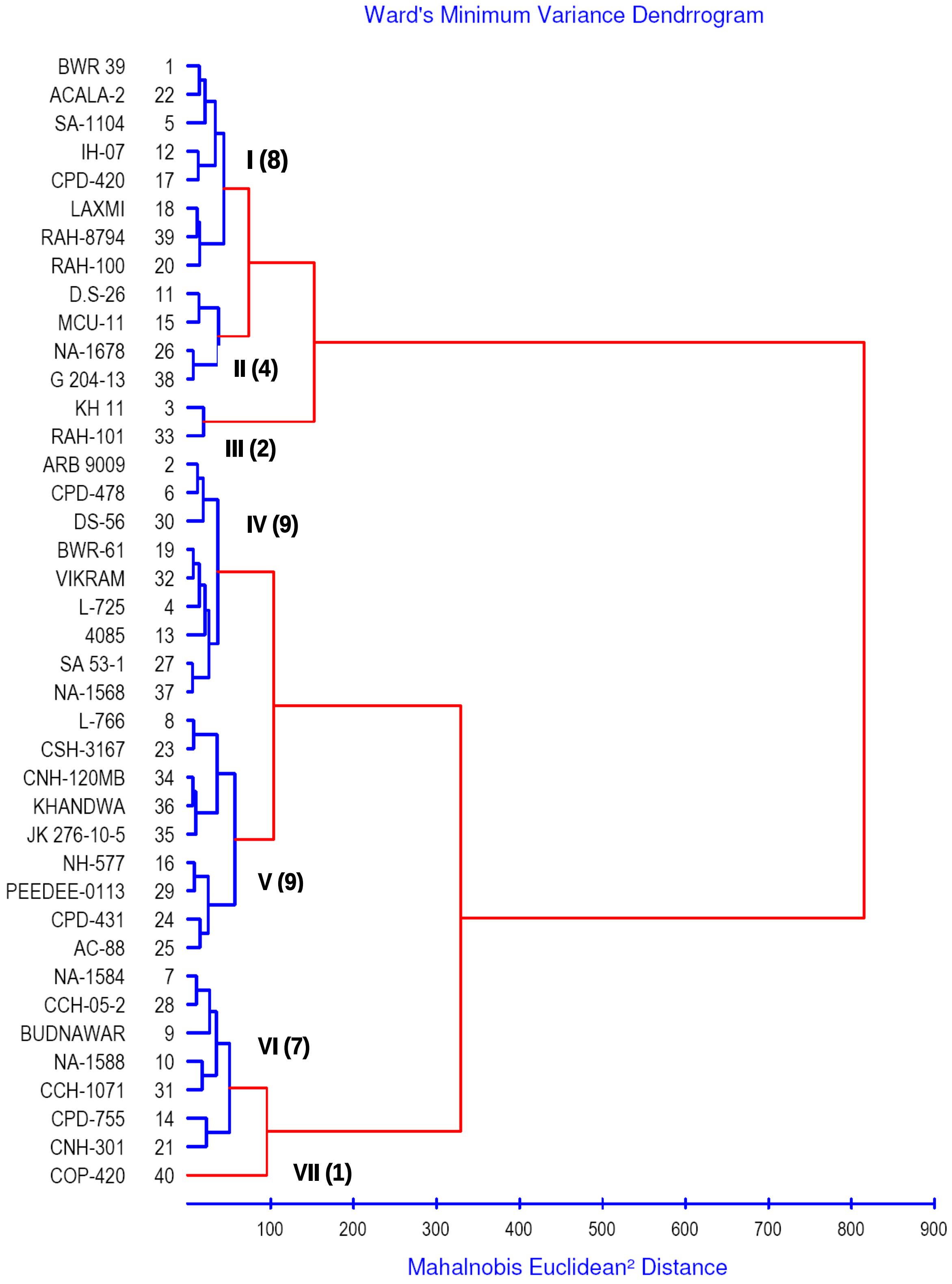
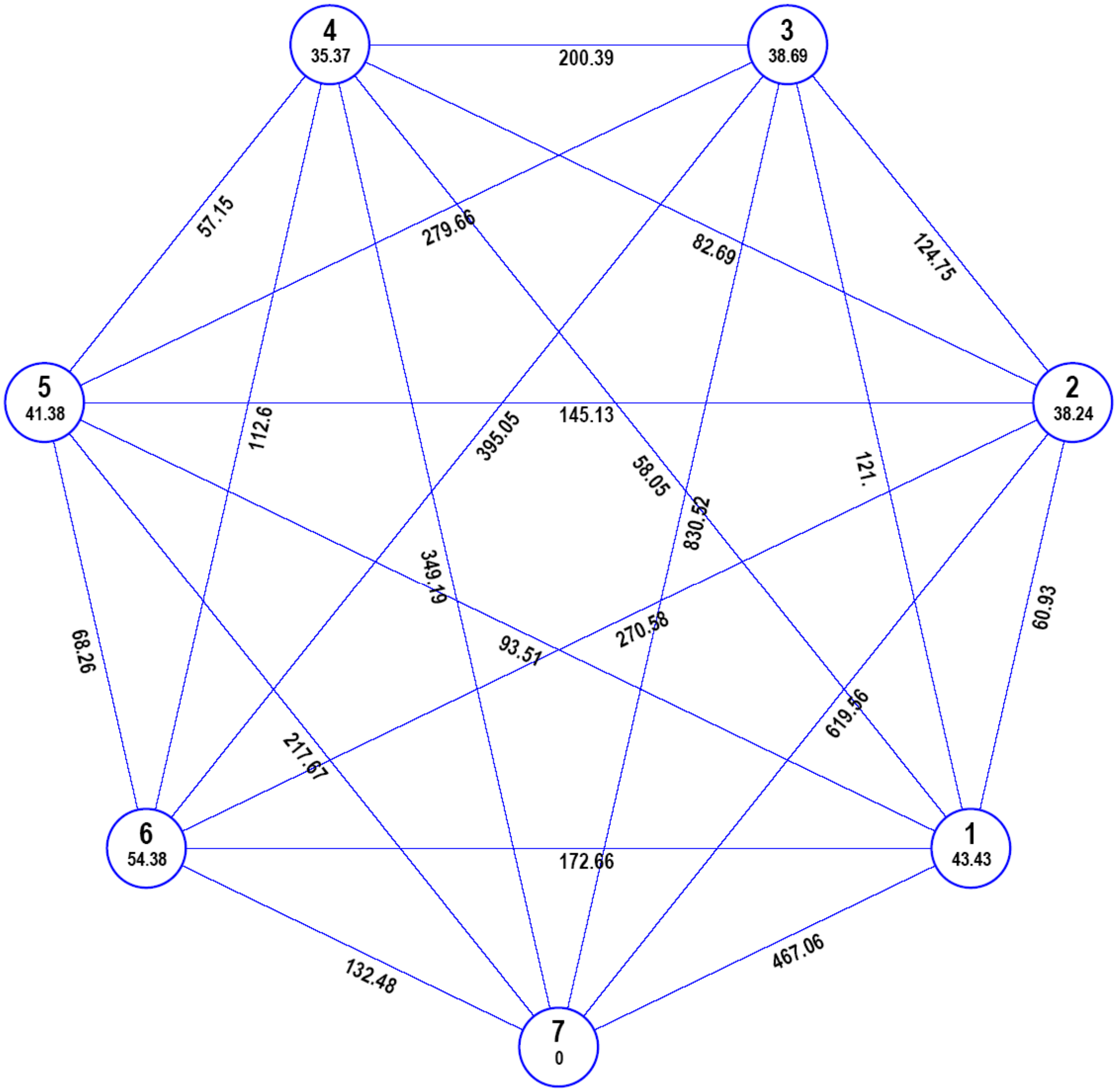


Fig-4.7: Dendrogram showing relationship of 40 cotton (*Gossypium hirsutum* L.) genotypes in seven clusters using Ward's minimum variance method.



Euclidean² Distance (Not to the Scale)

Fig-4.8: Intra-and inter-cluster distance of 40 cotton (*Gossypium hirsutum* L.) genotypes in seven clusters based on Euclidean ^{2} distances.

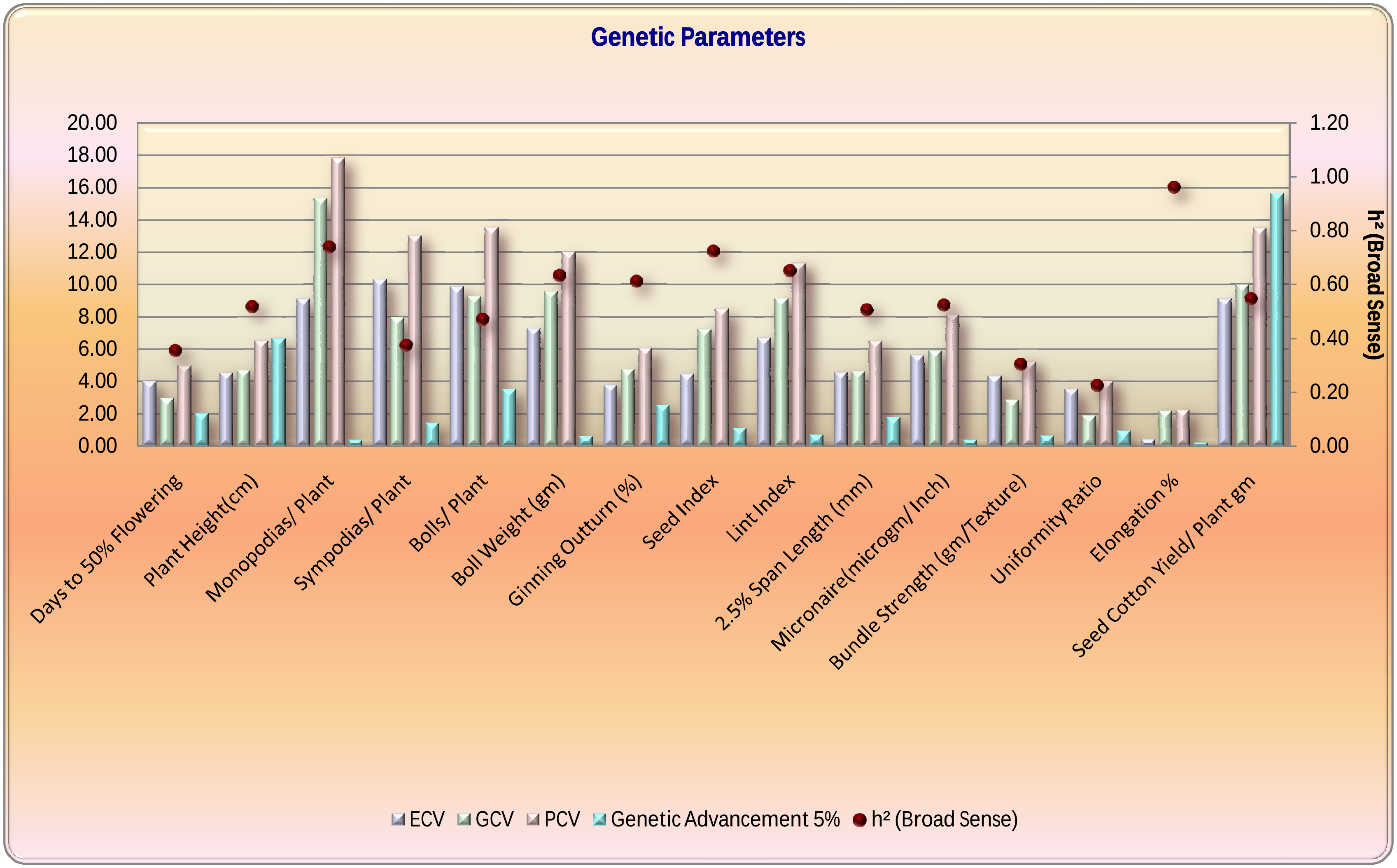


Fig.4.1: Environment, genotypic and phenotypic coefficients of variation, genetic advance as per cent of mean (GAM) and heritability for 15 characters in cotton (*Gossypium hirsutum* L.).

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)
21	CNH-301	57.00	94.66	1.54	16.46	29.66	4.21	**30.74**	9.03
22	ACOLA-2	55.66	100.33	1.83	15.66	26.66	4.56	34.22	9.06
23	CSH-3167	57.00	95.00	**0.95**	12.93	24.33	3.86	31.83	8.77
24	CPD-431	56.66	94.00	**2.00**	15.56	25.66	3.62	34.36	9.32
25	AC-88	56.33	89.43	1.71	16.33	**23.00**	4.31	32.46	9.75
26	NA-1678	55.66	96.50	1.40	13.33	25.33	3.67	33.16	8.74
27	SA 53-1	57.00	89.33	1.50	13.04	25.66	3.80	31.60	8.35
28	CCH-05-2	56.00	93.33	1.66	13.86	25.00	3.39	33.46	9.04
29	PEE DEE-0113	57.00	88.66	1.46	15.00	28.00	4.02	33.22	9.05
30	DS-56	56.00	96.00	1.87	12.30	30.00	3.53	34.56	8.12
31	CCH-1071	55.00	90.00	1.50	14.26	25.33	4.25	37.12	8.28
32	VIKRAM	54.33	97.93	1.73	14.50	30.00	3.88	35.85	9.10
33	RAH-101	51.66	108.00	1.75	17.00	31.00	5.21	36.36	9.71
34	CNH-120 MB	56.33	90.33	1.06	15.00	26.33	**3.32**	32.10	**7.56**
35	JK 276-10-5	58.66	93.00	1.40	13.06	25.66	3.81	31.28	8.47
36	KHANDWA	59.33	87.00	1.26	15.00	24.66	3.75	32.10	8.43
37	NA-1568	60.00	90.96	1.56	14.26	26.33	3.57	31.87	8.44
38	G 204-13	56.00	96.95	1.30	13.40	25.33	4.15	31.41	8.37
39	RAH-8794	56.66	97.73	1.90	15.53	29.66	4.18	35.35	9.88
40	COP-420	**61.33**	**86.66**	1.06	14.20	24.33	3.64	30.92	8.63
	Mean	**55.84**	**95.40**	**1.56**	**14.54**	**26.91**	**3.98**	**33.41**	**8.98**
	C.V.	4.021	4.55	9.09	10.31	9.85	7.27	3.79	4.48
	C.D at 5%	3.650	7.06	0.23	2.43	4.31	0.47	2.05	0.65

Table 4.4 (Contd.)

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	BWR 39	5.09	27.83	4.25	19.72	51.64	5.56	97.00
2	ARB 9009	4.17	24.51	4.77	19.35	52.20	5.53	92.66
3	KH 11	**5.73**	28.78	5.02	20.46	51.88	5.56	**140.33**
4	L-725	4.68	27.97	4.49	21.42	51.54	5.49	111.33
5	SA-1104	5.36	29.23	4.97	21.00	52.83	5.56	92.66
6	CPD-478	4.89	27.88	4.34	20.66	50.20	5.54	101.33
7	NA-1584	3.94	26.43	4.25	20.21	49.57	5.36	99.33
8	L-766	4.64	28.28	4.44	20.11	50.74	5.46	94.00
9	BADANWAR	4.80	27.53	4.40	19.97	50.81	5.23	91.66
10	NA-1588	5.58	27.39	4.52	19.45	51.74	5.32	97.33
11	DS-26	5.30	28.46	4.19	20.83	48.90	5.66	97.00
12	IH-07	5.49	27.62	4.35	20.95	52.70	5.53	124.66
13	4085	**3.91**	27.63	4.18	19.24	49.01	5.58	102.33
14	CPD-755	4.20	26.17	5.15	20.93	50.80	5.32	118.33
15	MCU-11	4.98	**29.77**	4.17	21.09	50.82	5.69	105.33
16	NH-577	4.57	25.87	4.31	19.79	50.99	5.41	119.00
17	CPD-420	5.47	28.81	4.00	19.88	48.16	5.50	109.33
18	LAXMI	4.94	25.21	5.14	20.50	51.87	5.57	123.00
19	BWR-61	4.59	26.83	4.69	19.42	50.52	5.50	107.66
20	RAH-100	5.02	26.15	4.39	19.48	50.05	5.61	97.44

Table 4.4 (Contd.)

Table 3.2: IBPGR Descriptors for morphological traits in cotton (*Gossypium hirsutum* L.)

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 = Embeded	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 3.1: Genotype name and source of cotton (*Gossypium hirsutum* L.) lines employed in the present study

S. No.	Genotype	Source
1	BWR-39	RARS, Lam, Guntur, Andhra Pradesh
2	ARB-9009	UAS, Arbhavi, Karnataka
3	KH-11	RARS, Lam, Guntur, Andhra Pradesh
4	L-725	RARS, Lam, Guntur, Andhra Pradesh
5	SA-1104	GAU, Surat, Gujarat
6	CPD-478	NAU, Surat, Gujarat
7	NA-1584	RARS, Nandyal
8	L-766	RARS, Lam, Guntur
9	BADANWAR	JNKV, Indore, Madya Pradesh
10	NA-1588	RARS, Nandyal, Andhra Pradesh
11	D.S-26	UAS, Dharwad, Karnataka
12	IH-07	JNKV, Indore, Madya Pradesh
13	4085	RARS, Nandyal, Andhra Pradesh
14	CPD-755	UAS, Dharwad, Karnataka
15	MCU-11	TNAU, Coimbatore, Tamilnadu
16	NH-577	AICCIP
17	CPD-420	UAS, Dharwad, Karnataka
18	LAXMI	UAS, Dharwad, Karnataka
19	BWR-61	RARS, Lam, Guntur, Andhra Pradesh
20	RAH-100	ARS, Raichur, Karnataka
21	CNH-301	CICR, Nagpur, Maharastra
22	ACOLA-2	USA
23	CSH-3167	CICR, Coimbatore, Tamilnadu
24	CPD-431	UAS, Dharwad, Karnataka
25	AC-88	CICR, Nagpur, Maharastra
26	NA-1678	RARS, Nandyal
27	SA 53-1	UAS, Arbhavi, Karnataka
28	CCH-05-2	CICR, Coimbatore, Tamilnadu
29	PEEDEE-0113	USA
30	DS-56	UAS, Dharwad,Karnataka
31	CCH-1071	CICR, Coimbatore, Tamilnadu
32	VIKRAM	RARS, Nandyal
33	RAH-101	ARS, Raichur, Karnataka
34	CNH-120MB	CICR, Nagpur
35	JK-276-10-5	UAS, Dharwad, Karnataka
36	KHANDWA	JNKV, Khandwa
37	NA-1568	RARS, Nandyal, Andhra Pradesh
38	G 204-13	GAU, Surat, Gujarat
39	RAH-8794	Dharwad, Karnataka
40	COP-420	RARS, Nandyal

Table 4.1 : Stem and leaf morphological descriptors in 40 cotton (*Gossypium hirsutum* L.) 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	BWR 39	1	3	1	2	2	5	1
2	ARB 9009	1	5	1	2	2	5	1
3	KH-11	1	3	1	2	2	5	1
4	L-725	1	5	1	2	2	5	1
5	SA-1104	1	5	1	2	2	5	1
6	CPD-478	1	5	1	3	2	5	1
7	NA-1584	1	5	1	2	2	5	1
8	L-766	1	5	1	3	2	5	1
9	BADANWAR	1	5	1	2	2	5	1
10	NA-1588	1	3	1	2	2	5	1
11	D.S-26	1	5	1	2	2	5	1
12	IH-07	1	5	4	3	2	5	1
13	4085	1	5	1	2	2	5	1
14	CPD-755	1	3	1	2	2	5	9
15	MCU-11	1	5	1	3	2	5	1
16	NH-577	1	5	1	2	2	5	1
17	CPD-420	1	5	1	2	2	5	1
18	LAXMI	1	5	1	2	2	5	1
19	BWR-61	1	5	1	2	2	5	1
20	RAH-100	1	5	1	3	2	5	1

Table 4.1 (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				
21	CNH-301	1	5	1	2	2	5	1
22	ACOLA-2	1	5	1	2	2	5	1
23	CSH-3167	1	5	1	2	2	9	1
24	CPD-431	1	5	1	3	2	5	1
25	AC-88	1	5	1	2	2	5	1
26	NA-1678	1	3	1	2	2	5	1
27	SA 53-1	1	3	1	2	2	5	1
28	CCH-05-2	1	5	1	2	2	5	1
29	PEEDEE-0113	1	5	1	2	2	5	1
30	DS-56	1	5	1	2	2	5	1
31	CCH-1071	1	5	1	2	2	5	1
32	VIKRAM	1	5	1	2	2	5	1
33	RAH-101	1	5	1	2	2	5	1
34	CNH-120MB	1	3	1	2	2	5	1
35	JK-276-10-5	1	5	1	2	2	5	9
36	KHANDWA	1	5	1	2	2	5	1
37	NA-1568	1	5	1	3	2	5	1
38	G 204-13	1	5	1	3	2	5	1
39	RAH-8794	1	5	1	2	2	5	1
40	COP-420	1	3	1	2	2	5	1

Table 4.2: Flower and boll morphological characters descriptors for 40 cotton (*Gossypium hirsutum* L.) lines

S.No	**Genotype**	Sepal pigmentation	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	BWR 39	1	2	1	2	1	2	5	1	3	2
2	ARB 9009	1	3	1	2	1	2	5	1	3	2
3	KH-11	1	2	1	2	1	2	5	1	3	2
4	L-725	1	2	1	2	1	3	3	1	2	1
5	SA-1104	1	3	1	2	1	3	5	1	3	2
6	CPD-478	1	3	1	2	1	2	5	1	2	2
7	NA-1584	1	2	1	2	1	2	5	1	2	2
8	L-766	1	2	1	2	9	2	5	1	3	2
9	BADANWAR	1	3	1	2	1	3	5	1	3	2
10	NA-1588	1	2	1	2	1	2	5	1	1	2
11	D.S-26	1	2	1	2	1	2	5	1	3	2
12	IH-07	1	2	1	2	1	2	5	1	2	2
13	4085	1	2	1	2	1	2	5	1	3	2
14	CPD-755	1	2	1	2	1	3	5	1	3	2
15	MCU-11	1	2	1	2	1	3	5	1	2	2
16	NH-577	1	3	1	2	1	3	5	1	3	2
17	CPD-420	1	2	1	2	1	3	5	1	2	2
18	LAXMI	1	3	1	2	1	2	5	1	3	1
19	BWR-61	1	2	1	2	1	2	5	1	3	2
20	RAH-100	1	3	1	2	1	2	5	1	3	2

Table 4.2 (Contd.)

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	
21	CNH-301	1	3	1	2	1	2	3	1	2	2
22	ACOLA-2	1	2	1	2	1	3	5	1	3	2
23	CSH-3167	1	2	9	2	1	3	5	1	3	2
24	CPD-431	1	2	1	2	9	2	5	1	3	2
25	AC-88	1	2	1	2	1	2	5	1	2	2
26	NA-1678	1	2	1	2	1	2	5	1	3	2
27	SA 53-1	1	2	1	1	1	3	3	1	2	2
28	CCH-05-2	1	2	1	2	1	2	5	1	3	2
29	PEEDEE-0113	1	2	1	2	1	3	5	1	3	1
30	DS-56	1	3	1	2	1	3	5	1	2	1
31	CCH-1071	1	2	1	2	1	2	5	1	2	1
32	VIKRAM	1	2	1	2	1	2	5	1	3	2
33	RAH-101	1	2	1	2	1	3	5	1	1	2
34	CNH-120MB	1	3	9	2	1	3	5	1	2	2
35	JK-276-10-5	1	2	1	2	1	2	5	1	3	2
36	KHANDWA	1	2	1	2	1	2	5	1	2	2
37	NA-1568	1	2	1	2	1	2	3	1	2	2
38	G 204-13	1	2	1	2	1	2	5	1	3	2
39	RAH-8794	1	3	1	2	1	2	5	1	3	2
40	COP-420	1	2	1	2	1	2	5	1	3	1

Table 4.3 : Frequency of cotton genotypes for the different morphological characters (Descriptors)

SCORE	**Stem Pigmentation**	**Stem hair**	**Leaf shape**	**Leaf lobes**	**Leaf size**	**Leaf colour**	**Leaf pubescence**	**Leaf appearance**	**Leaf Gossypol**	**Leaf nectaries**	**Petiole pigmentation**	**Bract**	**Bract no. of serrations**
	1= absent	3= Sparse	1=palmate	2= three	7= large	2= green	5= medium	2= flat	9=present	9= present	1= absent	1=normal	7=many
	9= present	5= medium	3=okra	3= five		4= dark red	9= strong				9=present		
			4=super okra										
1	**40**		**39**								**38**	**40**	
2				**32**		**40**		**40**					
3		**8**		**8**									
4			**1**										
5		**32**					**39**						
6													
7					**40**								**40**
8													
9							**1**		**40**	**40**	**2**		

SCORE	**Sepal pigmentation**	**Petal colour**	**Petal spot**	**Stigma position**	**Filament colour**	**Anther colour**	**Boll habit**	**Boll size**	**Boll colour**	**Boll shape**	**Boll surface**	**Boll tip**	**Boll open**	**Plant habit**
	1=absent	2=cream	1=absent	1= embedded	1=absent	2=cream	1= solitary	5= medium	1= green	1= round	1=smooth	1= blunt	3=open	3=prostrate
	9=present	3=yellow	9=present	2=exserted	9=present	3=yellow		3=Small	2=red	2= ovate		2=pointed		5=compact
		6=bicolour				4=purple				3=elliptic				7=erect
1	**40**		**38**	**1**	**38**		**40**		**40**	**2**	**40**	**6**		
2		**29**		**39**		**26**				**14**		**34**		
3		**11**				**14**		**4**		**24**			**40**	
4														
5								**36**						
6														
7														**40**
8														
9			**2**		**2**									

Table 4.4 : Mean performance of 40 genotypes for 15 quantitative characters in 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	BWR 39	54.66	94.19	1.65	16.10	23.33	4.45	36.01	8.60
2	ARB 9009	55.33	95.33	1.56	13.13	27.00	4.22	35.18	7.50
3	KH 11	52.33	**111.00**	1.80	**18.33**	**37.33**	**5.24**	**37.32**	10.06
4	L-725	56.66	95.84	1.41	13.30	29.66	3.71	31.50	9.46
5	SA-1104	55.00	92.66	1.70	14.46	23.66	3.68	33.28	9.95
6	CPD-478	56.00	95.33	1.80	13.40	26.66	3.82	34.33	8.06
7	NA-1584	58.00	91.00	1.60	**11.86**	25.00	3.68	31.27	8.30
8	L-766	57.66	93.00	1.05	13.66	24.00	3.92	33.60	9.25
9	BADANWAR	56.33	91.33	1.70	14.80	25.00	3.56	32.87	8.66
10	NA-1588	54.33	99.00	1.53	15.40	26.00	3.96	31.26	8.67
11	DS-26	55.00	92.33	1.60	13.73	24.33	3.96	34.32	9.01
12	IH-07	57.33	99.00	1.47	14.33	28.33	4.32	33.20	10.09
13	4085	54.00	98.00	1.62	14.10	24.00	4.36	32.22	9.32
14	CPD-755	56.33	99.33	1.21	15.00	30.33	4.04	34.41	8.79
15	MCU-11	53.00	96.33	1.85	17.73	28.00	4.19	35.43	9.50
16	NH-577	54.66	94.08	1.55	12.20	32.00	3.66	34.59	9.18
17	CPD-420	55.66	100.33	1.55	14.66	25.00	3.63	33.72	10.14
18	LAXMI	53.00	103.66	1.85	15.22	31.00	4.27	32.95	**10.39**
19	BWR 61	53.66	96.33	1.64	15.66	27.00	3.83	32.41	8.75
20	RAH 100	**51.00**	101.66	1.83	13.86	27.00	4.05	32.46	9.55

Table 4.4 (Contd.)

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)
21	CNH-301	4.15	24.59	**5.21**	18.87	51.17	5.36	104.33
22	ACOLA-2	4.80	27.25	4.60	21.32	52.12	5.58	**83.00**
23	CSH-3167	4.93	26.06	4.27	20.06	50.63	5.41	92.00
24	CPD-431	5.20	27.93	**3.91**	20.79	49.60	5.46	99.66
25	AC-88	5.29	27.95	4.33	20.51	51.64	5.43	94.66
26	NA-1678	4.83	25.20	4.25	20.72	51.74	5.66	99.33
27	SA 53-1	4.21	25.76	4.44	20.37	51.88	5.54	95.66
28	CCH-05-2	4.72	25.98	4.52	19.55	50.18	5.37	102.33
29	PEE DEE-0113	4.56	26.12	4.52	20.13	49.41	5.43	109.33
30	DS-56	4.69	25.24	4.70	20.31	48.37	5.46	103.66
31	CCH-1071	5.25	25.42	4.52	19.90	51.83	5.33	91.00
32	VIKRAM	4.69	27.04	4.81	20.33	51.38	5.52	109.00
33	RAH-101	5.55	28.15	4.66	**21.53**	**53.03**	**5.69**	121.33
34	CNH-120MB	4.37	24.98	4.52	18.98	49.60	5.42	90.66
35	JK 276-10-5	4.45	26.25	4.48	**18.70**	**46.02**	5.41	96.33
36	KHANDWA	4.45	25.88	4.37	19.27	49.53	5.43	93.66
37	NA-1568	4.32	26.01	4.59	18.73	50.60	5.55	95.00
38	G 204-13	4.89	25.26	4.26	19.12	49.78	5.61	99.33
39	RAH-8794	5.40	25.93	4.83	19.72	50.40	5.54	113.66
40	COP-420	4.26	**23.73**	4.32	19.29	49.52	**5.14**	94.00
	Mean	4.81	26.72	4.50	20.07	50.63	5.48	102.7
	C.V.	6.70	4.59	5.64	4.36	3.55	0.45	9.10
	C.D at 5%	0.52	1.99	0.41	1.42	2.92	0.040	15.20

Table 4.5 : Analysis of variance for seed cotton yield and its 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-out-turn (%)	Seed index (g)
		Mean squares							
Replications	2	8.95	0.82323	0.0069	1.5684	2.1583	0.0883	0.3523	0.1800
Varieties	39	13.35**	79.6199**	0.1922**	6.2894**	25.7564**	0.5197**	9.2123**	1.4345**
Error	78	5.04	18.8649	0.0202	2.2513	7.0301	0.0841	1.6059	0.1622

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	0.0149	0.7517	0.0399	0.2765	0.0746	0.00009	20.7802
Varieties	39	0.6857**	6.1371**	0.2785**	1.7733**	6.0628**	0.0449**	403.5929**
Error	78	0.1042	1.5092	0.0647	0.7681	3.2345	0.00062	87.5246

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

Table -4.6 : 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	55.84	51.00	61.33	5.00	2.97	35.44	3.65
2	Plant height (cm)	95.40	86.66	111.00	6.55	4.71	51.77	6.99
3	No. of monopodia plant^{-1}	1.56	0.95	2.00	17.82	15.32	73.94	27.15
4	No. of sympodia plant^{-1}	14.54	11.86	18.33	13.04	7.97	37.42	10.05
5	No. of bolls plant^{-1}	26.91	23.00	37.33	13.53	9.28	47.03	13.11
6	Boll weight (g)	3.98	3.32	5.24	12.01	9.56	63.31	15.67
7	Ginning out-turn (%)	33.41	30.74	37.32	6.09	4.76	61.22	7.68
8	Seed index (g)	8.98	7.56	10.39	8.51	7.24	72.33	12.69
9	Lint index (g)	4.81	3.91	5.73	11.34	9.14	65.02	15.19
10	2.5% span length (mm)	26.72	23.73	29.77	6.53	4.64	50.55	6.80
11	Micronaire (10^{-6} g/inch)	4.50	3.91	5.21	8.18	5.92	52.37	8.83
12	Bundle strength (g/tex)	20.07	18.70	21.53	5.23	2.88	30.37	3.27
13	Uniformity ratio (%)	50.63	46.02	53.03	4.03	1.91	22.57	1.87
14	Fibre elongation (%)	5.48	5.14	5.69	2.26	2.21	95.97	4.47
15.	Seed cotton yield plant^{-1} (g)	102.74	83.00	140.33	13.51	9.99	54.62	15.20

PCV = Phenotypic coefficient of variation

GCV = Genotypic coefficient of variation

Table 4.7 : Phenotypic (above diagonal) and genotypic (below diagonal) correlations of 15 characters in 40 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 out-turn	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	--	-0.4646**	-0.3093**	-0.3350**	-0.1600	-0.3393**	-0.3057**	-0.2102*	-0.2564**	-0.1977*	-0.0754	-0.1455	-0.1963*	-0.4139**	-0.1871*
Plant height	-0.9935**	--	0.2822**	0.2458**	0.3935**	0.4289**	0.2958**	0.4207**	0.3700**	0.2719**	0.1953*	0.1685	0.1479	0.3796**	0.4920**
No.of monopodia plant^{-1}	-0.7673**	0.4948**	--	0.2488**	0.2375**	0.2592**	0.3902**	0.3281**	0.3345**	0.2802**	0.0916	0.2971**	0.1129	0.3751**	0.1964*
No.of sympodia plant^{-1}	-0.4248**	0.5711**	0.4206**	--	0.1056	0.4558**	0.2500**	0.2513**	0.3038**	0.1976*	0.1252	0.1712	0.1424	0.1344	0.2109*
No. of bolls plant^{-1}	-0.6837**	0.9120**	0.3614**	0.5655**	--	0.2232*	0.3094**	0.2529**	0.0936	0.0227	0.4217**	0.1806*	0.1965*	0.1192	0.5831**
Boll weight	-0.7209**	0.8501**	0.3077**	0.7664**	0.6305**	--	0.3478**	0.2735**	0.3281**	0.1335	0.2038*	0.1687	0.2771**	0.3645**	0.3568**
Ginning out-turn	-0.7422**	0.5269**	0.4928**	0.4877**	0.5208**	0.6055**	--	0.1872*	0.3289**	0.1813*	0.1299	0.2959**	0.2522**	0.2793**	0.2365**
Seed index	-0.5591**	0.6127**	0.4005**	0.6425**	0.3682**	0.5026**	0.2037*	--	0.4730**	0.4283**	0.1098	0.3217**	0.1342	0.2640**	0.4411**
Lint index	-0.6672**	0.5553**	0.3932**	0.5951**	0.2218*	0.4534**	0.5886**	0.6349**	--	0.4034**	-0.0324	0.2543**	0.1404	0.2474**	0.2167*
2.5% span length	-0.5916**	0.3509**	0.4349**	0.6351**	-0.0608	0.4112**	0.4846**	0.6100**	0.6727**	--	-0.1771	0.3568**	-0.0334	0.3138**	0.1316
Micronaire	-0.2850**	0.4664**	0.1213	0.4413**	0.7406**	0.3609**	0.1606	0.1250	-0.1037	-0.3165**	--	-0.0331	0.2234*	-0.0526	0.2985**
Bundle strength	-0.5826**	0.5529**	0.3527**	0.1928*	0.3257**	0.4565**	0.5864**	0.5912**	0.6232**	0.8079**	0.0551	--	0.2542**	0.2637**	0.1564
Uniformity ratio	-0.6345**	0.5168**	0.2249*	0.6742**	0.3345**	0.7290**	0.4291**	0.4363**	0.5590**	0.4170**	0.6002**	0.8768**	--	0.1644	0.1243
Fibre elongation	-0.6937**	0.5688**	0.4327**	0.2246*	0.1942*	0.4598**	0.3861**	0.3293**	0.3513**	0.4513**	-0.0681	0.4762**	0.3247**	--	0.1642
Seed cotton yield plant^{-1}	-0.6154**	0.8226**	0.2993**	0.4609**	1.0618**	0.5321**	0.4755**	0.6910**	0.3813**	0.2471**	0.4111**	0.4804**	0.3013**	0.2362**	--

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

Table 4.8 : Direct and indirect effects (phenotypic) of yield components on seed cotton yield in 40 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 out-turn**	**Seed index**	**Lint index**	**2.5%span length**	**Micronaire**	**Bundle strength**	**Uniformity ratio**	**Fibre elongation**
Days to 50% flowering	**0.0462**	-0.0215	-0.0143	-0.0155	-0.0074	-0.0157	-0.0141	-0.0097	-0.0119	-0.0091	-0.0035	-0.0067	-0.0091	-0.0191
Plant height	-0.0981	**0.2111**	0.0596	0.0519	0.0831	0.0905	0.0625	0.0888	0.0781	0.0574	0.0412	0.0356	0.0312	0.0801
No.of monopodia plant^{-1}	0.0150	-0.0136	**-0.0483**	-0.0120	-0.0115	-0.0125	-0.0189	-0.0159	-0.0162	-0.0135	-0.0044	-0.0144	-0.0055	-0.0181
No. of sympodia plant^{-1}	-0.0105	0.0077	0.0078	**0.0313**	0.0033	0.0143	0.0078	0.0079	0.0095	0.0062	0.0039	0.0054	0.0045	0.0042
No. of bolls plant^{-1}	-0.0677	0.1664	0.1004	0.0447	**0.4229**	0.0944	0.1308	0.1070	0.0396	0.0096	0.1783	0.0764	0.0831	0.0504
Boll weight	-0.0498	0.0629	0.0380	0.0669	0.0328	**0.1467**	0.0510	0.0401	0.0481	0.0196	0.0299	0.0248	0.0407	0.0535
Ginning out-turn	-0.0008	0.0008	0.0010	0.0007	0.0008	0.0009	**0.0026**	0.0005	0.0009	0.0005	0.0003	0.0008	0.0007	0.0007
Seed index	-0.0547	0.1095	0.0854	0.0654	0.0658	0.0712	0.0487	**0.2602**	0.1231	0.1114	0.0286	0.0837	0.0349	0.0687
Lint index	0.0069	-0.0100	-0.0090	-0.0082	-0.0025	-0.0088	-0.0088	-0.0127	**-0.0269**	-0.0108	0.0009	-0.0068	-0.0038	-0.0067
2.5% span length	0.0045	-0.0061	-0.0063	-0.0045	-0.0005	-0.0030	-0.0041	-0.0097	-0.0091	**-0.0226**	0.0040	-0.0081	0.0008	-0.0071
Micronaire	-0.0022	0.0056	0.0026	0.0036	0.0122	0.0059	0.0038	0.0032	-0.0009	-0.0051	**0.0289**	-0.0010	0.0065	-0.0015
Bundle strength	0.0018	-0.0021	-0.0037	-0.0021	-0.0022	-0.0021	-0.0037	-0.0040	-0.0031	-0.0044	0.0004	**-0.0124**	-0.0031	-0.0033
Uniformity ratio	0.0101	-0.0076	-0.0058	-0.0074	-0.0102	-0.0143	-0.0130	-0.0069	-0.0073	0.0017	-0.0115	-0.0131	**-0.0517**	-0.0085
Fibre elongation	0.0121	-0.0111	-0.0109	-0.0039	-0.0035	-0.0106	-0.0082	-0.0077	-0.0072	-0.0092	0.0015	-0.0077	-0.0048	**-0.0292**
Correlation with seed cotton yield plant^{-1}	-0.1871**	0.4920**	0.1964*	0.2109*	0.5831**	0.3568**	0.2365**	0.4411**	0.2167*	0.1316	0.2985**	0.1564	0.1243	0.1642

*=Significant at 5% level **=Significant at 1% level, Bold and diagonal values indicate direct effects, Residual effect= 0.712

Table 4.9 : Direct and indirect effects (genotypic) of yield components on seed cotton yield in 40 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 out-turn	Seed index	Lint index	2.5%span length	Micronaire	Bundle strength	Uniformity ratio	Fibre elongation
Days to 50% flowering	**1.1501**	-1.1426	-0.8824	-0.4885	-0.7863	-0.8290	-0.8536	-0.6430	-0.7673	-0.6804	-0.3277	-0.6700	-0.729	-0.7978
Plant height	-0.8697	**0.8754**	0.4332	0.5000	0.7984	0.7443	0.4613	0.5364	0.4861	0.3072	0.4083	0.4840	0.4524	0.4980
No. of monopodia plant^{-1}	-0.1183	0.0763	**0.1541**	0.0648	0.0557	0.0474	0.0760	0.0617	0.0606	0.0670	0.0187	0.0544	0.0347	0.0667
No. of sympodia plant^{-1}	-0.0947	0.1273	0.0938	**0.2230**	0.1261	0.1709	0.1087	0.1433	0.1327	0.1416	0.0984	0.0430	0.1503	0.0501
No. of bolls plant^{-1}	-0.4531	0.6044	0.2395	0.3748	**0.6627**	0.4178	0.3451	0.2440	0.1470	-0.0403	0.4908	0.2158	0.2217	0.1287
Boll weight	0.0793	-0.0936	-0.0339	-0.0844	-0.0694	**-0.1101**	-0.0667	-0.0553	-0.0499	-0.0453	-0.0397	-0.0503	-0.0802	-0.0506
Ginning out-turn	-0.0868	0.0616	0.0576	0.0571	0.0609	0.0708	**0.1170**	0.0238	0.0689	0.0567	0.0188	0.0686	0.0502	0.0452
Seed index	-0.0822	0.0901	0.0589	0.0945	0.0542	0.0739	0.0300	**0.1471**	0.0934	0.0897	0.0184	0.0870	0.0642	0.0484
Lint index	-0.1087	0.0904	0.0640	0.0969	0.0361	0.0738	0.0959	0.1034	**0.1629**	0.1096	-0.0169	0.1015	0.0910	0.0572
2.5% span length	0.1116	-0.0662	-0.0820	-0.1198	0.0115	-0.0776	-0.0914	-0.1151	-0.1269	**-0.1886**	0.0597	-0.1524	-0.0786	-0.0851
Micronaire	-0.0179	0.0293	0.0076	0.0277	0.0465	0.0227	0.0101	0.0078	-0.0065	-0.0199	**0.0628**	0.0035	0.0377	-0.0043
Bundle strength	-0.5044	0.4786	0.3054	0.1669	0.2819	0.3952	0.5076	0.5118	0.5395	0.6994	0.0477	**0.8657**	0.7590	0.4122
Uniformity ratio	0.4456	-0.3630	-0.1580	-0.4736	-0.2350	-0.5121	-0.3014	-0.3064	-0.3926	-0.2929	-0.4216	-0.6158	**-0.7024**	-0.2281
Fibre elongation	-0.0663	0.0543	0.0413	0.0215	0.0185	0.0439	0.0369	0.0315	0.0336	0.0431	-0.0065	0.0455	0.0310	**0.0955**
Correlation with Seed cotton yield plant^{-1}	-0.6154**	0.8226**	0.2993**	0.4609**	1.0618**	0.5321**	0.4755**	0.6910**	0.3813**	0.2471**	0.4111**	0.4804**	0.3013**	0.2362**

*=Significant at 5% level **=Significant at 1% level, Bold and diagonal values indicate direct effects, Residual effect= Sqrt (1-1.231)

Table 4.10 : Contribution of different characters towards genetic divergence in 40 genotypes of cotton (*Gossypium hirsutum* L.)

Source	Times ranked first	Contribution % towards divergence
Fibre elongation (%)	491	62.95
Seed index (g)	83	10.64
Number of monopodia plant^{-1}	65	8.33
Boll weight (g)	28	3.59
Lint index (g)	19	2.44
Micronaire (10^{-6} g/in)	17	2.18
Ginning out-turn (%)	16	2.05
2.5% span length (mm)	14	1.79
Seed cotton yield plant^{-1} (g)	12	1.54
Uniformity ratio	11	1.41
Bundle strength (g/tex)	10	1.28
No. of bolls plant^{-1}	9	1.15
Days to 50% flowering	3	0.38
No. of sympodia plant^{-1}	2	0.26
Plant height (cm)	0	0.00

Table 4.11: Clustering of 40 genotypes of cotton (*Gossypium hirsutum* L.) by Tocher's method.

Cluster No.	No. of genotypes	Name of genotype(s)
I	13	SA 53-1, NA-1568, BWR-61, CPD-478, VIKRAM, ARB-9009, L-725, 4085, PEE DEE-0113, CPD-431, RAH-8794, BWR-39, CPD-420
II	13	CNH-120MB, KHANDWA, JK 276-10-5, CCH-05-2, NA-1584, CSH-3167, NH-577, NA-1588, CCH-1071, AC-88, L-766, CPD-755, D.S-56
III	9	NA-1678, G 204-13, D.S-26, RAH-100, ACOLA-2, SA-1104, IH-07, MCU-11, LAXMI
IV	2	KH-11, RAH-101
V	1	BADANWAR
VI	1	CNH-301
VII	1	COP-420

Table 4.12: Average intra-and inter-cluster D^2 values among seven clusters in 40 genotypes of cotton (*Gossypium hirsutum* L.).

Cluster No	I	II	III	IV	V	VI	VII
I	**13.50 (3.67)**	25.44 (5.04)	22.39 (4.73)	61.38 (7.83)	66.61 (8.16)	40.13 (6.33)	119.18 (10.91)
II		**17.60 (4.19)**	51.71 (7.19)	105.76 (10.28)	31.78 (5.63)	24.23 (4.92)	63.25 (7.95)
III			**17.91 (4.23)**	40.13 (6.33)	116.64 (10.80)	73.08 (8.54)	182.40 (13.50)
IV				**12.89 (3.59)**	190.65 (13.80)	126.05 (11.22)	276.84 (16.63)
V					**0.00 (0.00)**	27.27 (5.22)	20.87 (4.56)
VI						**0.00 (0.00)**	47.00 (6.855)
VII							**0.00 (0.00)**

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

Table 4.13 : The nearest and the farthest cluster from each cluster based on D^2 values using Tocher's method in 40 genotypes of cotton (*Gossypium hirsutum* L.)

Cluster No.	Nearest cluster with D^2 values	Farthest cluster with D^2 values
I	III (22.39)	VII (119.18)
II	VI (24.23)	IV (105.76)
III	I (22.39)	VII (182.40)
IV	III (40.13)	VII (276.84)
V	VII (20.87)	IV (190.65)
VI	II (24.23)	IV (126.05)
VII	V (20.87)	IV (276.84)

Values in parentheses indicate D^2 values

Table 4.14 : Mean values of seven clusters for 15 characters estimated from 40 genotypes of cotton (*Gossypium hirsutum* L.) by Tocher's method

Cluster No	Days to 50% flowering	Plant height (cm)	No. of mono podia plant^{-1}	No. of sympodia plant^{-1}	No.of bolls plant^{-1}	Boll weight (g)	Ginning out-turn (%)	Seed index (g)	Lint index (g)	2.5% span length (mm)	Micro-naire ((10^{-6} g/In)	Bundle strength (g/tex)	Unifor-mity ratio	Elon-gation (%)	Seed cotton yield/ plant^{-1} (g)
I	55.97	94.92	1.64	14.48	26.76	3.93	33.66	8.92	4.71	26.94	4.45	19.98	50.50	5.52	103.38
II	56.59	93.16	1.41	**13.91**	26.28	3.80	33.08	8.66	4.70	26.30	4.49	19.83	50.13	5.39	99.41
III	54.63	97.71	1.64	14.64	26.63	4.09	33.38	9.41	5.07	27.13	4.48	20.56	51.20	5.61	102.42
IV	**52.00**	**109.50**	**1.77**	**17.66**	**34.16**	**5.22**	**36.84**	**9.88**	**5.64**	**28.47**	4.84	**20.99**	**52.45**	**5.62**	**130.83**
V	56.33	91.33	1.70	14.80	25.00	**3.56**	32.87	8.66	4.80	27.53	4.40	19.97	50.81	5.23	**91.66**
VI	57.00	94.66	1.54	16.46	29.66	4.21	**30.74**	9.03	**4.15**	24.59	**5.21**	**18.87**	51.17	5.36	104.33
VII	**61.33**	**86.66**	**1.06**	14.20	**24.33**	3.64	30.92	**8.63**	4.26	**23.73**	**4.32**	19.29	**49.52**	**5.14**	94.00

Bold figures are minimum and maximum values

Table 4.15: Eigen values, proportion of the total variance represented by first five 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**
Eigene Value (Root)	**5.810**	**2.055**	**1.744**	**1.228**	**0.916**
% Var. Exp.	**38.731**	**13.698**	**11.624**	**8.187**	**6.107**
Cum. Var. Exp.	**38.731**	**52.429**	**64.053**	**72.240**	**78.346**
Days to 50% flowering	0.315	0.123	0.250	0.082	0.019
Plant height(cm)	-0.337	-0.257	-0.031	0.071	-0.168
No. of Monopodia/ plant	-0.222	-0.176	-0.344	-0.427	0.088
No. of Sympodia/ plant	-0.122	0.033	0.568	-0.315	0.335
No. of Bolls/ plant	-0.294	-0.391	0.088	0.146	0.092
Boll weight (gm)	-0.327	-0.169	0.197	0.151	0.058
Ginning out-turn (%)	-0.280	0.106	-0.091	0.286	0.578
Seed index (g)	-0.269	0.043	0.225	-0.323	-0.451
Lint index (g)	-0.243	0.365	-0.022	0.021	0.192
2.5% span length (mm)	-0.271	0.377	0.001	-0.145	0.227
Micronaire (microgm/ Inch)	-0.057	-0.494	0.355	0.128	0.046
Bundle strength (gm/Texture)	-0.148	0.272	0.153	0.634	-0.304
Uniformity ratio	-0.225	0.311	0.343	-0.167	-0.245
Fibre Elongation %	-0.280	0.050	-0.265	-0.024	-0.215
Seed cotton yield/ plant (gm)	-0.304	0.006	-0.231	0.089	-0.115

Table 4.16 : PCA scores of 40 genotypes of cotton (*Gossypium hirsutum* L.)

S.No.	Genotype	PCA1	PCA2	PCA3
		X Vector	Y Vector	Z Vector
1	BWR 39	-71.555	17.191	-18.120
2	ARB 9009	-69.507	14.703	-18.300
3	KH 11	-76.833	14.441	-17.010
4	L-725	-70.209	16.071	-16.848
5	SA-1104	-71.170	17.120	-17.220
6	CPD-478	-70.096	16.227	-19.137
7	NA-1584	-66.428	15.233	-17.325
8	L-766	-69.582	17.444	-15.988
9	BADANWAR	-66.902	15.932	-15.908
10	NA-1588	-69.112	15.931	-15.894
11	D.S-26	-71.738	17.662	-19.584
12	IH-07	-72.440	16.962	-16.968
13	4085	-70.148	15.008	-18.377
14	CPD-755	-69.439	14.431	-14.823
15	MCU-11	-73.646	16.819	-18.984
16	NH-577	-69.810	15.268	-18.248
17	CPD-420	-71.102	17.073	-18.213
18	LAXMI	-72.554	13.488	-17.538
19	BWR-61	-69.904	14.814	-17.585
20	RAH-100	-71.502	14.759	-19.457

Table 4.16 (contd.)

S. No	Genotype	PCA1	PCA2	PCA3
		X Vector	Y Vector	Z Vector
21	CNH-301	-67.943	12.923	-14.568
22	ACOLA-2	-71.462	15.502	-17.315
23	CSH-3167	-68.648	17.097	-16.042
24	CPD-431	-69.745	16.678	-18.541
25	AC-88	-69.857	17.112	-16.134
26	NA-1678	-70.698	16.572	-18.956
27	SA 53-1	-68.463	15.805	-17.727
28	CCH-05-2	-67.947	15.459	-17.388
29	PEEDEE-0113	-69.086	15.663	-16.642
30	DS-56	-68.754	14.267	-19.189
31	CCH-1071	-69.365	16.832	-16.803
32	VIKRAM	-71.296	15.071	-18.091
33	RAH-101	-76.401	15.829	-18.141
34	CNH-120 MB	-67.102	15.666	-16.477
35	JK 276-10-5	-67.143	14.873	-17.128
36	KHANDWA	-67.362	16.270	-16.176
37	NA-1568	-68.021	15.204	-17.480
38	G 204-13	-70.075	15.911	-18.378
39	RAH-8794	-71.794	14.977	-17.873
40	COP-420	-64.215	15.633	-13.672

Table 4.17 : Clustering of 40 cotton (*Gossypium hirsutum* L.) genotypes by Ward's minimum variance method.

Cluster No	No. of genotypes	Name of genotype(s)
I	8	BWR 39, ACOLA 2, SA-1104, IH-07, CPD-420, LAXMI, RAH-8794, RAH-100
II	4	D.S-26, MCU-11, NA-1678, G 204-13
III	2	KH-11, RAH-101
IV	9	ARB-9009, CPD-478, D.S-56, BWR-61, VIKRAM, L-725, 4085, SA 53-1, NA-1568
V	9	L-766, CSH-3167, CNH-120MB, KHANDWA, JK 276-10-5, NH-577, PEE DEE-0113, CPD-431, AC-88
VI	7	NA-1584, CCH-05-2, BADANWAR, NA-1588, CCH-1071, CPD-755, CNH-301
VII	1	COP-420

Table 4.18: Average intra – and inter- cluster Euclidean^2 values among the seven clusters in 40 cotton (*Gossypium hirsutum* L.) genotypes.

Cluster No	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**
I	**43.43**	60.93	121.00	58.05	93.51	172.65	467.06
II		**38.24**	124.75	82.68	145.12	270.57	619.56
III			**38.68**	200.39	279.66	395.05	830.52
IV				**35.36**	57.14	112.59	349.18
V					**41.37**	68.26	217.66
VI						**54.37.**	132.48
VII							**0.000**

Bold and diagonal values indicate intra-cluster distance

Table 4.19 : Mean values of seven clusters estimated from 40 cotton (*Gossypium hirsutum* L.) genotypes by Ward's minimum variance Method.

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)	Uniformi ty ratio	Elongation (%)	Seed cotton yield plant^{-1}
I	54.87	98.69	1.72	14.98	26.83	4.14	33.90	9.71	5.20	27.25	4.56	20.32	51.22	5.56	105.09
II	54.91	95.53	1.53	14.55	25.75	3.99	33.58	8.91	5.00	27.17	**4.22**	20.44	50.31	**5.66**	100.25
III	**52.00**	**109.50**	**1.77**	**17.66**	**34.16**	**5.22**	**36.84**	**9.88**	**5.64**	**28.47**	**4.84**	**20.99**	**52.45**	5.62	**130.83**
IV	55.88	95.00	1.63	**13.74**	27.37	3.86	33.28	**8.57**	4.46	26.54	4.55	19.98	50.63	5.52	102.07
V	57.07	91.68	1.38	14.30	25.96	3.81	32.84	8.86	4.72	26.59	4.35	19.82	49.79	5.43	98.81
VI	56.14	94.09	1.53	14.52	26.61	3.87	33.02	8.68	4.66	26.21	4.65	19.84	50.87	5.33	100.61
VII	**61.33**	**86.66**	**1.06**	14.20	**24.33**	**3.64**	**30.92**	8.63	**4.26**	**23.73**	4.32	**19.29**	**49.52**	**5.14**	**94.00**

Bold figures are minimum and maximum values

Chapter V

SUMMARY AND CONCLUSIONS

The present investigation was carried out during *kharif* 2010-11 at Agricultural College Farm, Bapatla, with 40 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 forty 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^{-6}g/in), bundle strength (g/tex), uniformity ratio (%), fibre elongation (%) and seed cotton yield plant^{-1} (g).

Variability was recorded for thirteen 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 effect of the environment.

The characters viz., number of sympodia plant^{-1}, number of bolls per plant, boll weight and seed cotton yield per plant exhibited moderate phenotypic coefficient of variation. Moderate heritability coupled with moderate genetic advance was noted for number of sympodia plant^{-1}, number of bolls per plant and seed cotton yield per plant. This indicates the presence of non-additive gene action and further improvement of these traits would be possible through heterosis breeding rather than simple selection.

The traits viz., days to 50% flowering, plant height, ginning outturn, 2.5% span length, micronaire and fibre elongation showed moderate to high heritability coupled with low genetic advance revealing the role of additive and non- additive gene action and further improvement of these characters would be easier through heterosis breeding. Low heritability and low genetic advance was reported for the traits, bundle strength and uniformity ratio indicating the operation of non additive gene action. These traits might be exploited through heterosis breeding, cyclic hybridization, biparental mating and diallel selective mating system.

The correlation and path coefficient analyses together indicated that plant height, number of sympodia plant^{-1}, number of bolls plant^{-1} and seed index had significant positive and positive direct effects on seed cotton yield per plant indicating the existence of true relationship between these characters and their exploitation in selection programmes.

The results of multivariate analysis revealed that the distribution of 40 cotton genotypes into seven clusters in case of D^{2} analysis and agglomerative cluster analysis which was at random indicating that the genetic diversity and geographical diversity were not related.

The inter cluster distance was maximum between clusters IV and VII (276.84) followed by clusters V and IV (190.65), III and VII (182.40), IV and VI (126.05), I and VII (119.18) and II and IV (105.76). The characters, fibre elongation, seed index, number of monopodia plant^{-1}, boll weight, lint index, micronaire, ginning out-turn, 2.5% span length, seed cotton yield per plant and uniformity ratio contributed maximum towards genetic divergence.

Based on the inter- cluster distances among the groups, crosses after confirming the general combining ability of the genotypes from clusters VII (COP-420) and IV (KH-11, RAH-101) may yield better and desirable segregants.

In the principal component analysis, first 5 principal components altogether explained 78.35% of the variability. The first component explained 38.73% of total variability and remaining ones accounted for progressive lesser and lesser amount of variation. The PC_1 was characterized by high loading values of plant height, boll weight, days to 50% flowering, seed cotton yield per plant, number of bolls per plant, fibre elongation, ginning out-turn, 2.5% span length, seed index and lint index and these characters contributed maximum for divergence towards variability.

Agglomerative cluster analysis revealed that wide genetic distance exists between cluster III and VII (830.52) followed by cluster II and VII (619.56). The hybridization programme can be attempted between the clusters III (KH-11 and RAH-101) and VII (COP-420) for the identification transgressive segregants for the desirable yield contributing traits.

The genotypes KH-11 and RAH-101, and COP-420 showed maximum inter-cluster distance in multivariate analysis and these genotypes can be exploited for the development of heterotic hybrids after testing their combining ability for yield and its yield contributing traits.

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

ANNEXURE

Monthly meteorological data during the crop growth period 2010-11.

Month	Temperature (^{0}C)		Relative humidity (%)		Rain fall (mm)	Wind velocity (km/hr)
	Maximum	Minimum	8.30 A.M	5.30 P.M		
August 2010	33.30	25.10	85	77	345.9	06/03
September 2010	32.60	25.30	87	79	350.3	06/03
October 2010	32.30	24.60	87	78	179.5	04/02
November 2010	30.40	23.10	90	82	152.5	05/02
December 2010	28.90	18.90	90	72	170.3	05/02
January 2011	29.80	17.20	92	66	000.0	04/02
February 2011	31.10	18.70	89	64	029.9	04/02

(Agricultural College Farm, Bapatla)