

**GENETIC DIVERGENCE STUDIES
IN AMERICAN COTTON
(*Gossypium hirsutum* L.) GENOTYPES**

By
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B.Sc. (Ag.)

**THESIS SUBMITTED TO THE
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CHAIRPERSON: Dr. Y. SATISH



**DEPARTMENT OF GENETICS AND PLANT BREEDING
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GUNTUR, ANDHRA PRADESH**

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2016

DECLARATION

I, **Mr. B. MANSINGH NAIK**, hereby declare that the thesis entitled **“GENETIC DIVERGENCE STUDIES IN AMERICAN COTTON (*Gossypium hirsutum* L.) GENOTYPES”**, submitted to **Acharya N. G. Ranga Agricultural University** for the degree of **Master of Science in Agriculture** in the major field of **Genetics and Plant Breeding** is the result of original research work done by me. I also declare that no material contained in the thesis has been published earlier in any manner.

Place:

(BANAVATH MANSINGH NAIK)

Date:

I. D. No. BAM-14-10

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LIST OF SYMBOLS AND ABBREVIATIONS

%	:	Per cent
*	:	Significance at 5% level
**	:	Significance at 1% level
/ or ⁻¹	:	Per
AICRP	:	All India Coordinated Research Project on cotton
ANGRAU	:	Acharya N.G Ranga Agricultural University
ANOVA	:	Analysis of Variance
ARS	:	Agricultural Research Station
CCSHAU	:	Chaudhary Charan Singh Haryana Agricultural University
CICR	:	Central Institute for Cotton Research
Cm	:	Centimeter
Cont.	:	Continued
CV	:	Coefficient of Variation
df	:	Degrees of freedom
<i>et al.</i> ,	:	And others
G	:	Gram
g/in	:	Grams per inch
g/tex	:	Grams per tex
GA	:	Genetic Advance
GAM	:	Genetic Advance as per cent of Mean
GCV	:	Genotypic Coefficient of Variation
h^2_b	:	Heritability in broad sense
h^2_n	:	Heritability in narrow sense
ha	:	Hectare
<i>i.e.</i> ,	:	That is
IARI	:	Indian Agricultural Research Institute
JAU	:	Junagadh Agricultural University
JNKVV	:	Jawaharlal Nehru Krishi Viswa Vidyalaya

Kg	:	Kilogram
M	:	Meter
Mm	:	Millimeter
MAU	:	Marathwada Agricultural University
MPKV	:	Mahatama Phule Krishi Vidyapeeth
NAU	:	Navsari Agricultural University
No.	:	Number
OUAT	:	Orissa University of Agriculture and Technology
PAU	:	Punjab Agricultural University
PCV	:	Phenotypic Coefficient of Variation
PCA	:	Principal component analysis
PCs	:	Principal components
RARS	:	Regional Agricultural Research Station
RAU	:	Rajasthan Agricultural University
RBD	:	Randomized block design
SCY	:	Seed Cotton Yield Per Plant
SD	:	Standard Deviation
TNAU	:	Tamil Nadu Agricultural University
UAS	:	University of Agricultural Sciences
viz.,	:	Namely
2D	:	Two dimensional
3D	:	Three dimensional
BALE	:	170 Kg

LIST OF CONTENTS

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

LIST OF TABLES

S.No.	Title	Page No.
2.1	Review of literature on genetic variability in cotton (<i>G.hirsutum</i> L.)	
2.2	Review of literature on heritability (h^2_b) and genetic advance (GA) in cotton (<i>G.hirsutum</i> L.)	
2.3	Review of literature on association of component characters with seed cotton yield in cotton (<i>G.hirsutum</i> L.)	
2.4	Review of literature on association among component characters of seed cotton yield in cotton (<i>G.hirsutum</i> L.)	
2.5	Review of literature on direct effects of component characters on seed cotton yield in cotton (<i>G.hirsutum</i> L.)	
3.1	Experimental details of the present investigation	
3.2	Name and source of cotton (<i>G.hirsutum</i> L.) germplasm employed in the present study	
4.1	Mean performance of 50 genotypes of cotton (<i>G.hirsutum</i> L.) for 15 characters	
4.2	Analysis of variance for yield and yield components in cotton (<i>G.hirsutum</i> L.)	
4.3	Mean, genetic variability, heritability (broad sense) and genetic advance as per cent of mean for seed cotton yield and yield components in cotton (<i>G.hirsutum</i> L.)	
4.4	Phenotypic (above diagonal) and genotypic (below diagonal) correlations among 15 characters in 50 cotton (<i>G.hirsutum</i> L.) genotypes	
4.5	Direct and indirect effects (phenotypic) of yield components on seed cotton yield per plant in 50 genotypes of cotton (<i>G.hirsutum</i> L.)	
4.6	Direct and indirect effects (genotypic) of yield components on seed cotton yield per plant in 50 genotypes of cotton (<i>G.hirsutum</i> L.)	
4.7	Contribution of different characters towards genetic divergence in 50 cotton (<i>G.hirsutum</i> L.) genotypes	
4.8	Clustering pattern of 50 cotton (<i>G.hirsutum</i> L.) genotypes by Tocher's method	
4.9	Average intra-and inter-cluster D^2 values among eight clusters in 50 cotton (<i>G.hirsutum</i> L.) genotypes	
4.10	The nearest and farthest cluster from each cluster based on D^2 values	

4.11	Mean values of eight clusters estimated by Tocher's method from 50 genotypes of cotton (<i>G.hirsutum</i> L.)	
4.12	Eigen values, proportion of the total variance represented by first six principal components, cumulative per cent variance and component loading of different characters in cotton (<i>G.hirsutum</i> L.)	
4.13	PCA scores of 50 genotypes of cotton (<i>G.hirsutum</i> L.)	
4.14	Clustering of 50 cotton (<i>G.hirsutum</i> L.) genotypes by Ward's minimum variance method	
4.15	Average intra-and inter-cluster Euclidean ² values among eight clusters in 50 cotton (<i>G.hirsutum</i> L.) genotypes	
4.16	Mean values of 8 clusters estimated from 50 genotypes of cotton Average intra-and inter-cluster D ² values among eight clusters in 50 cotton (<i>G.hirsutum</i> L.) genotypes by Ward's minimum variance method	

LIST OF FIGURES

S.No.	Title	Page No.
4.1	Phenotypic path diagram showing cause and effect relationship of yield components with seed cotton yield per plant in cotton (<i>G.hirsutum</i> L.)	
4.2	Genotypic path diagram showing cause and effect relationship of yield components with seed cotton yield per plant in cotton (<i>G.hirsutum</i> L.)	
4.3	Contribution of different characters towards genetic divergence in 50 cotton (<i>G.hirsutum</i> L.) genotypes	
4.4	Dendrogram showing relationship among 50 cotton (<i>G.hirsutum</i> L.) genotypes in eight clusters based on Mahalanobis D ² values	
4.5	Intra-and inter cluster distance of 50 cotton (<i>G.hirsutum</i> L.) genotypes in eight clusters based on Euclidean distance	
4.6	Two dimensional graph showing relative position of 50 cotton (<i>G.hirsutum</i> L.) genotypes based on PCA scores	
4.7	Three dimensional graph showing relative position of 50 cotton (<i>G.hirsutum</i> L.) genotypes based on PCA scores	
4.8	Dendrogram showing relationship among 50 cotton (<i>G.hirsutum</i> L.) genotypes in eight clusters based on Mahalanobis Euclidean ² distance	
4.9	Intra-and inter cluster distance of 50 cotton (<i>G.hirsutum</i> L.) genotypes in eight clusters based on Euclidean ² distance	

ABSTRACT

Name of the Author : **B. MANSINGH NAIK**

Title of the thesis : **GENETIC DIVERGENCE STUDIES IN AMERICAN COTTON (*Gossypium hirsutum* L.)**

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The present investigation was carried out during *kharif*, 2015-16 at Regional Agricultural Research Station, Lam Farm, Guntur, Andhra Pradesh to characterize 50 genotypes of cotton (*G. hirsutum*), to study the variability, heritability, genetic advance as per cent of mean, genetic divergence, character association and the magnitude of direct and indirect effects of 15 yield component traits with seed cotton yield per plant viz., plant height (cm), days to 50% flowering, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight (g), ginning out-turn (%), seed index (g), lint index (g), 2.5% span length (mm), micronaire (10^6 g/in), bundle strength (g/tex), uniformity ratio, seed cotton yield per plant (g) and lint yield per plant (g).

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. Moderate to high variability and high heritability coupled with high genetic advance as per cent of mean was observed for plant height, boll weight and micronaire indicating the predominance of additive gene action and hence, direct phenotypic selection may be useful with respect to these traits.

Correlation study indicated that plant height, number of sympodia per plant, number of bolls per plant, boll weight, ginning out turn, seed index, lint index, micronaire and lint yield per plant had positive significant association with seed cotton yield per plant.

. The path analysis indicated that as plant height, number of sympodia per plant, number of bolls per plant, boll weight, ginning out turn, seed index, lint index, micronaire and lint yield per plant showed positive and significant correlation, direct selection based on these attributes may be helpful in evolving high yielding varieties of upland cotton.

The results of multivariate analysis indicated the presence of considerable genetic divergence among the 50 genotypes studied. The 50 genotypes were grouped into 8 clusters by using Tocher's method in D^2 analysis indicating that the genetic diversity and geographical diversity were not related.

By Mahalanobis's D^2 statistic, it could be inferred that seed index, days to 50% flowering, boll weight, 2.5% span length and micronaire contributed maximum towards genetic divergence. Based on intra-and inter-cluster distance among the groups, it is suggested to make crosses between the genotypes of cluster VI (ARBH 1402) and cluster VII (HYPS 152), between genotypes of cluster I (SSGR 105) and cluster VIII (L 788), between the genotypes of cluster I (SSGR 105) and cluster IV (L 799), between the genotypes of cluster V (GJHV 497) and cluster VIII (L 788) after confirming their general combining ability.

Principal component analysis identified six principal components (PCs), which contributed 81.99 per cent of cumulative variance. The significant factors loaded in PC1 towards maximum genetic divergence were seed cotton yield per plant, bundle strength, lint index, micronaire, number of bolls per plant, number of sympodia per plant, plant height and uniformity ratio. 2D and 3D graphs showed wide divergence between L 788, MCU 5, HYPS 152, GISV 267, TSH 0499, SSGR 105, ARBH1402 and HS 294 signifying their usefulness in cotton breeding to develop high heterotic hybrids.

The genotypes L 788, HS 294, MCU 5, HYPS 152 and GISV 267 showed maximum inter-cluster distance in Mahalanobis D^2 analysis, principal component analysis and cluster analysis and also have better *per se* performance in sympodia per plant, number of bolls per plant, boll weight, seed index, lint index and quality characters. So they can be exploited for the development of heterotic hybrids in future breeding programmes.

Table 2.2. Review of literature on heritability ($h^2_{(b)}$) and genetic advance (GA) in cotton (*G. hirsutum* L.).

S. No.	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
1.	Plant height (cm)	Neelam <i>et al.</i> (2002) Kale <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007) An <i>et al.</i> (2008) Ravikesavan <i>et al.</i> (2008) Khan <i>et al.</i> (2009) Lakshmi <i>et al.</i> (2012) Haritha <i>et al.</i> (2012) Hafiz <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Abbas <i>et al.</i> (2014) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Khan <i>et al.</i> (2015)	Kaushik and Kapoor (2006) Verma <i>et al.</i> (2006) Mahantesh (2009)	---	Rajanna (2010)
2.	Days to 50% flowering	Neelam <i>et al.</i> (2002) Rao (2008) Mahantesh (2009) Hafiz <i>et al.</i> (2013)	Muraleedhar (2005) Kale <i>et al.</i> (2007) An <i>et al.</i> (2008) Ravikesavan <i>et al.</i> (2008) Mahantesh (2009) Rajanna (2010) Patel <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Dhivya <i>et al.</i> (2014)	---	Neelima (2002) Sivaprasad (2003) Raju (2005) Rao (2008)

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.	Number of monopodia plant ⁻¹	Raju (2005) Kaushik and Kapoor (2006) Pratap (2006) Rao (2008) Mahantesh (2009) Lakshmi <i>et al.</i> (2012) Hafiz <i>et al.</i> (2013) Patel <i>et al.</i> (2013) Abbas <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Dahipale <i>et al.</i> (2015)	Reddy (2001) Farooq <i>et al.</i> (2014) Khan <i>et al.</i> (2015)	Neelima (2002) Sivaprasad (2003)	Rao and Reddy (2001) Kale <i>et al.</i> (2007) Rajamani and Rao (2009) Rajanna (2010)
4.	Number of sympodia plant ⁻¹	Girase and Mehetre (2002) Neelam <i>et al.</i> (2002) Kaushik <i>et al.</i> (2003) Kaushik and Kapoor (2006) Verma <i>et al.</i> (2006) Sakthi <i>et al.</i> (2007) An <i>et al.</i> (2008) Ravikesavan <i>et al.</i> (2008) Rajanna (2010) Haritha <i>et al.</i> (2012) Lakshmi <i>et al.</i> (2012) Hafiz <i>et al.</i> (2013) Abbas <i>et al.</i> (2014) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015) Narendra (2015)	Gururajan (2000) Reddy (2001) Vinodhana <i>et al.</i> (2013) Farooq <i>et al.</i> (2014)	Mahantesh (2009)	Rao and Reddy (2001) Sivaprasad <i>et al.</i> (2004) Rajamani and Rao (2009) Bazi (2011) Patel <i>et al.</i> (2013)

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.	Number of bolls plant ⁻¹	Kaushik <i>et al.</i> (2003) Sivaprasad (2003) Kaushik and Kapoor (2006) Pratap (2006) Kale <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007) An <i>et al.</i> (2008) Khan <i>et al.</i> (2009) Mahantesh (2009) Rajanna (2010) Bazi (2011) Lakshmi <i>et al.</i> (2012) Dinakaran <i>et al.</i> (2012) Hafiz <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Abbas <i>et al.</i> (2014) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015) Ahsan <i>et al.</i> (2015b)	Gururajan and Sundar (2004) Patel <i>et al.</i> (2013) Farooq <i>et al.</i> (2014)	---	Rajamani and Rao (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)	Sakthi <i>et al.</i> (2007) An <i>et al.</i> (2008) Ravikesavan <i>et al.</i> (2008) Khan <i>et al.</i> (2009) Rajanna (2010) Bazi (2011) Lakshmi <i>et al.</i> (2012) Haritha <i>et al.</i> (2012) Dinakaran <i>et al.</i> (2012) Santhoshkumar <i>et al.</i> (2012) Vinodhana <i>et al.</i> (2013) Abbas <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015) Ahsan <i>et al.</i> (2015b) Rajamani <i>et al.</i> (2015)	Gururajan (2000) Gururajan and Sundar (2004) Kale <i>et al.</i> (2007) Mahantesh (2009) Farooq <i>et al.</i> (2014)	Sivaprasad (2003) Dhivya <i>et al.</i> (2014)	Rajamani and Rao (2009)
7.	Ginning out-turn (%)	Gururajan and Sundar (2004) Ravikesavan <i>et al.</i> (2008) Dinakaran <i>et al.</i> (2012) Haritha <i>et al.</i> (2012) Abbas <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015b)	An <i>et al.</i> (2008) Mahantesh (2009) Rajanna (2010) Bazi (2011) Vinodhana <i>et al.</i> (2013) Patel <i>et al.</i> (2013) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Khan <i>et al.</i> (2015) Ahsan <i>et al.</i> (2015a)	---	Sivaprasad (2003)

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)	Raju (2005) Kaushik and Kapoor (2006) An <i>et al.</i> (2008) Ravikesavan <i>et al.</i> (2008) Mahantesh (2009) Naqib <i>et al.</i> (2010) Bazi (2011) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015a) Ahsan <i>et al.</i> (2015b) Rajamani <i>et al.</i> (2015) Narendra (2015)	Gururajan (2000) Neelam <i>et al.</i> (2002) Sivaprasad (2003) Sakthi <i>et al.</i> (2007) Rajanna (2010) Haritha <i>et al.</i> (2012) Vinodhana <i>et al.</i> (2013) Khan <i>et al.</i> (2015)	---	Reddy (2001) Gururajan and Sundar (2004)
9.	Lint index (g)	Raju (2005) Kaushik and Kapoor (2006) Sambamurthy <i>et al.</i> (2006) An <i>et al.</i> (2008) Ravikesavan <i>et al.</i> (2008) Mahantesh (2009) Naqib <i>et al.</i> (2010) Bazi (2011) Lakshmi <i>et al.</i> (2012) Haritha <i>et al.</i> (2012) Santhoshkumar <i>et al.</i> (2012) Vinodhana <i>et al.</i> (2013) Dhivya <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015a) Ahsan <i>et al.</i> (2015b) Rajamani <i>et al.</i> (2015)	Sakthi <i>et al.</i> (2007) Rajanna (2010) Khan <i>et al.</i> (2015)	Erande <i>et al.</i> (2014)	---

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) Bazi (2011) Dinakaran <i>et al.</i> (2012) Hafiz <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014)	Sakthi <i>et al.</i> (2007) An <i>et al.</i> (2008) Ravikesavan <i>et al.</i> (2008) Mahantesh (2009) Rajamani and Rao (2009) Rajanna (2010)	---	Haritha <i>et al.</i> (2012)
11.	Micronaire value (10 ⁻⁶ g/inch)	Rao and Reddy (2001) An <i>et al.</i> (2008) Ravikesavan <i>et al.</i> (2008) Bazi (2011) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Narendra (2015)	Reddy (2001) Sakthi <i>et al.</i> (2007) Mahantesh (2009) Dinakaran <i>et al.</i> (2012) Haritha <i>et al.</i> (2012) Khan <i>et al.</i> (2015)	---	Sivaprasad (2003) Rajamani and Rao (2009) Rajanna (2010)
12.	Bundle strength (g/tex)	Reddy (2001) Sambamurthy <i>et al.</i> (2006) An <i>et al.</i> (2008) Ravikesavan <i>et al.</i> (2008) Vinodhana <i>et al.</i> (2013) Abbas <i>et al.</i> (2014)	Rao and Reddy (2001) Sakthi <i>et al.</i> (2007) Rajanna (2010)	---	Rao (2008) Mahantesh (2009) Rajamani and Rao (2009) Bazi (2011)

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
13.	Uniformity ratio	---	Sakthi <i>et al.</i> (2007) Mahantesh (2009) Bazi (2011) Dinakaran <i>et al.</i> (2012) Haritha <i>et al.</i> (2012) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)	Neelima (2002) Raju (2005)	Muraleedhar (2005) Rajamani and Rao (2009) Rajanna (2010)
14.	Seed cotton yield plant ⁻¹ (g)	An <i>et al.</i> (2008) Khan <i>et al.</i> (2009) Mahantesh (2009) Rajanna (2010) Bazi (2011) Dinakaran <i>et al.</i> (2012) Haritha <i>et al.</i> (2012) Vinodhana <i>et al.</i> (2013) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Khan <i>et al.</i> (2015) Ahsan <i>et al.</i> (2015) Narendra (2015) Dahipale <i>et al.</i> (2015)	Gururajan and Sundar (2004) Kale <i>et al.</i> (2007)	---	Rajamani and Rao (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
15.	Lint yield plant ⁻¹ (g)	Pratap (2006) Rao (2008) Mahantesh (2009) Rajanna (2010) Dinakaran <i>et al.</i> (2012) Erande <i>et al.</i> (2014) Dahipale <i>et al.</i> (2015)	---	---	---

Chapter I

INTRODUCTION

Cotton (*Gossypium* spp.) is the most important renewable natural fiber crop of global importance and continues to be the predominant and sustainable fiber in the Indian textile scene (Asha *et al.*, 2015). It contribute raw materials to the textile industry such as cotton lint as an export item, crude oil and cotton seed cake to oil and live stock industries, respectively (Ali *et al.*, 2009). Cotton is widely cultivated profitable fiber crop to boost up national economy and gained too much attention toward research (Haidar *et al.*, 2012). It plays a key role in the national economy in terms of its contribution to trade, industrial activities, employment and foreign exchange earnings (Gite *et al.*, 2006). Despite stiff competition from the man made synthetic fiber cotton retains its reputation as “queen of the fiber plants”. For multiple uses of lint and by-products, cotton is also referred as “white gold”.

India has prime place in the global cotton scenario due to several distinct features such as largest cotton growing area, cultivation of all the four cultivated species, large area under tetraploid cotton, one of the largest producers of extra-long staple cotton, possibly the only country to grow hybrid cotton, native home of old world cotton and wide diversity in agro-climatic conditions under which cotton is grown.

Cotton belongs to the genus *Gossypium* of the family Malvaceae and consists of approximately 50 species, including 45 diploids ($2n = 26$) and 5 allotetraploids ($2n = 52$). Of which four cultivated species viz., *G. hirsutum* L. [$n=2x=26$, (AD)1], *Gossypium barbadense* L. [$n=2x=26$, (AD)2], *Gossypium herbaceum* L. ($n=x=13$, A1), and *Gossypium arboreum* L. ($n=x=13$, A2). The former two species are allotetraploids and known as new world cottons, dominate the world cotton production, the later two are diploids and known as old world or Desi or Asiatic cottons. *G. hirsutum* and *G. barbadense* account for 90% and 8% of the world cotton production, respectively.

Among four linted cotton species, upland cotton (*G. hirsutum*) is a predominant species of cotton in the world as well as in India. By virtue of its wider adaptability, higher yield and good fibre quality, it gradually replaced Asiatic diploid cottons and was grown under irrigated as well as rain fed conditions. Varieties and hybrids of *G. hirsutum* occupy about 75 per cent of area and 85 per cent of cotton production.

India is the largest cotton growing country with an area of 118.81 lakh hectares and production of 352.00 lakh bales of cotton. Average productivity in India is 503 kg lint per hectare. In Andhra Pradesh, cotton is a crop of great economic value and playing a significant role in the socio-economic status of the farmers. It occupies an area of about 6.63 lakh hectares with an annual production of 19.10 lakh bales (170 kg each) and productivity of 641 kg lint per hectare (AICRP, Annual Report, 2015-16).

For developing high yielding cotton varieties or hybrids with superior fiber quality traits, genetically divergent parents are very important. Genetic diversity of germplasm plays an important role in cotton breeding. Genetic diversity is the basic portion of biological diversity, base of biological polymorphism and species diversity. The precise evaluation of the genetic diversity of germplasm will provide a guide for choosing parents and predicting the degree of inheritance, variation and level of heterosis, which are essential for realizing the breeding goal (Chen and Du, 2006).

The knowledge of genetic variation existing in germplasm is an important and essential aspect for initiating any crop breeding program because hybrids between lines of diverse origin generally display greater heterosis than those between closely related parents. Before actual breeding programme is taken up under crop improvement, it is desirable to elicit information on the extent of genetic variability present in the material (Swarup and Chaugle, 1962). The extent of heritability of the selected traits and the magnitude of genetic advance are equally important. The crosses involving genotypes with wider genetic base are likely to generate desirable recombinants in the progeny. The quantification of the degree of divergence present in the population is of immense value in

identifying diverse genotypes for recombination breeding programmes. Mahalanobis D^2 statistic is a powerful tool for quantifying genetic divergence in germplasm collections with respect to the characters considered together.

Correlation determines the degree and direction of relationship that exist between yield and its various components which will facilitate in selecting plants of desirable characteristics. In cotton, as both quantity and quality of the fiber are equally important, selection based on correlation without regard to the direct and indirect effects *via* other characters may not be fruitful. Path coefficient analysis helps to determine the direct and indirect effects of each independent variable on dependent variable, in order to make selection more effective (Dewey and Lu, 1959).

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

1. To assess the variability, genetic advance and heritability for seed cotton yield and fiber quality traits among the cotton genotypes.
2. To assess the genetic divergence among the cotton genotypes.
3. To assess the character association among yield components and fiber quality traits on seed cotton yield.
4. To study the direct and indirect effects of yield components and fiber quality traits on seed cotton yield.

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*** Original not seen**

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Chapter III

MATERIALS AND METHODS

The present investigation entitled, “Genetic divergence studies in American cotton (*G. hirsutum* L.)” was taken up during *kharif*, 2015-16 at Regional Agricultural Research Station, Lam Farm, Guntur, Andhra Pradesh. The site of the experiment is situated at 16⁰2' North and 80⁰3' East longitude at a height of 31.5 m above mean sea level. The soils are black cotton type with clay texture.

3.1 MATERIALS

The experimental material used in the present study comprised of 50 genotypes of cotton (*G. hirsutum* L.), which were obtained from different cotton research centers across the country. The information on source of these 50 genotypes is presented in Table 3.1.

3.2 METHODS

3.2.1 Experimental Technique

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

Table 3.2. Experimental details of the present investigation

Location	:	RARS Lam Farm, Guntur
Season	:	<i>Kharif</i> , 2015-16
Design	:	Randomized Block Design
Entries	:	50 genotypes of cotton (<i>G. hirsutum</i> L.)
Replications	:	Three
No. of rows/ genotype	:	One
No. of plants /row	:	10
Row length	:	6 m
Spacing	:	105 cm × 60 cm
Fertilizers	:	120 N: 60 P ₂ O ₅ : 60 K ₂ O kg/ha
Plant protection	:	Need based

Table 3.1 Cotton (*G. hirsutum* L.)genotypes employed in the study and their source

S. No.	NAME OF THE GENOTYPE	SOURCE
1	MCU 5	TNAU, Coimbatore
2	HS 294	CCSHAU, Sirsa
3	CCH 14-1	CICR, Coimbatore
4	L 604	ANGRAU, Lam
5	H 1442	CCSHAU, Hisar
6	LH 2256	PAU, Ludhiana
7	GJHV 497	JAU, Junagarh
8	TCH 1806	TNAU, Coimbatore
9	PBH 13	PAU, Bhatinda
10	NDLH 1938	ANGRAU, Nandyal
11	CCH 14-2	CICR, Coimbatore
12	L 770	ANGRAU, Lam
13	F 2501	PAU, Fairdkot
14	HYPs 152	AICCIP
15	PBH 10	PAU, Bhatinda
16	GSHV 177	NAU, Surat
17	TCH 1741	TNAU, Coimbatore
18	CPD 1401	UAS, Dharwad
19	SHAKTHI SULTAN (SSGR 105)	Shakti Agrotech
20	L 389	ANGRAU, Lam
21	L RK 516	TNAU, Coimbatore
22	ARBH 1402	UAS, Arabhavi
23	GTHV 13/37	SDAU, Talod
24	NA 1325	RARS, Nandyal
25	SURAJ	CICR, Coimbatore
26	RAH 1066	UAS, Bheemarayangudi
27	H 1447	CCSHAU, Hisar
28	SCS 1214	UAS, Raichur.
29	BS 26	OUAT, Bhavanipatna
30	CNH 5	CICR, Nagpur

31	BS 23	OUAT, Bhavanipatna
32	TSH 0533-2	TNAU, Srivalliputtur
33	SCS 1061	UAS, Raichur.
34	F 2493	PAU, Faridkot
35	TSH 0533-1	TNAU, Srivalliputtur
36	CSH 2838	CICR, Sirsa
37	RAH 1033	UAS, Bheemarayangudi
38	TSH 0499	TNAU, Srivalliputtur
39	SCS 1207	UAS, Raichur
40	L 1060	ANGRAU, Lam
41	GISV 267	NAU, Surat
42	GJHV 510	JAU, Junagarh
43	CNH 1118	CICR, Nagpur
44	L 788	ANGRAU, Lam
45	L 1008	ANGRAU, Lam
46	L 799	ANGRAU, Lam
47	ARBH 1401	UAS, Arabhavi
48	CPD 1402	UAS, Dharwad
49	RS 2765	ARS, Sriganganagar
50	RS 2767	ARS, Sriganganagar

3.2.2 Recording Observations

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

3.2.2.1 Plant height (cm)

At maturity, when the apical bud ceased to grow, the height of plant was recorded with the measuring rod in centimeters from ground to the apical bud.

3.2.2.2 Days to 50% flowering

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

3.2.2.3 Number of monopodia per plant

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

3.2.2.4 Number of sympodia per plant

Sympodial branches are direct fruit bearing branches that are extra-axillary in position with zigzag branching. These are generally short, appearing towards the top of the stem. At maturity, the sympodial branches on each plant were counted.

3.2.2.5 Number of bolls per plant

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

3.2.2.6 Boll weight (g)

The boll weight was obtained by taking the average weight of seed cotton from randomly collected 25 bolls per plot.

3.2.2.7 Ginning-out turn (%)

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

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

3.2.2.8 Seed index (g)

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

3.2.2.9 Lint index (g)

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

3.2.2.10 2.5% span length (mm)

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

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

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

3.2.2.12 Bundle strength (g/tex)

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

3.2.2.13 Uniformity ratio

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

3.2.2.14 Lint yield per plant (g)

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

3.2.2.15 Seed cotton yield per plant (g)

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

3.3 STATISTICAL ANALYSIS

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

3.3.1 Analysis of variance

Analysis of variance of the characters was done as per standard statistical procedure for randomized complete block design as given by Panse and Sukhatme (1978).

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

Where,

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

μ = General mean

t_i = i^{th} genotype effect

r_j = j^{th} block effect

e_{ij} = Random error

The structure of analysis of variance was as follows.

ANOVA Table for Randomized Block Design

Source of variation	Degrees of freedom	Mean sum of squares	Expected mean sum of squares	“F” calculated value
Replications	$r-1$	M_r	$\sigma_e^2 + t \sigma_r^2$	M_r / M_e
Treatments	$t-1$	M_t	$\sigma_e^2 + r \sigma_g^2$	M_t / M_e
Error	$(r-1)(t-1)$	M_e	σ_e^2	
Total	$(rt-1)$			

Where,

r = Number of replications

g = Number of genotypes

M_r = Mean sum of square of replication

M_t = Mean sum of square of treatment

M_e = Mean sum of square of error

σ_e^2 = Environmental variance

σ_r^2 = Variance due to replications

σ_g^2 = Variance due to genotypes

3.3.2 Estimation of genetic parameters

3.3.2.1 Estimation of variance components

Phenotypic and genotypic variances were estimated using the following formula,

$$\text{Genotypic variance } (\sigma^2_g) = \frac{M_t - M_e}{r}$$

$$\text{Phenotypic variance } (\sigma^2_p) = \sigma^2_g + M_e = \frac{M_t - M_e}{r} + M_e$$

The test of significance was carried out using 'F' table value of Fisher and Yates (1963).

3.3.2.2 Coefficient of variation

The genotypic and phenotypic coefficients of variation were calculated using the formula by Burton (1952).

- a. Genotypic coefficient of variation (GCV)

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

- b. Phenotypic coefficient of variation (PCV)

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

The GCV and PCV values were classified as described by Sivasubramanian and Menon (1973).

Classification	GCV/ PCV
Low	Less than 10%
Moderate	10 – 20%
High	More than 20%

3.3.2.3 Heritability

Heritability in broad sense was computed as the ratio of genetic variance to the total phenotypic variance and narrow sense heritability was the ratio of additive genetic variance to the total phenotypic variance as suggested by Hanson *et al.* (1956) and expressed as percentage.

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

Heritability in broad sense was categorized as per the classification given by Johnson *et al.* (1955).

Classification	Heritability
Low	Less than 30%
Moderate	30 – 60%
High	More than 60%

3.3.2.4 Expected genetic advance

Genetic advance was calculated based on formula given by Johnson *et al.* (1955).

$$\text{Expected genetic advance (GA)} = K \times \sigma_p \times h^2_b$$

Where,

K = Selection differential at 5% selection intensity (2.06)

σ_p = Phenotypic standard deviation

h^2_b = Heritability in broad sense

3.3.2.5 Genetic advance as per cent of mean (GAM)

$$\text{GAM} = \frac{\text{GA}}{\bar{X}} \times 100$$

Where,

GA = Genetic advance

$\bar{X}$ = Grand mean of the character

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

Classification	GAM
Low	Less than 10%
Moderate	10 – 20%
High	More than 20%

3.3.3 Correlation studies

The phenotypic and genotypic correlation coefficients were worked out to determine the degree of association of a character with yield and also among the yield components by using covariance technique as per Falconer (1964).

$$\text{Phenotypic coefficients of correlation (r}_p\text{)} = r(x_i x_j)_p = \frac{\text{Cov}(x_i x_j)_p}{\left[V(x_i)_p \cdot V(x_j)_p \right]^{1/2}}$$

Where,

$r(x_i x_j)_p$ = Phenotypic correlation between i^{th} and j^{th} characters
 $\text{Cov}(x_i x_j)_p$ = Phenotypic covariance between i^{th} and j^{th} characters
 $V(x_i)_p$ and $V(x_j)_p$ = Phenotypic variance of i^{th} and j^{th} characters respectively

$$\text{Genotypic coefficients of correlation (r}_g\text{)} = r(x_i x_j)_g = \frac{\text{Cov}(x_i x_j)_g}{\left[V(x_i)_g \cdot V(x_j)_g \right]^{1/2}}$$

Where,

$r(x_i x_j)_g$ = Genotypic correlation between i^{th} and j^{th} characters
 $\text{Cov}(x_i x_j)_g$ = Genotypic covariance between i^{th} and j^{th} characters
 $V(x_i)_g$ and $V(x_j)_g$ = Genotypic variance of i^{th} and j^{th} characters respectively

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 was carried out by using the correlation coefficients to know the direct and indirect effects of the component characters on yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959).

Path coefficients were obtained by solving the simultaneous equations which express the basic relationship between correlations and path coefficients.

The equations were as follows:

$$\begin{array}{l} r_{1,y} = \quad P_{1,y} + r_{1,2} P_{2,y} + r_{1,3} P_{3,y} + \dots + r_{1,k} P_{k,y} \\ r_{2,y} = r_{2,1} P_{1,y} + \quad P_{2,y} + r_{2,3} P_{3,y} + \dots + r_{2,k} P_{k,y} \\ .. \qquad \cdot \qquad \qquad \qquad \cdot \qquad \qquad \qquad \cdot \\ \cdot \qquad \cdot \qquad \qquad \qquad \cdot \qquad \qquad \qquad \cdot \\ \cdot \qquad \cdot \qquad \qquad \qquad \cdot \qquad \qquad \qquad \cdot \\ r_{k,y} = r_{k,1} P_{1,y} + r_{k,2} P_{2,y} + r_{k,3} P_{3,y} + \dots + r_{k,k} P_{k,y} \end{array}$$

Where,

$$r_{1,y} \text{ to } r_{k,y} = \text{Correlation coefficients between independent characters}$$

$r_{1,2}$ to $r_{k-1,k}$ = Correlation coefficients between all possible combinations of independent characters

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

The residual effect was computed by using the formula

$$R = \left[1 - (P_{1,y} r_{1,y} + P_{2,y} r_{2,y} + P_{3,y} r_{3,y} + \dots) \right]^{1/2}$$

Where,

R = Residual effect

$P_{1,y}$ = Direct effect of independent character '1' on dependent character 'y'

$$r_{1,y} = \text{Correlation coefficient of independent character '1' on dependent character 'y'}$$

3.3.5 Genetic divergence

3.3.5.1 Mahalanobis D² analysis

The data collected on different yield contributing characters was analysed using Mahalanobis's D² analysis to determine the genetic divergence among the genotypes in terms of 'generalised group distance' (Mahalanobis, 1928).

3.3.5.1.1 Test of significance

Variances were calculated for all the characters studied and test of significance was done. For the character pairs analysis of covariance was estimated on the basis of mean values (Panse & 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.

$$\Lambda = \frac{|E|}{|E+V|}$$

Where,

Λ = Wilk's criterion

$|E|$ = Determinant of error matrix and

$|E+V|$ = Determinant of error + variety matrix

$$\log_e \Lambda V_{(stat)} = -m \log_e \left(1 - \frac{pq}{n} \right) \log_e \hat{g}_e \dots\dots\dots (\text{ at } pq \text{ df})$$

Where,

$$m = n - (p + q + 1)/2 = 2.3026 \log 10 \Lambda$$

n = degree of freedom for error + varieties

p = number of variables /characters (15)

q = number of varieties –1 (or d.f.)

$V_{(stat)}$ is distributed as χ^2 with pq (735) 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.*, $\sum d_i^2$. Therefore transformation of the correlated variables into uncorrelated ones was done before working out the D^2 values. Transformation was done using pivotal condensation method.

3.3.5.1.2 Computation of D^2 values

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

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

Where,

y_i^t is uncorrelated mean value of i^{th} genotype for character 't'

y_j^t is uncorrelated mean value of j^{th} genotype for character 't'

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

3.3.5.1.3 Testing the significance of D^2 values

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

3.3.5.1.4 Contribution of individual characters towards divergence

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

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

Where,

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

M = All possible combinations of number of genotypes considered.

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 $\Sigma D_i^2/n$ where, ΣD_i^2 was the sum of distances between all possible combinations (n) of the populations included in a cluster.

3.3.5.1.7 Average inter-cluster distance

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

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

Where,

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

n_1 & n_2 = 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.

$$\text{Per cent variance explained for PC}_1 = \frac{\text{eigen value (PC}_1\text{)}}{\text{Sum of eigen values}}$$

The eigen vector (loading) defines the correlation of each variable with the principal components. The principal components were identified by following procedure. The j^{th} principal component (Y_j) of the observations X is the linear combination given as follows:

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

Where,

A_{ij} are found such that Y_j is uncorrelated $Y_1, Y_2, \dots, Y_{j-1}$ the j^{th} largest variance. The A_{ij} are the elements of the normalized eigen vector associated with largest j^{th} eigen value. The variance of the j^{th} principal component of the λ_j and the total system variance trace (S) = $\lambda_1 + \lambda_2 + \dots + \lambda_p$.

The importance of the j^{th} principal component is given by,

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

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

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

Where, S_i is the standard deviation of X_i .

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

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

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

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

3.3.5.2.2 Cluster analysis

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

3.3.5.2.2.1 Obtaining data matrix

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

3.3.5.2.2 Standardizing the data matrix

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

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

$$Z_{ij} = \bar{X}_{ij} - X_j / S_{ij}$$

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

$$\text{Where, } S_{ij} = \frac{\sum_{i=1}^n X_{ij} - \bar{X}_j / n}{n-1}$$

For, i = genotypes *i.e.*, 50

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

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

3.3.5.2.3 Computing the resemblance matrix

A resemblance coefficient, which measures the overall resemblance (the degree of similarity or distance) between a pair of genotypes, was computed. Here 50 genotypes were taken in data matrix therefore resemblance coefficient was computed.

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

$$\text{Squared Euclidean distance } [d_{ij}] = \sum_{k=1}^P (X_{ik} - X_{jk})^2$$

Where,

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

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

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

3.3.5.2.4 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 two 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 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 .

Table 2.5. Review of literature on direct effects of component characters on seed cotton yield in cotton (*G. hirsutum* L.)

S.No.	Character	Positive direct effect	Negative direct effect
1.	Plant height (cm)	Redddy (2001) Neelima (2002) Altaher and Singh (2003a) Sivaprasad (2003) Muthu <i>et al.</i> (2004) Kaushik and Kapoor (2006) Sakthi <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a) Dahiphale <i>et al.</i> (2015)	Raju (2005) Verma <i>et al.</i> (2006) Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Kumar <i>et al.</i> (2010) Farooq <i>et al.</i> (2013) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015a) Latif <i>et al.</i> (2015) Reddy <i>et al.</i> (2015) Chandrashekhar <i>et al.</i> (2016)
2.	Days to 50% flowering	Kumar <i>et al.</i> (2010) Rajanna <i>et al.</i> (2011) Patel <i>et al.</i> (2013) Rajamani <i>et al.</i> (2013) Ranjan <i>et al.</i> (2014a) Asha <i>et al.</i> (2015)	Gururajan (2000) Muthu <i>et al.</i> (2004) Kaushik and Kapoor (2006) Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Reddy <i>et al.</i> (2015) Chandrashekhar <i>et al.</i> (2016)
3.	No. of monopodia plant ⁻¹	Vijayalaxmi <i>et al.</i> (2008) Ekinici <i>et al.</i> (2010) Salahuddin <i>et al.</i> (2010) Srinivasulu <i>et al.</i> (2010) Mohan (2011) Rajanna <i>et al.</i> (2011) Patel <i>et al.</i> (2013) Chitti <i>et al.</i> (2013) Ranjan <i>et al.</i> (2014a) Dahiphale <i>et al.</i> (2015)	Raju (2003) Sivaprasad (2003) Kaushik and Kapoor (2006) Verma <i>et al.</i> (2006) Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Tulasi <i>et al.</i> (2012) Farooq <i>et al.</i> (2013) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Reddy <i>et al.</i> (2015) Chandrashekhar <i>et al.</i> (2016)

S.No.	Character	Positive direct effect	Negative direct effect
4	No. of sympodia plant ⁻¹	Vijayalaxmi <i>et al.</i> (2008) Kumar <i>et al.</i> (2010) Ekinci <i>et al.</i> (2010) Salahuddin <i>et al.</i> (2010) Srinivasulu <i>et al.</i> (2010) Patel <i>et al.</i> (2013) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Dahiphale <i>et al.</i> (2015)	Gururajan (2000) Reddy (2001) Sivaprasad (2003) Muthu <i>et al.</i> (2004) Raju (2005) Venkateswarlu <i>et al.</i> (2010a) Farroq <i>et al.</i> (2013) Reddy <i>et al.</i> (2015) Chandrashekhar <i>et al.</i> (2016)
5.	No. of bolls plant ⁻¹	Vijayalaxmi <i>et al.</i> (2008) Kumar <i>et al.</i> (2010) Ekinci <i>et al.</i> (2010) Salahuddin <i>et al.</i> (2010) Srinivasulu <i>et al.</i> (2010) Mohan (2011) Lakshmi <i>et al.</i> (2012) Tulasi <i>et al.</i> (2012) Patel <i>et al.</i> (2013) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a) Ahsan <i>et al.</i> (2015a) Asha <i>et al.</i> (2015) Reddy <i>et al.</i> (2015) Dahiphale <i>et al.</i> (2015) Latif <i>et al.</i> (2015) Chandrashekhar <i>et al.</i> (2016)	Kaushik <i>et al.</i> (2003) Farroq <i>et al.</i> (2013) Farroq <i>et al.</i> (2014)

S.No.	Character	Positive direct effect	Negative direct effect
6	Boll weight (g)	Vijayalaxmi <i>et al.</i> (2008) Kumar <i>et al.</i> (2010) Ekinci <i>et al.</i> (2010) Salahuddin <i>et al.</i> (2010) Srinivasulu <i>et al.</i> (2010) Mohan (2011) Lakshmi <i>et al.</i> (2012) Patel <i>et al.</i> (2013) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Farroq <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a) Ahsan <i>et al.</i> (2015a) Asha <i>et al.</i> (2015) Reddy <i>et al.</i> (2015) Chandrashekhar <i>et al.</i> (2016)	Ladole and Meshram (2000) Verma <i>et al.</i> (2006) Tulasi <i>et al.</i> (2012) Farooq <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
7	Seed index (g)	Vijayalaxmi <i>et al.</i> (2008) Kumar <i>et al.</i> (2010) Mohan (2011) Rajanna <i>et al.</i> (2011) Tulasi <i>et al.</i> (2012) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a) Ahsan <i>et al.</i> (2015a) Reddy <i>et al.</i> (2015)	Ladole and Meshram (2000) Neelima (2002) Altaher and Singh (2003a) Gururajan and Sundar (2004) Raju (2005) Kale <i>et al.</i> (2007) Farooq <i>et al.</i> (2013) Dahiphale <i>et al.</i> (2015) Chandrashekhar <i>et al.</i> (2016)
8	Lint index (g)	Vijayalaxmi <i>et al.</i> (2008) Kumar <i>et al.</i> (2010) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a) Ahsan <i>et al.</i> (2015a) Chandrashekhar <i>et al.</i> (2016)	Sivaprasad (2003) Muthu <i>et al.</i> (2004) Kaushik and Kapoor (2006) Pratap <i>et al.</i> (2007) Venkateswrlu <i>et al.</i> (2010a) Tulasi <i>et al.</i> (2012) Farooq <i>et al.</i> (2013) Reddy <i>et al.</i> (2015)

S.No.	Character	Positive direct effect	Negative direct effect
9	Ginning out-turn (%)	Gururajan (2000) Reddy (2001) Muthu <i>et al.</i> (2004) Kaushik and Kapoor (2006) Verma <i>et al.</i> (2006) Kale <i>et al.</i> (2007) Pratap <i>et al.</i> (2007) Mohan (2011) Tulasi <i>et al.</i> (2012) Patel <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a)	Vijayalaxmi <i>et al.</i> (2008) Kumar <i>et al.</i> (2010) Salahuddin <i>et al.</i> (2010) Venkateswarlu <i>et al.</i> (2010a) Farooq <i>et al.</i> (2013) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015a) Dahiphale <i>et al.</i> (2015) Reddy <i>et al.</i> (2015) Chandrashekhar <i>et al.</i> (2016)
10	2.5% span length (mm)	Raju (2005) Kaushik and Kapoor (2006) Kale <i>et al.</i> (2007) Kumar <i>et al.</i> (2010) Mohan (2011) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Dahiphale <i>et al.</i> (2015) Reddy <i>et al.</i> (2015) Chandrashekhar <i>et al.</i> (2016)	Reddy (2001) Neelima (2002) Muhammad <i>et al.</i> (2003) Sakthi <i>et al.</i> (2007) Mahantesh <i>et al.</i> (2010) Venkateswarlu <i>et al.</i> (2010a) Farooq <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013)
11	Micronaire value (10^{-6} g/inch)	Neelima <i>et al.</i> (2005) Sambamurthy <i>et al.</i> (2006) Pratap <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rasheed <i>et al.</i> (2009) Kumar <i>et al.</i> (2010) Mohan (2011) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Reddy <i>et al.</i> (2015) Chandrashekhar <i>et al.</i> (2016)	Gururajan and Sundar (2004) Raju (2005) Verma <i>et al.</i> (2006) Venkateswarlu <i>et al.</i> (2010a) Vinodhana <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)

S.No.	Character	Positive direct effect	Negative direct effect
12	Bundle strength (g/tex)	Neelima <i>et al.</i> (2002) Sivaprasad (2003) Sambamurthy <i>et al.</i> (2006) Sakthi <i>et al.</i> (2007) Rasheed <i>et al.</i> (2009) Rajanna <i>et al.</i> (2011)	Raju (2005) Vijayalaxmi <i>et al.</i> (2008) Kumar <i>et al.</i> (2010) Venkateswarlu <i>et al.</i> (2010a) Farooq <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014) Reddy <i>et al.</i> (2015) Chandrashekhar <i>et al.</i> (2016)
13.	Uniformity ratio	Sivaprasad (2003) Raju (2005) Sambamurthy <i>et al.</i> (2006) Vijayalaxmi <i>et al.</i> (2008) Srinivasulu <i>et al.</i> (2010) Mohan (2011) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)	Neelima (2002) Muthu <i>et al.</i> (2004) Pratap <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007) Padmavathi (2008) Anandan (2009) Venkateswarlu <i>et al.</i> (2010a) Reddy <i>et al.</i> (2015) Chandrashekhar <i>et al.</i> (2016)
14	Lint yield plant ⁻¹	Dedaniya and Pethani (1994) Tomar and Singh (1996) Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Reddy <i>et al.</i> (2015) Dahiphale <i>et al.</i> (2015)	

Chapter IV

RESULTS AND DISCUSSION

A systematic study was conducted to characterize the 50 cotton germplasm lines to study the variability, heritability, genetic advance as percent of mean, association and direct and indirect effects of yield components on seed cotton yield at Regional Agricultural Research Station, Lam Farm, Guntur, Andhra Pradesh, India. The results along with statistical analysis of the data are discussed and presented under the following headings.

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

4.2 Character association

4.3 Path coefficient analysis

4.4 Genetic divergence

ANALYSIS OF VARIANCE

The mean performance of 50 genotypes is presented in Table 4.1. The analysis of variance (Table 4.2.) revealed significant differences among the genotypes for all the 15 characters indicating the presence of genetic variability in the genotypes studied.

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

In any successful crop improvement programme, the availability of adequate variability in basic genetic stocks and their proper use through breeding for building up improved strains are very necessary. The genetic improvement of plant population depends on the presence of magnitude of genetic variability and the extent to which the desirable traits are transmissible. Thus, besides genetic variability knowledge on heritability and expected genetic advance plays a predictive role in breeding, expressing the reliability of phenotype as a guide to its breeding value. The higher the heritability the greater would be the response to selection that is gain in yield as heritability is directly proportional to genetic

advance making selection more effective. This was supported by Burton (1952) and Swarup and Chaugle (1962). So, the magnitude of heritable variability is the most important aspect of genetic contribution of the breeding material, which has close relationship on its response to selection (Panse, 1957).

In the present investigation estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability in broad sense (h^2_b) and genetic advance as per cent of mean (GAM) were calculated for 50 genotypes and are presented in Table 4.3 and discussed character-wise here under.

4.1.1 Plant Height (cm)

The plant height ranged from 97.00 cm (LRK 516) to 165.33 cm (BS 26) with a mean of 131.21 cm. The estimates of PCV and GCV were moderate to low (10.65 and 9.55), respectively and difference between them is low indicating that there is less influence of environment. Similar results were reported by Erande *et al.* (2014), Ahsan *et al.* (2015a), Ahsan *et al.* (2015b), Dahiphale *et al.* (2015) and Rajamani *et al.* (2015).

High heritability (80.50) coupled with high genetic advance as per cent of mean (22.63) was observed for the trait indicating the preponderance of additive gene action making selection effective. Similar results were reported by Haritha *et al.* (2012), Lakshmi *et al.* (2012), Hafiz *et al.* (2013), Vineela *et al.* (2013), Vinodhana *et al.* (2013), Dhivya *et al.* (2014), Erande *et al.* (2014), Farooq *et al.* (2014) and Khan *et al.* (2015).

4.1.2 Days to 50% Flowering

The mean value recorded for the trait was 63.76 days ranging from 53.67 (ARBH 1402) to 76.67 days (GISV 267). The estimates of PCV and GCV were low (6.57 and 6.41) and there was a close correspondence between phenotypic and genotypic variance indicating less environmental influence. Similar results were reported by Rajanna (2010), Sarada *et al.* (2010), Kulkarni *et al.* (2011), Venkatesh (2012), Dhivya *et al.* (2014) and Erande *et al.* (2014).

High heritability (95.43) coupled with moderate genetic advance as per cent of mean (16.54) was observed for days to 50% flowering indicating the presence of both additive and non additive gene actions and desired results may not be obtained by simple selection. Similar results were reported by Rao (2008), Mahantesh (2009) and Hafiz *et al.* (2013).

4.1.3 Number of Monopodia per plant

The number of monopodia per plant ranged from 1.10 (RS 2765) to 2.17 (GJHV 497 & L 799) with a mean of 1.67. The estimates of PCV and GCV were 21.88 (high) and 15.79 (moderate) respectively, which revealed the influence of environment is more on this trait than that of the genotype. These results were in conformity with Erande *et al.* (2014).

Moderate heritability (52.09) and high genetic advance as per cent of mean (30.09) was observed for this trait indicating the role of additive gene action making selection effective. These results were in agreement with the findings of Abbas *et al.* (2014), Erande *et al.* (2014) and Dahipale *et al.* (2015).

4.1.4 Number of Sympodia per plant

The number of sympodia per plant ranged from 13.93 (ARBH 1401) to 21.40 (CCH 14-1) with a mean of 19.00. The estimates of PCV and GCV (9.70 and 6.01) were low and indicating narrow range of variability for this trait. These results were in agreement with the findings of Farooq *et al.* (2014) and Rajamani *et al.* (2015).

Moderate heritability (38.40) coupled with low genetic advance as per cent of mean (9.84) indicating the operation of non additive gene action. The heritability is being exhibited due to favourable influence of environment rather than genotype and indicating the possibility of improvement of these traits through heterosis breeding rather than simple selection. These results were similar to those described by Sivaprasad *et al.* (2004), Bazi (2011) and Patel *et al.* (2013).

4.1.5 Number of Bolls per Plant

The number of bolls per plant ranged from 34.67(HYPS 152) to 59.67(HS 294) with an average of 45.51. The estimates of PCV and GCV (16.13 and 10.85) were moderate and there is high difference between them indicating influence of environment. These results were in agreement with Girase and Mehetre (2002), Pratap (2006) and Hafiz *et al.* (2013).

Moderate heritability (45.20) coupled with moderate genetic advance as per cent of mean (19.25) was observed for this trait indicating the presence of both additive and non additive gene action and desired results may not be obtained by simple selection.

4.1.6 Boll Weight (g)

The boll weight ranged from 3.13 g (ARBH 1401) to 5.05 g (L 788) with a mean of 4.00 g. The estimates of PCV and GCV (11.26 and 10.47) were moderate. Lower difference of magnitude was observed between them indicating that this trait is less affected by environment and variability among the studied genotypes. Similar results were reported by Vinodhana *et al.* (2013), Erande *et al.* (2014), Dhivya *et al.* (2014) and Ahsan *et al.* (2015a).

High heritability (86.54) and high genetic advance as per cent of mean (25.72) were recorded for this trait indicating preponderance of additive gene action making selection effective. Similar results were reported by Dinakaran *et al.* (2012), Santhoshkumar *et al.* (2012), Vinodhana *et al.* (2013), Abbas *et al.* (2014), Erande *et al.* (2014), Ahsan *et al.* (2015b), Khan *et al.* (2015) and Rajamani *et al.* (2015).

4.1.7 Ginning Out-turn (%)

The range of variation among the genotypes for this trait was 32.63 (NDLH 1938) to 35.51 (HS 294) with a mean of 34.08. The estimates of PCV and GCV (2.11 and 1.91) were low indicating there is less variability among the genotypes studied. Similar results were reported by Mohan (2011), Vinodhana *et al.* (2013), Dhivya *et al.* (2014), Erande *et al.* (2014), Farooq *et al.* (2014) and Khan *et al.* (2015).

High heritability (82.24) coupled with low genetic advance as per cent of mean (4.58) indicating the operation of non additive gene action. The heritability is being exhibited due to favourable influence of environment rather than genotype and indicating the possibility of improvement of these traits through heterosis breeding rather than simple selection. Similar results were reported by Patel *et al.* (2013), Vinodhana *et al.* (2013), Dhivya *et al.* (2014), Erande *et al.* (2014), Farooq *et al.* (2014) and Khan *et al.* (2015).

4.1.8 Seed Index (g)

Seed index was in the range of 7.85 g (TCH 1806) to 10.50 g (L 788) with a mean of 8.86 g. The estimates of PCV and GCV (6.02 and 5.42) were low and difference between them is low indicating there is less influence of environment. Similar results were reported by Ahsan *et al.* (2015b) and Dahiphale *et al.* (2015).

High heritability (81.27) and moderate genetic advance as per cent of mean (12.91) were observed for this trait indicating the operation of both additive and non additive gene action and desired results may not be obtained by simple selection. Similar findings were reported by Rajanna (2010), Haritha *et al.* (2012), Vinodhana *et al.* (2013) and Khan *et al.* (2015).

4.1.9 Lint Index (g)

The range of variation observed for this character was from 3.95g (TCH 1806) to 5.71 g (L 788) with a mean of 4.59 g. The estimates of PCV and GCV (8.25 and 7.49) were low and difference between them is low indicating there is less influence of environment. Similar findings were reported by Naquib *et al.* (2010), Rajanna *et al.* (2010) and Vinodhana *et al.* (2013).

High heritability (82.49) and moderate genetic advance as per cent of mean (17.96) were observed for lint index indicating the operation of both additive and non additive gene action and desired results may not be obtained by simple selection. These results are in agreement with the findings of Khan *et al.* (2015).

4.1.10 2.5% Span Length (mm)

The mean span length ranged from 24.13 (PBH 10) to 31.71 (MCU 5) with a mean of 26.85. The estimates of PCV and GCV (5.71 and 5.36) were low indicating there is less variability among the genotypes studied. Similar findings were reported by Kishore *et al.* (2011), Mohan (2011), Vinodhana *et al.* (2013), Dhivya *et al.* (2014), Erande *et al.* (2014), Dahiphale *et al.* (2015), Narendra *et al.* (2015) and Rajamani *et al.* (2015).

High heritability (88.19) coupled with moderate genetic advance as per cent of mean (13.29) was observed for this trait indicating the operation of both additive and non additive gene action and desired results may not be obtained by simple selection. Similar findings were reported by Mahantesh *et al.* (2009), Rajamani and Rao (2009) and Rajanna (2010).

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

The range of variation for the character was from 3.19 (TSH 0499) to 4.78 (RAH 1033) with a mean of 3.96. The estimates of PCV and GCV (11.20 and 10.31) were moderate and difference between them is low indicating there is less influence of environment. Similar findings were reported by Vinodhana *et al.* (2013), Khan *et al.* (2013), Narendra (2015) and Rajamani *et al.* (2015).

High heritability (84.81) coupled with high genetic advance as per cent of mean (25.07) was recorded for this trait indicating the preponderance of additive gene action making selection effective. Similar findings were reported by Ravikesavan *et al.* (2008), Bazi (2011), Vinodhana *et al.* (2013), Erande *et al.* (2014) and Narendra (2015).

4.1.12 Bundle Strength (g/tex)

The range of variation for bundle strength was from 18.74 (L 1008) to 21.91 (SURAJ) with a mean of 20.39. The estimates of PCV and GCV (4.27 and 3.73) were low indicating there is less variability among the genotypes studied. Similar results were observed by Sarada *et al.* (2010), Bazi (2011) and Rajamani *et al.* (2015).

High heritability (76.35) coupled with low genetic advance as per cent of mean (8.61) was recorded for this trait indicating the operation of non additive gene action. The heritability is being exhibited due to favourable influence of environment rather than genotype and indicating the possibility of improvement of these traits through heterosis breeding rather than simple selection. Similar results were observed by Rao and Reddy (2001), Sakthi *et al.* (2007) and Rajanna (2010).

4.1.13 Uniformity Ratio

The range of variation was from 45.72 (NA 1325) to 46.96 (CCH 14-1) with a mean of 46.25. The estimates of PCV and GCV (0.96 and 0.40) were low indicating there is less variability among the genotypes studied. Similar results were observed by Bazi (2011), Mohan (2011), Kishore *et al.* (2011), Vinodhana *et al.* (2013), Erande *et al.* (2014), Khan *et al.* (2015) and Rajamani *et al.* (2015).

Low heritability (16.92) coupled with low genetic advance as per cent of mean (0.43) was observed for uniformity ratio indicating that the trait is highly influenced by environmental effects and selection would be ineffective. This was in agreement with the findings of Muraleedhar (2005), Rajamani and Rao (2009) and Rajanna (2010).

4.1.14 Seed Cotton Yield per plant (g)

The range of variation was from 79.85 g (LRK 516) to 164.65 g (HS 294) with a mean of 118.01 g. The estimates of PCV and GCV (19.98 and 12.65) were moderate and there is high difference between them indicating influence of environment. Similar results were observed by Ahsan *et al.* (2015a).

Moderate heritability (40.08) coupled with high genetic advance as per cent of mean (21.14) was observed for seed cotton yield per plant indicating the role of additive gene action making selection effective.

4.1.15 Lint Yield per plant (g)

The mean variation ranged from 26.80 g (ARBH 1401) to 58.33 g (HS 294) with an average of 40.57 g. The PCV and GCV estimates (20.52 and 12.93) were high and moderate respectively and there is high difference between them indicating influence of environment.

Moderate heritability (39.71) coupled with high genetic advance as per cent of mean (21.52) was observed for seed cotton yield per plant indicating the role of additive gene action making selection effective.

4.2 CHARACTER ASSOCIATION

Yield is a complex quantitative trait, considerably affected by environment. Therefore, selection of genotypes based on yield alone is not effective. So, appraisal of genetic correlation measures the magnitude of relationship between various plant characters that determine the component characters on which selection can be made for improvement in yield (Johnson *et al.*, 1955). Genotypic correlation is the inherent association between two variables. It may be either due to pleiotropic action of genes or linkage. If the correlation between seed cotton yield and a character is due to the direct effect of the character, it reflects a true relationship between them and selection can be practiced for such characters in order to improve yield. But if the correlation is mainly due to indirect effect of the character through another component trait, the breeder has to select for the trait through which the indirect effect is expected. So, correlation coefficients are useful if indirect selection of a secondary trait is to be used for improving the primary trait of interest. A great yield response is obtained when the character for which indirect selection is practiced has a high heritability and a positive correlation with yield. Thus, correlation is an important asset to cotton breeder helping him in deciding the breeding procedure for genetic improvement of seed cotton.

In the present investigation, phenotypic and genotypic correlation coefficients between seed cotton yield and other related component characters and among themselves were estimated and presented in Table 4.4.

4.2.1 Plant Height (cm)

Plant height showed significant positive association with number of bolls per plant (0.3039** and 0.1801*), boll weight (0.3059** and 0.2653**), seed cotton yield per plant (0.4909** and 0.2748**) and lint yield per plant (0.4764** and 0.2640**) at both genotypic and phenotypic levels respectively indicating that increase in one character will lead to increase in second and vice versa. The trait showed significant positive association with days to 50% flowering (0.1819*) and number of sympodia per plant (0.1610*) at genotypic level indicating simultaneous improvement of these traits and significant negative association was observed with number of monopodia per plant (-0.2069*) where increase in one variable cause decrease in another variable and vice versa at genotypic level.

The selection for high seed cotton yield per plant based on plant height is beneficial as their association is significantly positive at both genotypic and phenotypic levels. Similar results were also reported by Ranjan *et al.* (2014a), Kumar *et al.* (2014), Farooq *et al.* (2014), Erande *et al.* (2014), Asha *et al.* (2015) and Ullah *et al.* (2015).

4.2.2 Days to 50% Flowering

The trait showed significant positive association with number of monopodia per plant (0.2414** and 0.1682*), boll weight (0.1911* and 0.1728*), ginning out turn (0.2254** and 0.1836*) and 2.5% span length (0.3601** and 0.3308**) at both genotypic and phenotypic levels and significant positive association with uniformity ratio (0.2532**) at genotypic level indicated that increase in one character will lead to increase in second and vice versa.

The non-significant positive association with seed cotton yield at both genotypic and phenotypic levels (0.0853 and 0.0538) clearly indicated the independent nature of two characters. Hence, improvement of seed cotton yield is not possible through days to 50% flowering. These results were in agreement with Kaushik and Kapoor (2006), Kale *et al.* (2007) and Erande *et al.* (2014).

4.2.3 Number of Monopodia per plant

At both genotypic and phenotypic levels, number of monopodia per plant was found to have significant positive association with days to 50% flowering (0.2414** and 0.1682*) and number of bolls per plant (0.2257** and 0.3463**) indicating simultaneous improvement of these traits. The trait showed positive and significant association with micronaire (0.2277**) at genotypic level and with sympodia per plant (0.3147**), seed index (0.2424**), lint index (0.2044*), seed cotton yield per plant (0.3145**) and lint yield per plant (0.3079**) at phenotypical level, respectively.

4.2.4 Number of Sympodia per plant

This trait showed significant positive association with number of bolls per plant (0.2123** and 0.5646**), boll weight (0.3291** and 0.3990**), seed cotton yield per plant (0.4309** and 0.6989**) and lint yield per plant (0.4471** and 0.6979**) at both genotypic and phenotypic level and uniformity ratio (0.2367**) at genotypic level indicating simultaneous improvement of these traits.

The selection for high seed cotton yield per plant based on number of sympodia per plant is beneficial as their association is significantly positive at both genotypic and phenotypic levels. Similar results were also reported by Batool *et al.* (2010), Ekinci *et al.* (2010), Patnaik and Sial (2010), Mohan (2011), Rajanna *et al.* (2011), Erande *et al.* (2014), Asha *et al.* (2015), Baloch *et al.* (2015b), Dahiphale *et al.* (2015) and Khan *et al.* (2015).

4.2.5 Number of Bolls per plant

Number of bolls per plant showed significant positive association with plant height (0.3039** and 0.1801*), monopodia per plant (0.2257** and 0.3463**), sympodia per plant (0.2123** and 0.5646**), micronaire (0.2916** and 0.1656*), seed cotton yield per plant (0.6446** and 0.8292**) and lint yield per plant (0.5985** and 0.8064**) at both genotypic and phenotypic levels indicating that simultaneous improvement of these traits. While, it showed negative and significant association with boll weight (-0.2618**), 2.5% span length (-0.2971**) and uniformity ratio (-0.4485**) at genotypic level indicating that simultaneous improvement of these traits is not possible.

The trait showed significant positive association with seed cotton yield per plant (0.6446** and 0.8292**) and lint yield per plant (0.5985** and 0.8064**) at both genotypic and phenotypic levels indicating that selection for high seed cotton yield per plant based on number of bolls per plant is beneficial. These results were in conformity with the reports of Vinodhana *et al.* (2013), Erande *et al.* (2014), Farooq *et al.* (2014), Kumar *et al.* (2014), Ranjan *et al.* (2014a), Ahasan *et al.* (2015a), Asha *et al.* (2015), Baloch *et al.* (2015b), Reddy *et al.* (2015), Ullah *et al.* (2015) and Chandrasekhar *et al.* (2016).

4.2.6 Boll Weight (g)

Boll weight showed significant positive association with plant height (0.3059** and 0.2653**), days to 50% flowering (0.1911* and 0.1728*), number of sympodia per plant (0.3291** and 0.3990**), ginning out turn (0.2949** and 0.2904**), seed index (0.2892** and 0.3687**), lint index (0.3250** and 0.3880**), 2.5% span length (0.2883** and 0.2637**) bundle strength (0.1925* and 0.1764*), uniformity ratio (0.4440** and 0.1723*), seed cotton yield per plant (0.5693** and 0.5686**) and lint yield per plant (0.6076** and 0.5919**) at both genotypic and phenotypic level indicating simultaneous selection for these traits.

The selection for high seed cotton yield per plant based on boll weight is beneficial as their association is significantly positive at both genotypic and phenotypic levels. These results were in conformity with the reports of Tulasi *et al.* (2012), Rao and Gopinath (2013), Kumar *et al.* (2014), Ranjan *et al.* (2014a), Ahasan *et al.* (2015a), Asha *et al.* (2015), Baloch *et al.* (2015b), Reddy *et al.* (2015), Ullah *et al.* (2015) and Chandrasekhar *et al.* (2016).

4.2.7 Ginning Out-turn (%)

This trait showed significant positive association with days to 50% flowering (0.2254** and 0.1836), boll weight (0.2949** and 0.2904**), seed index (0.5753** and 0.5308**), lint index (0.8169** and 0.7605**), 2.5% span length (0.3476** and 0.2835**), seed cotton yield per plant (0.1626* and 0.2185**) and lint yield per plant (0.2749** and 0.2868**) at genotypic and phenotypic level indicating simultaneous selection for these traits. It showed positive and highly significant association with uniformity ratio (0.3208**) at genotypic level.

The selection for high seed cotton yield per plant based on ginning out-turn is beneficial as their association is significantly positive at both genotypic and phenotypic levels. These results were in conformity with the reports of Salahuddin *et al.* (2010), Naqib *et al.* (2010), Erande *et al.* (2014), Farooq *et al.* (2014) and Dahiphale *et al.* (2015).

4.2.8 Seed Index (g)

At both genotypic and phenotypic levels, this trait showed significant positive association with boll weight (0.2892** and 0.3687**), ginning out turn (0.5753** and 0.5308**), lint index (0.9469** and 0.9458**), 2.5% span length (0.2378** and 0.2087*), seed cotton yield per plant (0.2103** and 0.4298**) and lint yield per plant (0.3034** and 0.4801**) and at genotypic level, this trait showed significant positive association with uniformity ratio (0.3181**) indicating simultaneous selection for these traits. The trait showed negative significant association with micronaire (-0.2828** and -0.2393**) at both genotypic and phenotypic level indicating that simultaneous selection for these trait was not possible.

The selection for high seed cotton yield per plant based on seed index is beneficial as their association is significantly positive at both genotypic and phenotypic levels. These results were in conformity with the reports of Mahantesh (2009), Kumar *et al.* (2010), Mohan (2011), Tulasi *et al.* (2012), Rao and Gopinath (2013), Kumar *et al.* (2014) and Ranjan *et al.* (2014a).

4.2.9 Lint Index (g)

Lint index showed significant positive association with uniformity ratio (0.3562**) at genotypic level and with boll weight (0.3250** and 0.3880**), ginning out turn (0.8169** and 0.7605**), seed index (0.9469** and 0.9458**), 2.5% span length (0.3048** and 0.2619**), seed cotton yield per plant (0.2167** and 0.4069**) and lint yield per plant (0.3272** and 0.4706**) at both genotypic and phenotypic level indicating selection for yield based on lint index would be beneficial. Naqib *et al.* (2010), Salahuddin *et al.* (2010) and Kumar *et al.* (2014) reported that lint index had positive and significant association with seed cotton yield.

The trait showed significant negative association with micronaire (-0.2414** and -0.1987*) at both genotypic and phenotypic levels indicating simultaneous selection for these traits was not possible.

4.2.10 2.5% Span Length (mm)

The trait showed significant positive association with bundle strength (0.4585** and 0.4160**) and uniformity ratio (0.9245** and 0.6483**) at both genotypic and phenotypic levels indicating simultaneous selection for these traits.

The trait showed significant negative association with micronaire (-0.1627* and -0.1638*) at both genotypic and phenotypic levels indicating simultaneous selection for these traits was not possible. Rajamani *et al.* (2013), Rao and Gopinath (2013), Vinodhana *et al.* (2013), Erande *et al.* (2014) and Kumar *et al.* (2014) also reported significant negative association of 2.5% span length with micronaire.

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

The trait showed significant positive association with bundle strength (0.4329** and 0.3565**) at both genotypic and phenotypic level. Seed cotton yield per plant (0.1718*) showed significant positive association with micronaire at genotypic level indicated that simultaneous improvement of these traits was possible.

4.2.12 Bundle Strength (g/tex)

The non significant association of seed cotton yield with bundle strength (0.1009 and 0.0714) at both genotypic and phenotypic levels clearly indicates the independent nature of these traits and selection for high seed cotton yield based on bundle strength is not reliable. Kumar *et al.* (2010), Bazi (2011) and Mohan (2011) also reported similar results.

4.2.13 Uniformity Ratio

This trait showed negatively non-significant association with seed cotton yield per plant (-0.0794 and -0.0274) at both genotypic and phenotypic levels were in conformity with results of Tuteja *et al.* (2005), Kishore *et al.* (2011), Mohan (2011), Rajanna *et al.* (2011) and Kumar *et al.* (2014) and lint yield per plant (-0.0424) at genotypic level indicated that simultaneous improvement of these traits is not possible. Vijayalaxmi *et al.* (2008) and Erande *et al.* (2014) reported negatively non-significant association of the trait with lint yield per plant.

4.2.14 Lint Yield Per Plant (g)

This trait showed highly significant positive association with seed cotton yield per plant (0.9891** and 0.9927**) both at genotypic and phenotypic levels. Rajanna *et al.* (2011), Lakshmi *et al.* (2012), Erande *et al.* (2014), Dahiphale *et al.* (2015) and Reddy *et al.* (2015) also reported similar results.

The genetic factors responsible for correlated response are linkage and pleiotropy (manifold effects of a gene). If the association between two traits (whether positive or negative) remains same in the parental population as well as segregating populations, it means the association is due to pleiotropy and if it changes in segregating populations it is most likely due to linkage due to recombination between genes (Mallikarjun *et al.*, 2003). The pleiotropy or linkage may involve two desirable traits like seed cotton yield per plant with number of bolls per plant and boll weight or one desirable and one undesirable trait like seed cotton yield with plant height and days to 50% flowering hindering the progress. In light of above results we can infer that genotypic correlation is more stable as it excludes environmental effects and is paramount importance for a plant breeder to bring about genetic improvement in one character by selecting the other character of a pair that is genetically correlated.

4.3 PATH COEFFICIENT ANALYSIS

The information on the extent of association between the yield and other factors is important to bring the simultaneous improvement in correlated traits. Although, knowledge of phenotypic correlation of agronomic characters with yield in cotton is indispensable in the characterization of component influences on manifesting the characters, these associations yet do not provide explicit information on the relative importance of direct and indirect effects of each component character on seed cotton yield.

With the increase in number of variables, it becomes imperative to measure the contribution of each variable towards the observed correlation. Therefore, partitioning the observed correlation coefficients into unidirectional pathways and alternate pathways facilitate the characterizations of more complex traits like seed cotton yield devised by Wright (1921) and utilized by Dewey and Lu (1959) in selection programmes. In light of above inferences, path coefficient analysis, which splits the correlation coefficients, provides precise information on the direct and indirect effects in order to perceive the most influencing characters to be utilized as selection criteria in cotton breeding programme.

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

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

- If the correlation coefficient between a causal factor and the effect is almost equal to its direct effect, then correlation explains the true relationship and a direct selection through this trait will be effective.
- If the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effects seem to be the cause of positive correlation. In such situations, the indirect causal factors are to be considered simultaneously for selection.
- Correlation coefficient may be negative but the direct effect is positive and high. Under these circumstances, a restricted simultaneous selection model is to be followed *i.e.*, restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect.
- If correlation coefficient is negative and direct effect is also negative, then we have to drop the selection based on the character.
- The residual effect determines how best the causal factors account for the variability of the dependent factor. If the residual effect is high, some other factors which have not been considered in the study need to be included in the analysis to account fully for the variation in yield.

So, in the present study direct and indirect effects of different yield component traits on seed cotton yield per plant were estimated through path analysis at phenotypic and genotypic levels and are presented in Tables 4.5 and 4.6. respectively. The phenotypic and genotypic path diagrams are given in Fig. 4.1 and 4.2 respectively.

4.3.1 Plant Height (cm)

At phenotypic level the direct contribution of this character on seed cotton yield per plant was positive and low (0.0080). The indirect effects sympodia per plant (0.0007), number of bolls per plant (0.0486), boll weight (0.0450), seed index (0.0014), 2.5% span length (0.0001), uniformity ratio (0.0006) and lint yield per plant (0.1816) were positive. While, days to 50% flowering (-0.0002), monopodia per plant (-0.0011), ginning out turn (-0.0026), lint index (-0.0067) and micronaire (-0.0006) were negative.

At genotypic level this trait showed negative direct effects with seed cotton yield per plant (-0.0453). It showed positive indirect effects through number of bolls per plant (0.5111), boll weight (0.4977), ginning out turn (0.0242), seed index (0.0004), 2.5% span length (0.0220) and bundle strength (0.0027). Whereas, days to 50% flowering (-0.0083), monopodia per plant (-0.0056), sympodia per plant (-0.0057), lint index (-0.0080), micronaire (-0.0048), uniformity ratio (-0.0166) and lint yield per plant (-0.4730) were negative.

Plant height had positive significant correlation with seed cotton yield per plant (0.4909** and 0.2748**) both at genotypic level and phenotypic level respectively. The negative direct effect and positive correlation with seed cotton yield per plant at genotypic level suggests the indirect effects seem to be the cause of positive correlation, the indirect causal factors are to be considered simultaneously for selection. This was in agreement with the previous work of Kumar *et al.* (2014).

4.3.2 Days to 50% Flowering

At phenotypic level, it exhibited negligible negative direct effect (-0.0015). The indirect effects via plant height (0.0012), monopodia per plant (0.0022), boll weight (0.0293), seed index (0.0004), micronaire (0.0010) and lint yield per plant (0.0405) were positive. While, sympodia per plant (-0.0007), number of bolls (-0.0089), ginning out turn (-0.0032), lint index (-0.0053), 2.5% span length (-0.0004) and uniformity ratio (-0.0008) were negative.

At genotypic level, the direct contribution of this character with seed cotton yield per plant was negative (-0.0454). The indirect effects via monoodia per plant (0.0065), sympodia per plant (0.0044), boll weight (0.3109), ginning out turn (0.0363), seed index (0.0001), micronaire (0.0078), bundle strength (0.0019) and uniformity ratio (0.0132) were positive. While, plant height (-0.0082), number of bolls per plant (-0.0737), lint index (-0.0058), 2.5% span length (-0.0658) and lint yield per plant (-0.0969) were negative.

This trait had positive non significant correlation with seed cotton yield per plant (0.0853 and 0.0538) both at genotypic and phenotypic levels, respectively. The above results were in agreement with Kaushik and Kapoor (2006), Kale *et al.* (2007) and Erande *et al.* (2014). The negative direct effect indicated that selection for this trait would not be realized in increased seed cotton yield per plant. Thus, indirect positive effects are to be considered. The results were in agreement with Gururajan (2000), Muthu *et al.* (2004), Erande *et al.* (2014), Kumar *et al.* (2014) and Chandrashekhar *et al.* (2016). Further non significant correlations indicate the independent association of this trait in improving yield per plant. Selection for early maturing and short duration varieties in cotton may also bring about yield improvement.

4.3.3 Number of monopodia per plant

At phenotypic level direct contribution of this character on seed cotton yield per plant was positive (0.0130). The indirect effects *via* sympodia per plant (0.0029), number of bolls (0.0935), boll weight (0.0052), seed index (0.0035)

and lint yield per plant (0.2117) were positive. While, plant height (-0.0006), days to 50% flowering (-0.0002), ginning out-turn (-0.0013), lint index (-0.0116), micronaire (-0.0013) and uniformity ratio (-0.0003) were negative.

At genotypic level, the direct contribution of this character with seed cotton yield per plant was positive (0.0270). The indirect effect via plant height (0.0094), number of bolls per plant (0.3796), ginning out turn (0.0022), seed index (0.0005), 2.5% span length (0.0022), bundle strength (0.0048) and uniformity ratio (0.0028) were positive. Whereas, days to 50% flowering (-0.0110), sympodia per plant (-0.0037), boll weight (-0.1758), lint index (-0.0060), micronaire (-0.0164) and lint yield (-0.1105) were negative.

This trait had positive non significant correlation with seed cotton yield per plant (0.1049) at genotypic level and positive significant (0.3145**) at phenotypic level. The above result was reported by earlier works of Rajanna *et al.* (2011), Erande *et al.* (2014) and Khan *et al.* (2015) The low positive direct effect indicated the number of monopodia per plant had little effect on yield as its own but its effect on yield per plant may be through its component traits. The results are in agreement with Salahuddin *et al.* (2010), Rajanna *et al.* (2011), Chitti *et al.* (2013), Ranjan *et al.* (2014a) and Dahiphale *et al.* (2015). Further non significant correlations indicate the independent association of this trait in improving yield per plant.

4.3.4 Number of Sympodia per plant

At phenotypic level, the direct contribution of this character on seed cotton yield per plant was low and positive (0.0092). The indirect effects of this trait through plant height (0.0006), days to 50% flowering (0.0001), monopodia per plant (0.0041), number of bolls per plant (0.1542), boll weight (0.0677), seed index (0.0047) and lint yield per plant (0.4800) were positive. While, ginning out turn (-0.0023), lint index (-0.0167), micronaire (-0.0004) and uniformity ratio (-0.0005) showed negative effects.

The direct contribution of this character on seed cotton yield per plant was negative (-0.0357) at genotypic level. The indirect effects *via* days to 50% flowering (0.0056), monopodia per plant (0.0028), number of bolls per plant (0.3571), boll weight (0.5354), ginning out turn (0.0062), seed index (0.0002), bundle strength (0.0105) and uniformity ratio (0.0123) were positive. While, plant height (-0.0073), lint index (-0.0027), 2.5% span length (-0.0038), micronaire (-0.0058) and lint yield per plant (-0.4438) were negative.

This trait had positive significant correlation with seed cotton yield per plant (0.4309** and 0.6989**) both at genotypic and phenotypic levels respectively. This was in agreement with earlier work of Asha *et al.* (2015), Baloch *et al.* (2015b), Dahipale *et al.* (2015) and Khan *et al.* (2015). The negative direct effect and positive correlation with seed cotton yield per plant at genotypic level suggests the indirect effects seems to be the cause of positive correlation, indirect causal factors are to be considered simultaneously for selection. These results were in conformity with earlier works of Gururajan (2000), Muthu *et al.* (2004), Farooq *et al.* (2013) and Chandrashekhar *et al.* (2016). Further significant correlations indicate the dependent association of this trait in improving yield per plant.

4.3.5 Number of Bolls per plant

Direct effect of this trait on seed cotton yield per plant was positive (0.2699) at phenotypic level and its indirect effects through plant height (0.0014), monopodia per plant (0.0045), sympodia per plant (0.0052), boll weight (0.0053), seed index (0.0041), 2.5%span length (0.0002), uniformity ratio (0.0009) and lint yield per plant (0.5546) were positive. While, ginning out turn (-0.0014), lint index (-0.0141) and micronaire (-0.0016) showed negative effects.

At genotypic level, the direct effect of this character on seed cotton yield per plant was positive and high (1.6820). The indirect effects through days to 50% flowering (0.0020), number of monopodia per plant (0.0061), lint index (0.0011) and 2.5%span length (0.0543) were positive. While negative effects were observed through plant height (-0.0138), sympodia per plant (-0.0076), boll weight (-0.4259), ginning out turn (-0.0106), micronaire (-0.0210), uniformity ratio (-0.0233) and lint yield per plant (-0.5941).

This trait expressed significant positive (0.6446** and 0.8292**) correlations with seed cotton yield per plant at both genotypic and phenotypic levels. High direct effects and positive correlations with seed cotton yield suggests number of bolls per plant as one of the major contributor towards seed cotton yield per plant which was in agreement with an earlier works of Tulasi *et al.* (2012), Vinodhana *et al.* (2013), Kumar *et al.* (2014), Ranjan *et al.* (2014a), Ahsan *et al.* (2015a), Reddy *et al.* (2015) and Chandrashekhar *et al.* (2016).

4.3.6 Boll Weight (g)

With respect to phenotypic level, this trait recorded a positive (0.1696) direct effect on seed cotton yield per plant. The indirect effects of this trait *via* plant height (0.0021), monopodia per plant (0.0004), Sympodia per plant (0.0037), number of bolls per plant (0.0084), seed index (0.0053), micronaire (0.0008) and lint yield per plant (0.4070) were positive. Days to 50% flowering (-0.0003), ginning out turn (-0.0050), lint index (-0.0221), 2.5% span length (-0.0003) and uniformity ratio (-0.0011) showed negative effects.

At genotypic level, the direct influence of this character on seed cotton yield per plant was positive and high (1.6269). The indirect effects *via* ginning out turn (0.0475), seed index (0.0010), micronaire (0.0068), uniformity ratio (0.0231) and bundle strength (0.0147) were positive. Plant height (-0.0138), days to 50% flowering (-0.0087), number of monopodia per plant (-0.0029), sympodia per plant (-0.0117), number of bolls per plant (-0.4404), lint index (-0.0173), 2.5%span length (-0.0527) and lint yield per plant (-0.6031) showed negative effects.

This trait showed significant positive association with seed cotton yield per plant (0.5693** and 0.5686**) at both genotypic and phenotypic levels. High direct effects and pronounced correlations with seed cotton yield per plant suggest that direct selection for seed cotton yield per plant through this trait will be rewarding. These results were in conformity with earlier works of Erande *et al.* (2014), Ranjan *et al.* (2014a), Asha *et al.* (2015), Ahsan *et al.* (2015a), Reddy *et al.* (2015) and Chandrashekhar *et al.* (2016).

4.3.7 Ginning out-turn (%)

The direct effect of ginning out-turn on seed cotton yield per plant was negative (-0.0173) at phenotypic level. However, the indirect effects of this trait *via* plant height (0.0012), monopodia per plant (0.0010), sympodia per plant (0.0012), number of bolls (0.0222), boll weight (0.0492), seed index (0.0077), micronaire (0.0005) and lint yield per plant (0.1972) showed positive effects. Days to 50% flowering (-0.0003), lint index (-0.0433), 2.5% span length (-0.0003) and uniformity ratio (-0.0005) showed negative effects.

This trait showed a positive (0.1612) direct effect on seed cotton yield per plant at genotypic level. The indirect effects *via* monopodia per plant (0.0004), boll weight (0.4798), seed index (0.0019), micronaire (0.0074), bundle strength (0.0045) and uniformity ratio (0.0167) showed positive effects. Plant height (-0.0068), days to 50% flowering (-0.0102), sympodia per plant (-0.0014), number of bolls per plant (-0.1109), lint index (-0.0435), 2.5% span length (-0.0635) and lint yield per plant (-0.2729) showed negative indirect effects through this character.

The character, ginning out-turn showed significant positive correlation with seed cotton yield per plant (0.1626* and 0.2185**) at both genotypic and phenotypic levels. The low direct effects indicate that this trait had little effect on yield as its own but its effect on yield per plant may be through its component traits. Further significant correlations indicate the dependent association of this trait in improving yield per plant. The results were in conformity with the findings of Kale *et al.* (2007), Tulasi *et al.* (2012), Erande *et al.* (2014) and Farooq *et al.* (2014).

4.3.8 Seed Index (g)

The direct effect exhibited by seed index on seed cotton yield per plant was positive (0.0144) at phenotypic level. However, the indirect effect of this trait *via* plant height (0.0007), number of monopodia per plant (0.0031), number of sympodia per plant (0.0030), number of bolls per plant (0.0774), boll weight (0.0625), micronaire (0.0022) and lint yield per plant (0.3302) were positive. Ginning out turn (-0.0092), lint index (-0.0539), 2.5% span length (-0.0002) and uniformity ratio (-0.0006) showed negative effects.

The direct effect exhibited by seed index on seed cotton yield per plant was positive (0.0033) at genotypic level. Monopodia per plant (0.0039), number of bolls per plant (0.0136), boll weight (0.4705), ginning out turn (0.0927), micronaire (0.0204) and uniformity ratio (0.0165) showed positive effects. While, plant height (-0.0055), days to 50% flowering (-0.0014), sympodia per plant (-0.0020), lint index (-0.0504), 2.5% span length (-0.0434), bundle strength (-0.0069) and lint yield per plant (-0.3012) showed negative effects.

This trait possessed significant positive correlation with seed cotton yield per plant at (0.2103** and 0.4298**) at both genotypic and phenotypic levels. Low direct effects indicate that this trait had little effect on yield as its own but its effect on yield per plant may be through its component traits. Further significant correlations indicate the dependent association of this trait in improving yield per plant. These findings are in agreement with Mohan *et al.* (2011), Tulasi *et al.* (2012), Kumar *et al.* (2014) and Ranjan *et al.* (2014a).

4.3.9 Lint Index (g)

The trait, lint index revealed a negative (-0.0570) direct effect on seed cotton yield per plant at phenotypic level. The indirect effects of this trait through, plant height (0.0009), monopodia per plant (0.0027), sympodia per plant (0.0027), number of bolls per plant (0.0667), boll weight (0.0658), seed index (0.0137), micronaire (0.0019) and lint yield per plant (0.3237) were positive. Days to 50% flowering (-0.0001), ginning out turn (-0.0132), 2.5% span length (-0.0003) and uniformity ratio (-0.0006) showed negative effects.

At genotypic level, the direct influence of this character on seed cotton yield per plant was negative (-0.0532). The indirect effects through monopodia per plant (0.0030), boll weight (0.5287), ginning out turn (0.1317), seed index (0.0032), micronaire (0.0174) and uniformity ratio (0.0185) were positive. Negative effects were exhibited in plant height (-0.0068), days to 50% flowering (-0.0049), sympodia per plant (-0.0018), number of bolls per plant (-0.0350), 2.5% span length (-0.0557), bundle strength (-0.0035) and lint yield per plant (-0.3248).

This trait exhibited significant positive association with seed cotton yield per plant (0.2167** and 0.4069**) at both genotypic and phenotypic levels. The negative direct effect and positive correlation with seed cotton yield per plant at genotypic and phenotypic level suggests the indirect effects seem to be the cause of positive correlation, the indirect causal factors are to be considered simultaneously for selection. These findings were in agreement with Sivaprasad *et al.* (2003) and Tulasi *et al.* (2012).

4.3.10 2.5% Span Length (mm)

At phenotypic level, the direct effect of this character on seed cotton yield per plant was low and positive (-0.0011). The indirect effects through sympodia per plant (0.0003), boll weight (0.0447), seed index (0.0030), micronaire (0.0015) and lint yield (0.0137) were positive. Whereas, the traits plant height (-0.0011), days to 50% flowering (-0.0005), monopodia per plant (-0.0004), number of bolls per plant (-0.0457), ginning out turn (-0.0049), lint index (-0.0149) and uniformity ratio (-0.0041) showed negative indirect effects.

At genotypic level, the direct contribution of this character on seed cotton yield per plant was low and negative (-0.1827). The indirect effect of this trait through Plant height (0.0055), boll weight (0.4691), ginning out turn (0.0560), seed index (0.0008), micronaire (0.0117), bundle strength (0.0349), uniformity ratio (0.0659) and lint yield per plant (0.0120) showed positive effects. Days to 50% flowering (-0.0163), monopodia per plant (-0.0003), sympodia per plant (-0.0008), number of bolls per plant (-0.4997) and lint index (-0.0162) showed negative effects.

This trait had non-significant negative correlations with seed cotton yield per plant (-0.0602 and -0.0094) at both genotypic and phenotypic levels. The results were in agreement with earlier work of Vijayalaxmi *et al.* (2008), Rajanna *et al.* (2011) and Farooq *et al.* (2013). The non-significant negative correlations and low indirect effects indicate its weak association with seed cotton yield per plant and selection for 2.5% span length cannot guarantee for high yield in cotton. The results were in agreement with earlier work of Farooq *et al.* (2013).

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

The direct contribution of this character on seed cotton yield per plant was very low and negative (-0.0094) at phenotypic level. The indirect effects of this trait through plant height (0.0005), days to 50% flowering (0.0002), monopodia per plant (0.0018), sympodia per plant (0.0004), number of bolls per plant (0.0447), ginning out turn (0.0010), lint index (0.0113), 2.5% span length (0.0002), uniformity ratio (0.0003) and lint yield per plant (0.0556) showed positive effects. Boll weight (-0.0142) and seed index (-0.0035) were negative.

The direct influence of this character was low and negative (-0.0720) on seed cotton yield per plant at genotypic level. The indirect effects through days to 50% flowering (0.0049), monopodia per plant (0.0062), number of bolls per plant (0.4905), lint index (0.0128), 2.5% span length (0.0297) and bundle strength (0.0329) were showed positive effects. While, plant height (-0.0030), sympodia per plant (-0.0029), boll weight (-0.1544), ginning out turn (-0.0166), seed index (-0.0009), uniformity ratio (-0.0011) and lint yield per plant (-0.1545) were negative.

This trait showed significant positive correlation and non significant positive correlation with seed cotton yield per plant (0.1718* and 0.0889) at genotypic and phenotypic levels respectively. The negative direct effect and positive correlation with seed cotton yield per plant at genotypic level suggests the indirect effects seem to be the cause of positive correlation, the indirect causal factors are to be considered simultaneously for selection. The results are in agreement with earlier effects of Raju *et al.* (2005) and Venkateswarlu *et al.* (2010a).

4.3.12 Bundle Strength (g/tex)

At phenotypic level, the direct contribution of this character on seed cotton yield per plant was low and positive (0.0001). This trait showed positive effects with plant height (0.0002), monopodia per plant (0.0008), sympodia per plant (0.0009), boll weight (0.0299), lint index (0.0016) and lint yield per plant

(0.0548). While, number of bolls per plant (-0.0090), ginning out turn (-0.0007), seed index (-0.0008), 2.5% span length (-0.0005), micronaire (-0.0033) and uniformity ratio (-0.0024) showed negative effects.

The direct contribution of this character on seed cotton yield per plant was low and positive (0.0761) at genotypic level. The indirect effect of this trait *via* monopodia per plant (0.0017), boll weight (0.3132), ginning out turn (0.0094), lint index (0.0025), and uniformity ratio (0.0402) showed positive effects. Plant height (-0.0016), days to 50% flowering (-0.0011), sympodia per plant (-0.0049), number of bolls per plant (-0.1014), seed index (-0.0003), 2.5% span length (-0.0838), micronaire (-0.0312) and lint yield per plant (-0.1178) showed negative effects.

This trait had positive non significant correlation with seed cotton yield per plant (0.1009 and 0.0714) at both genotypic and phenotypic levels. Non significant association and low positive direct effects indicate that greater emphasis in selection should be placed on above positive direct effects for improvement in seed cotton yield per plant. The results were in agreement with the earlier effects of Neelima *et al.* (2002).

4.3.13 Uniformity Ratio

At phenotypic level, the direct effect of this trait on seed cotton yield per plant was very low and negative (-0.0064). The indirect effects of this trait *via* monopodia per plant (0.0006), sympodia per plant (0.0007), boll weight (0.0292), seed index (0.0013) and micronaire (0.0004) were positive. Plant height (-0.0007), days to 50% flowering (-0.0002), number of bolls per plant (-0.0393), ginning out turn (-0.0014), lint index (-0.0051), 2.5% span length (-0.0007) and lint yield per plant (-0.0057) were negative.

Direct effect of uniformity ratio on seed cotton yield per plant was low and positive (0.0520) at genotypic level. Plant height (0.0144), monopodia per plant (0.0014), boll weight (0.7223), ginning out turn (0.0517), seed index (0.0011), micronaire (0.0015), bundle strength (0.0588) and lint yield (0.0421)

were positive. Days to 50% flowering (-0.0115), Sympodia per plant (-0.0084), number of bolls per plant (-0.7544), lint index (-0.0189) and 2.5% span length (-0.2314) were negative.

This trait had negative non-significant correlation with seed cotton yield per plant (-0.0794 and -0.0274) at genotypic and phenotypic levels respectively. The above results indicate that uniformity ratio cannot be used as criteria of yield improvement in cotton. The results were supported by earlier works of Mohan (2011), Rajanna *et al.* (2011) and Kumar *et al.* (2014).

4.3.14 Lint Yield per plant (g)

At phenotypic level, the direct contribution of this trait on seed cotton yield per plant was high and positive (0.6877). The indirect effects *via* plant height (0.0021), monopodia per plant (0.0040), number of sympodia per plant (0.0064), number of bolls per plant (0.2177), boll weight (0.1004), seed index (0.0069) and uniformity ratio (0.0001) were positive. While, days to 50% flowering (-0.0001), ginning out turn (-0.0050), lint index (-0.0268) and micronaire (-0.0008) were negative.

At genotypic level, the direct contribution of this trait on seed cotton yield per plant was high and negative (-0.9927). The indirect effects *via* monopodia per plant (0.0030), number of bolls per plant (1.0066), boll weight (0.9884), ginning out turn (0.0443), seed index (0.0010), 2.5% span length (0.0022) and bundle strength (0.0090) were positive. While, plant height (-0.0216), days to 50% flowering (-0.0044), sympodia per plant (-0.0160), lint index (-0.0174), micronaire (-0.0112) and uniformity ratio (-0.0022) were negative.

This trait showed significant positive association with seed cotton yield per plant (0.9891** and 0.9927**) at both genotypic and phenotypic levels (Erande *et al.* 2014; Reddy *et al.* 2015). The negative direct effect and positive correlation with seed cotton yield per plant at genotypic level suggests the indirect effects seem to be the cause of positive correlation, the indirect causal factors are to be considered simultaneously for selection.

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 *i.e.*, residual effect measures the role of the possible independent variables which were not included in the study. The residual effect at phenotypic level was 0.0759 indicating that the characters included in the study are contributing more than 90 per cent of variability pertaining to the dependent variable *i.e.*, yield. Less than 10 per cent of contribution is from the few other characters which were not included in the present study.

The residual effect determines how best the causal factors account for the variability of the dependent factor. In present investigation residual effect is very low, indicating that the characters included in the study are contributing high variability pertaining the dependent variable *i.e.*, yield. Low per cent of contribution is from the few other characters which were not included in the present study.

The character association studies revealed that seed cotton yield per plant had positive significant association with plant height, number of sympodia per plant, number of bolls per plant, boll weight, ginning out turn, seed index, lint index, micronaire and lint yield per plant suggesting that these were the major yield contributing traits.

Path coefficient analysis revealed that number of bolls per plant exerted highest positive direct effect on seed cotton yield per plant followed by boll weight, ginning out turn, bundle strength, uniformity ratio, number of monopodia per plant and seed index. Lint yield per plant, 2.5% span length, micronaire, lint index, plant height, days to 50% flowering and number of sympodia per plant exerted negative direct effect on seed cotton yield per plant.

The correlation and path coefficient analysis revealed that major emphasis should be laid on balancing between yield component traits *i.e.*, number of bolls per plant and boll weight for the improvement of seed cotton yield per plant without sacrificing desirable fiber quality traits.

4.4 GENETIC DIVERGENCE

Genetic divergence played a key role in analyzing the general distance among the genotypes selected as parents. Within a certain limit, hybridization of more diverged parents is expected to enhance the level of heterosis in hybrids and generate wide range of variability in segregating generations.

Generally, geographical diversity was considered as a measure of genetic diversity when no scientific tools were available. But geographical distribution of genotypes is not the only factor that causes genetic diversity. This may be due to exchange of breeding material over the locations and further selections at different locations which could result in genetic drift. However, this is an inferential criterion and may not be used for discrimination among the populations occupying ecologically marginal habitats (Arunachalam and Ram, 1967). So, selection of parents for hybridization programme should be based on genetic rather than geographical diversity as there is no parallelism between genetic divergence and geographical divergence of genotypes.

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

The data was collected on 15 characters from 50 genotypes of cotton studied during *Kharif* 2015-16 were subjected to multivariate analysis like Mahalanobis D^2 statistic and principal component. The magnitude of values suggested that there was considerable variability in the material studied, which led to genetic diversity.

4.4.1 Mahalanobis D^2 Analysis

4.4.1.1 Test with *Wilk's criterion* ' Λ '

Significant differences among the genotypes for individual characters were first determined and later the statistical significant differences between the genotypes based on the pooled effects of all the characters were carried out using the *Wilk's criterion* ' Λ '. The *Wilk's criterion* thus obtained was used in calculations of ' V ' statistic. The statistic was highly significant indicating that genotypes differ significantly when all the characters were considered simultaneously. The value of ' V ' statistic was 2908.7 in the present investigation.

4.4.1.2 Mahalanobis D^2 values

To estimate the D^2 values, correlated mean of characters were transformed into standardized uncorrelated characters using pivotal condensation method. It measures the degree of diversification and determines the relative proportion of each component character to total divergence. The statistical differences (D^2) between pairs of genotypes was obtained as the sum of squares of the differences between the pairs of corresponding uncorrelated values of any two genotypes considered at a time. Thus the possible 780 combinations and the corresponding D^2 values were obtained.

The per cent contribution towards genetic divergence by all the 15 contributing characters is presented in Table 4.7 and Fig 4.3. The knowledge on characters influencing divergence is an important aspect to a breeder. Character-wise rank has shown that no single character lonely had a greater contribution to total genetic divergence. The maximum contribution towards genetic divergence was by seed index (37.80) followed by days to 50% flowering (21.80), boll weight (17.71), 2.5% span length (6.53), micronaire (4.98), ginning out-turn (4.57), plant height (3.35), number of bolls per plant (0.90), bundle strength (0.82), seed cotton yield per plant (0.57), number of monopodia per plant (0.33), lint yield per plant (0.33), sympodia per plant (0.16), lint index (0.16) and uniformity ratio (0.00).

4.4.1.3 Grouping of genotypes into various clusters

The 50 genotypes were grouped into 8 clusters using the Tocher's method with the criterion that the intra-cluster average D^2 values should be less than the inter-cluster D^2 values.

From Table 4.8 it is infer that the distribution of 50 genotypes into 8 clusters was at random with maximum number of genotypes in cluster II (22 genotypes) from different locations. Cluster III was the second largest with 12 genotypes followed by cluster I (8 genotypes) and cluster VII (4 genotypes). Cluster IV, V, VI and VIII were solitary clusters with nil intra-cluster D^2 values. The formation of distinct solitary clusters may be due to the fact that geographic barriers preventing gene flow or intensive natural and human selection for diverse and adoptable gene complexes must be responsible for this genetic diversity. The mutual relationship between clusters is represented diagrammatically (Fig. 4.5.) by taking average intra and inter cluster Euclidean distances.

This pattern of grouping has indicated that the diversity need not be necessarily related to geographical diversity and it may be the outcome of several other factors like natural selection, exchange of breeding material, genetic drift and environmental variation. Therefore, selection of varieties for hybridization should be based on genetic diversity rather than geographical diversity. Raju (2005), Lakshmi *et al.* (2009), Rajamani and Rao (2009), Satish *et al.* (2009), Asha *et al.* (2013), Haritha and Ahamed (2013), Kavithamani *et al.* (2013), Bhailume *et al.* (2014), Tulasi *et al.* (2014) and Kumar *et al.* (2015) also reported that there is no parallelism between genetic divergence and geographical divergence of genotypes.

The mutual relationships between the clusters were represented diagrammatically by taking average intra and inter cluster D^2 values. The tree like structure called dendrogram (Fig. 4.4.) was constructed based on clustering by Tocher's method.

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

The average intra and inter-cluster D^2 values estimated as per the procedure given by Singh and Chaudhary (1977) are presented in the Table 4.9. The proximity and divergence among 8 clusters are indicated in Table 4.10.

The maximum intra-cluster distance was observed for cluster VII (70.13) followed by cluster III (47.79), cluster II (38.88) and cluster I (30.59), while, it was zero for clusters IV, V, VI and VIII. The high intra-cluster distance in cluster VII indicates the presence of wide genetic diversity among the genotypes present within this cluster.

Cluster I was with eight genotypes. It was nearest to cluster II (71.15) followed by cluster V (95.59) and it was farthest from cluster VIII (275.78) followed by cluster IV (195.67).

Cluster II, with 22 genotypes was the largest of all clusters. It was nearest to cluster V (60.21) followed by cluster III (68.25) and it was farthest from cluster VIII (177.85) and followed by cluster VII (145.89).

Cluster III was with 12 genotypes. It was nearest to cluster II (68.25) followed by cluster IV (80.07) and it was farthest from cluster VII (133.11) followed by cluster I (130.37).

Cluster IV was monogenotypic (L 799). It was nearest to cluster V (58.37) followed by cluster III (80.07) while, it was farthest from cluster I (195.67) followed by cluster VI (151.40).

Cluster V was monogenotypic (GJHV 497). It was nearest to the cluster IV (58.37) followed by cluster II (60.21) and it was farthest from cluster VIII (194.82) followed by cluster VI (181.93).

Cluster VI was monogenotypic (ARBH 1402). It was closest to the cluster II (77.86) followed by cluster III (92.85) and was farthest from cluster VII (296.37) followed by cluster V (181.93).

Cluster VII was with four genotypes. It was closest to the cluster V (75.38) followed by cluster IV (124.11) and was farthest from cluster VI (296.37) followed by cluster VIII (202.06).

Cluster VIII was monogenotypic (L 788). It was closest to the cluster III (80.02) followed by cluster IV (136.14) and was farthest from cluster I (275.78) followed by cluster VII (202.06).

The intra- and inter-cluster distances revealed that inter-cluster distance values were greater than intra-cluster distance values.

Genotypes grouped into the same cluster presumably differ little from one another as the aggregate of characters measured. General notion exists that the larger is the divergence between the genotypes, the higher will be the heterosis.

In the present study, inter-cluster distances were worked out considering 15 characters and these distances ranged from 58.37 (between cluster IV and V) to 296.37 between cluster VI and VII.

The inter-cluster distance was maximum between cluster VI and VII (296.37), followed by cluster I and VIII (275.78), cluster I and IV (195.67), cluster V and VIII (194.82), cluster II and VIII (177.85) and cluster III and VII (133.11). This suggested that there is wide genetic diversity between these clusters. Based on these studies crosses can be made between genotypes of these clusters to obtain desirable transgressive segregants.

Choice of the particular cluster and selection of particular genotype from selected cluster are the two important points to be considered before initiating the crossing programme. The hybrids between varieties of different clusters will express high heterosis and throw more useful segregants. Further, one or two varieties from different clusters may be chosen for further genetic studies either by diallel or line X tester analysis.

4.4.1.5 Cluster mean values

The cluster mean values for 15 characters are presented in Table 4.11. The data indicated a wide range of mean values between the characters. Plant height had a range of 128.24 for cluster II to 145.00 for cluster IV; Days to 50% flowering had a range of 53.67 for cluster VI to 73.67 for cluster VII; number of monopodia per plant ranged from 1.54 for cluster I to 2.17 for cluster IV and cluster V; number of sympodia per plant ranged from 18.28 for cluster IV to 20.77 for cluster V; number of bolls per plant varied from 39.33 for cluster VII to 55.33 for cluster IV; boll weight ranged from 3.55 for cluster IV to 5.05 for cluster VIII; ginning out-turn ranged from 33.46 for cluster VI to 35.21 for cluster VIII; seed index varied from 8.30 for cluster I to 10.50 for cluster VIII; lint index ranged from 4.22 for cluster I to 5.71 for cluster VIII; 2.5% span length varied from 25.72 for cluster VI to 29.21 for cluster VII; micronaire ranged from 3.47 for cluster VI to 4.67 for cluster V; bundle strength varied from 19.09 for cluster IV to 20.95 for cluster VII; uniformity ratio ranged from 46.01 for clusters IV to 46.49 for cluster VII; seed cotton yield per plant ranged from 109.05 for cluster VI to 150.07 for cluster VIII and lint yield per plant ranged from 37.04 for cluster VI to 52.81 for cluster VIII.

Higher mean values for boll weight were seen in cluster VIII and VII and higher means for number of boll per plant were observed in clusters IV and V which are major contributors in improving seed cotton yield per plant in cotton. Based on mean values, series of diallel analysis may prove highly successful.

The success and usefulness of Mahalanobis D^2 analysis in quantifying genetic divergence has been studied by Rao *et al.* (2009), Gopinath *et al.* (2009), Lakshmi *et al.* (2009), Rajamani and Rao (2009), Satish *et al.* (2009), Basavaraddi and Katageri (2011), Punitha *et al.* (2012), Asha *et al.* (2013), Haritha and Ahamed (2013), Kavithamani *et al.* (2013), Malik *et al.* (2013), Bhailume *et al.* (2014), Haritha *et al.* (2014), Laise *et al.* (2014), Ranjan *et al.* (2014a), Tulasi *et al.* (2014), Kumar *et al.* (2015), Saeed *et al.* (2015) and Ullah *et al.* (2015).

4.4.2 Application of Principal Component Analysis in Genetic Divergence

Principal component analysis or canonical (vector) analysis is a sort of multivariate analysis where canonical vectors or roots representing different axes of differentiation and amount of variation accounted for by each of such axes, respectively, are derived (Rao, 1952). It is called principal component analysis as it reflects the importance of the largest contributor to the total variation at each axes of differentiation. It measures divergence between varieties in terms of spatial distance rather than quantifying it as D^2 does. It gives group constellations as varietal distribution in two-way pictorial graph fixing the relative position of each variety.

In principal component analysis on correlation matrix, the standardization of columns (here characters) created 15 new variables for 50 genotypes without changing their relative positions. These 15 new variables are the principal components ($PC_1, PC_2, \dots, PC_{15}$). Each principal component is a linear combination of the 15 attributes of data matrix. The loading values are scaled or standardized in such a manner that the sum of square of loadings within a principal component is equal to one. The loadings are viewed as weights defining the contribution of characters in respective principal component. Like regression coefficients, loadings sign (+ / -) are indicative of the direction of contribution. But unlike regression, only the relative contributions are important, so all signs can be changed without affecting the analysis (Jackson, 1991).

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

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

Principal components (eigen value greater than one), eigen values (Latent Root), per cent variability, cumulative per cent variability and component loading of different characters are presented in Table 4.12.

In the present study, the first six principal components with eigen values more than one contributed 81.99 per cent towards the total variability. It was therefore inferred that the essential features of data set had been represented in the first six principal components. The first principal component contributed maximum towards variability (27.33). The characters viz., days to 50% flowering (-0.24), number of bolls per plant (0.12), ginning out turn (-0.35), seed index (-0.38), lint index (0.22), 2.5% span length (-0.35), micronaire (0.20), bundle strength (0.30), seed cotton yield per plant (0.46) and lint yield per plant (-0.35) explained the maximum variance in the first principal component (PC₁) and signifying their importance in divergence.

The second principal component (PC₂) described 19.12 per cent of total variance and the characters viz., plant height (0.30), days to 50% flowering (0.31), number of monopodia per plant (-0.26), number of sympodia per plant (0.37), number of bolls per plant (-0.18), boll weight (0.29), ginning out turn (0.21), seed index (-0.25), lint index (0.38), 2.5% span length (0.20), micronaire (0.20) and uniformity ratio (-0.43) showed the maximum variance in this principal component.

The third principal component (PC₃) was characterized by 13.70 per cent contribution towards the total variability. The characters viz., plant height (0.16), days to 50% flowering (-0.30), monopodia per plant (-0.37), sympodia per plant (0.26), boll weight (-0.31), seed index (0.22), lint index (-0.19), micronaire (-0.41), bundle strength (-0.20), lint yield (-0.26), 2.5% span length (-0.17) and uniformity ratio (0.39) showed the maximum variance in this principal component.

The fourth principal component (PC₄) was conspicuously characterized by high loading of plant height (0.54), days to 50% flowering (0.16), monopodia per plant (-0.31), number of bolls per plant (0.60), boll weight (-0.36), ginning out-turn (-0.07), seed index (0.18), lint index (-0.08), micronaire (0.02), uniformity ratio (0.08) and lint yield per plant (0.15). Contribution of this principal component towards the total variability was 9.37 per cent.

The fifth principal component (PC₅) described 6.78 per cent of total variance. The characters viz., days to 50% flowering (-0.33), number of monopodia per plant (-0.17), 2.5% span length (0.25), number of sympodia per plant (0.40), number of bolls per plant (-0.28), ginning out-turn (-0.05), seed index (0.16), micronaire (0.27), bundle strength (0.56), uniformity ratio (0.15), seed cotton yield per plant (-0.18) and lint yield (0.28) showed the maximum variance in this principal component.

The sixth principal component (PC₆) was characterized by 5.71 per cent contribution towards the total variability. The characters viz., plant height (0.20), number of sympodia per plant (-0.29), number of bolls per plant (0.28), boll weight (0.47), ginning out-turn (0.32), micronaire (0.45), bundle strength (0.20) seed index (0.24), 2.5% span length (0.23), uniformity ratio (0.12), and lint yield per plant (-0.32) showed the maximum variance in this principal component.

The PCA scores for 50 cotton genotypes in the first three principal components were computed. Principal component I, II and III were considered as three axes as X, Y and Z and squared distance of each genotype from these three axes were calculated and presented in Table 4.13.

The analysis thus identified the maximum contributing variables *i.e.*, seed cotton yield per plant, bundle strength, lint index, micronaire, number of bolls per plant, number of sympodia per plant, plant height and uniformity ratio were significantly loaded in PC1 and contributed more towards variability. It is important to study the variance as the relative contribution than the signs (indicative of direction) in principal component analysis.

These three PCA scores for 50 genotypes were plotted in graph to get two dimensional and three dimensional scatter diagrams (Fig. 4.6. and Fig. 4.7.) revealed diversity between the genotypes These genotypes may be used in crop improvement programmes for generating transgressive segregants.

The success and usefulness of principal component analysis in quantifying genetic divergence has been studied by Lakshmi *et al.* (2009), Rajamani and Rao (2009), Srinivasulu (2009), Venkateswarulu *et al.* (2010b), Asha *et al.* (2013), Haritha and Ahamed (2013), Tulasi *et al.* (2014), Baloch *et al.* (2015a), Saeed *et al.* (2015), Liaqat *et al.* (2015a), Liaqat *et al.* (2015b), Latif *et al.* (2015), Shakeel *et al.* (2015) and Talib *et al.* (2015).

4.4.3 Cluster analysis

To group the 50 genotypes into various clusters, agglomerative hierarchical cluster analysis was followed. Principal component scores for genotypes were used as an input for clustering using Ward's minimum variance method. The tree like structure called dendrogram (Fig. 4.8) was constructed based on Euclidean² distance computed from PCA scores of genotypes.

The 50 genotypes were grouped into 8 clusters. The distribution of genotypes into 8 clusters is represented in table 4.14. among all the clusters, cluster VII was the largest containing 12 genotypes followed by cluster III with 9 genotypes, cluster VI with 8 genotypes, cluster VIII with 7 genotypes, cluster IV with 6 genotypes, cluster V with 4 genotypes and clusters I & II with 2 genotypes each. This random distribution of genotypes indicated absence of parallelism between geographical and genetic diversity. The mutual relationship between clusters is represented diagrammatically (Fig. 4.9) by taking average intra- and inter cluster Euclidean² distances.

4.4..3.1 Average intra-and inter- cluster Euclidean² distance values

The average intra- and inter- cluster Euclidean² distance were estimated based on Ward's minimum variance and presented in the table 4.15.

By Ward's method, 50 genotypes were grouped into 8 clusters. Of the 7 clusters formed. Cluster V has minimum intra cluster Euclidean² distance value of 75.90 followed by cluster VI (85.00), cluster VIII (92.61), cluster IV (99.09), cluster VII (114.35), cluster II (119.88), cluster I (146.41) and cluster III (161.58). The inter cluster Euclidean² distances varied from 131.57 (cluster VI and cluster VII) to 719.28 (cluster I and cluster VIII).

Cluster I closest to cluster II (249.02) followed by cluster V (318.54) and farthest from cluster VIII (719.28) followed by cluster VII (570.10).

Cluster II was nearest to cluster I (249.02) followed by cluster V (267.58) and farthest from cluster III (436.50) followed by cluster IV (421.88).

Cluster III was closest to cluster IV (185.92) followed by cluster VIII (228.12) and farthest from cluster VIII (439.08) followed by cluster II (436.50).

Cluster IV was nearest to cluster V (159.64) followed by cluster III (185.92) and farthest from cluster VIII (465.27) followed by cluster II (421.88).

Cluster V was closest to cluster VI (137.15) followed by cluster IV (159.64) and farthest from cluster I (318.54) followed by cluster VIII (280.75).

Cluster VI was nearest to cluster VII (131.57) followed by cluster V (137.15) and farthest from cluster I (534.45) followed by cluster II (387.22).

Cluster VII was closest to cluster VI (131.57) followed by cluster V (177.07) and farthest from cluster I (570.10) followed by cluster II (404.54).

Cluster VIII was nearest to cluster VI (203.91) followed by cluster VII (223.23) and farthest from cluster I (719.28) followed by cluster IV (465.27).

Results of cluster analysis based on PCA scores were compared with the results of the principal component analysis on a visual aid in desecrating clusters in 2D and 3D scattered diagram.

Rao *et al.* (2009), Rajmani and Rao (2009), Vijayalaxmi *et al.* (2009), Srinivasulu *et al.* (2010a), Venakateswarlu *et al.* (2010a), Kulakarni *et al.* (2011b), Shakeel *et al.* (2015) and Talib *et al.* (2015) studied utilization of principal component analysis combined with clustering of Ward's method in genetic divergence studies in cotton.

4.4.3.2 Cluster means

Cluster means were computed for the 15 characters studied on pooled basis and are presented in Table 4.16.

Cluster I registered high mean values for plant height (138.83), days to 50% flowering (75.83), 2.5% span length (29.31), bundle strength (20.96) and uniformity ratio (46.53). While low mean values for number of sympodia per plant (18.06).

Cluster II recorded high mean values for boll weight (4.52) while low mean values for number of bolls per plant (39.00) and micronaire (3.26).

Cluster III recorded high mean values for lint index (4.95) along with cluster IV (4.95)

Cluster IV recorded high mean values for seed index (9.38) and lint index (4.95). While low mean values for bundle strength (19.77) and uniformity ratio (46.08).

Cluster V recorded highest mean values for number of monopodia per plant (1.93), number of sympodia per plant (19.88), number of bolls per plant (53.25) and ginning out turn (35.07).

Cluster VI recorded lowest mean values for plant height (124.63), boll weight (3.58), ginning out turn (33.47) and seed cotton yield per plant (113.40).

Cluster VII recorded low mean values for days to 50% flowering (61.25).

Cluster VIII recorded highest mean values for micronaire (4.35) and seed cotton yield per plant (126.98) while lowest mean values for number of monopodia per plant (1.54), seed index (8.27), lint index (4.19) and 2.5% span length (25.83).

Thus, cluster V showed high mean value for number of monopodia per plant (1.93), number of sympodia per plant (19.88), number of bolls per plant (53.25) and ginning out turn (35.07). So genotypes from this cluster (HS 294, GTHV 13/37, GJHV 510 and GJHV 497) can be used for cotton yield improvement programme. Among the quality attributes, high mean values for 2.5% span length (29.31), bundle strength (20.96) and uniformity ratio (46.53) were recorded in cluster I. Cluster VIII recorded high mean values for micronaire (4.35) and seed cotton yield per plant (126.98). So, the genotypes from these clusters can be used for cotton fibre improvement.

4.4.4 Comparative Study of Both D² Analysis and Principal Component Analysis and cluster analysis

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

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

Mahalanobis's D² statistic and Jackson's principal component analysis both are the tools for analyzing multivariate data. PCA confirms the group constellations obtained by D² analysis. It determines the effective number of

axes of differentiation primary and secondary or so based on number of canonical vectors. The advantage of PCA over D^2 analysis is that it reduces the dimensionality of the data set by creating significant principal components which contributed towards maximum variability of the genotypes. The largest element (absolute value) in each vector constitutes the greatest contributor for divergence. In PCA, standardization of data, made attributes to contribute equally towards the divergence studies irrespective of the units taken.

The principal component analysis sorted only significant principal components out of the total 15 attributes. The contribution of the main characters for variance easily identified by the characters loaded on the PC1 with high loading values. PCA facilitates the in depth analysis for genetic diversity. In D^2 analysis, seed index, days to 50% flowering, boll weight, 2.5% span length and micronaire contributed maximum towards the divergence. While in PCA the characters viz., seed cotton yield per plant, bundle strength, lint index, micronaire, number of bolls per plant, number of sympodia per plant, plant height and uniformity ratio were significantly loaded in PC1 and contributed more towards variability. It can be concluded that the characters which contributed more towards divergence in D^2 analysis were loaded in PC₁.

Both D^2 analysis and Ward's method grouped the 50 genotypes into 8 clusters. In D^2 analysis cluster II is the largest with 22 genotypes followed by cluster III (12 genotypes), cluster I (8 genotypes) and cluster VII (4 genotypes), where as in Ward's method cluster VII is the largest comprising of 12 genotypes followed by cluster III (9 genotypes), cluster VI (8 genotypes), cluster VIII (7 genotypes), cluster IV (6 genotypes) and cluster V (4 genotypes).

The pattern of distribution of genotypes into different clusters was at random. Furthermore, the two clustering methods grouped differently and clustering for genotypes are not same. There was no solitary cluster formed in Ward's minimum variance method, where as in D^2 analysis cluster IV, V, VI and VIII represent solitary clusters due to absence of intra cluster distance indicating that genetic diversity was the outcome of several factors along with geographical diversity. Hence, the selection for hybridization should be more based on genetic diversity rather than geographic diversity.

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

FUTURE LINE OF WORK

The genotypes L 788, HS 294, MCU 5, HYPS 152 and GISV 267 showed maximum inter-cluster distance in Mahalanobis D^2 analysis, principal component analysis and cluster analysis and also have better *per se* performance in sympodia per plant, number of bolls per plant, boll weight, seed index, lint index and quality characters . So they can be exploited for the development of heterotic hybrids in future breeding programmes.

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. Genetic variability

2.2. Heritability and genetic advance as per cent of mean

2.3. Character association

2.4. Path analysis

2.5. Genetic diversity

2.1. GENETIC VARIABILITY

The information on the nature and magnitude of variability for different quantitative and qualitative traits in any crop species plays a vital role 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.

2.2. HERITABILITY (h^2_b) AND GENETIC ADVANCE (GA) AS PERCENT 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 behavior of succeeding generations, making desirable selection and assessing the magnitude of genetic improvement through selection (Hafiz *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 $\times$ 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.

2.3. 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.

2.3.1 Association of Component Characters with Seed Cotton Yield

The available literature on the association of component characters with seed cotton yield is presented in Table 2.3.

2.3.2 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 fiber 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

The information on the nature and magnitude of genetic variability present in the crop species will play an important role in formulating a successful breeding programme. It has been well known that genetically diverse parents are likely to produce high heterotic effects and yield superior transgressive segregants in segregating generations.

Mahalanobis's 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).

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 like yellowness followed by fiber length, fiber fineness and elongation towards genetic divergence in their study involving 85 genotypes of Egyptian cotton.

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

Raju (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.

Padmavathi (2008) reported maximum contribution of number of monopodia per plant, seed index (g), number of sympodia per plant, plant height (cm), ginning out-turn (%) and micronaire towards genetic divergence in the study involving 60 genotypes.

Rao *et al.* (2009) evaluated 60 genotypes of upland cotton from different geographic regions and grouped them into 14 clusters using Tocher's method. The variation in the composition of individual cluster with regard to the number of genotypes indicated the presence of large amount of diversity in the population.

Gopinath *et al.* (2009) reported maximum contribution of boll weight, boll number and 2.5% span length towards total divergence in their study with 60 genotypes of cotton.

Lakshmi *et al.* (2009) assessed genetic divergence among 72 genotypes of cotton based on 18 traits and grouped them into eight clusters. The results clearly indicated that there is no parallelism between geographic diversity and genetic diversity.

Rajamani and Rao (2009) studied genetic divergence in 63 genotypes of cotton and grouped them into seven clusters. Genotypes originated at different agro-climatic situations were grouped into one cluster and *vice-versa* indicating that there is no parallelism between genetic and geographic diversity.

Satish *et al.* (2009) studied genetic diversity in 70 genotypes of cotton and assessed diversity using Mahalanobis D^2 statistic. The genotypes were grouped into 15 clusters. The distribution of genotypes indicated that geographical diversity and genetic diversity were not related and there were forces other than geographical separation which were responsible for diversity.

Basavaraddi and Katageri (2011) assessed genetic diversity in 24 derivatives of F_8 generation of cross between *G. hirsutum* var. DS-28 and *G. barbadense* var. SB (YF)-425 based on seventeen characters using Mahalanobis D^2 statistic and grouped them into eight clusters. The contribution

of various characters towards expression of genetic divergence indicated that the seed cotton yield (kg ha^{-1}) contributed highest followed by number of sympodia, uniformity ratio, ginning out turn and lint index, respectively.

Punitha *et al.* (2012) studied genetic variability in 45 upland cotton genotypes based on five characters using metroglyph analysis resulted in nine distinct groups. Group V had the largest genotypes with moderate kapas yield and medium span length.

Asha *et al.* (2013) studied genetic diversity in 40 genotypes of cotton for 15 quantitative characters which were grouped into seven clusters based on Mahalanobis D^2 analysis with cluster I and III being the largest each with eight genotypes followed by seven genotypes in cluster IV. The random distribution of genotypes indicated absence of parallelism between geographical diversity and genetic diversity.

Haritha and Ahamed (2013) studied genetic diversity in 40 genotypes of cotton for 21 morpho physiological characters. The 40 genotypes were grouped into seven clusters based on hierarchical analysis. Among all the clusters, cluster II was the largest containing 11 genotypes followed by cluster I with eight genotypes and cluster III with seven genotypes. The mutual relationship between the clusters revealed that inter cluster distance values were greater than intra-cluster values. The random distribution of genotypes indicated absence of parallelism between geographical diversity and genetic diversity.

Kavithamani *et al.* (2013) studied genetic diversity in 48 genotypes of *Gossypium barbadense* using multivariate Mahalanobis D^2 analysis and these genotypes were grouped into 13 clusters. Grouping of these genotypes into different clusters was independent of their geographical origin indicating other forces are responsible for diversity. The mutual relationship between the clusters revealed that inter cluster distance values were greater the intra-cluster values.

Malik *et al.* (2013) studied genetic diversity in 20 coloured and white cotton genotypes based on fifteen morphological traits using cluster and biplot analysis and grouped coloured and white cotton genotypes into four clusters.

Bhailume *et al.* (2014) studied genetic diversity in 50 genotypes of *Gossypium arboreum* for 12 characters and assessed diversity using Mahalanobis D^2 statistic. The genotypes were grouped into 19 clusters. Genetic diversity was found to be unrelated with geographic origin of the genotypes.

Haritha *et al.* (2014) studied genetic diversity in 40 genotypes of cotton for 21 characters and assessed diversity using Mahalanobis D^2 statistic. The genotypes were grouped into eight clusters. The mutual relationship between the clusters revealed that inter cluster distance values were greater than the intra-cluster values.

Laise *et al.* (2014) studied genetic diversity in 40 genotypes of cotton and stated that the mean boll weight presented the highest contribution to genetic diversity.

Ranjan *et al.* (2014b) studied D^2 analysis in 60 genotypes of Asiatic cotton and reported that the crossing between the genotypes of clusters VI and VIII would generate desirable genetic variability, suggested that days to flowering followed by seed cotton yield per plant, number of monopods and plant height contributed maximum towards divergence.

Tulasi *et al.* (2014) studied genetic divergence analysis with 40 genotypes of cotton based on 15 quantitative characters in upland cotton and grouped them into seven clusters based on Mahalanobis D^2 analysis. Cluster I and II were the largest with 13 genotypes each. Based on hierarchical cluster analysis all the genotypes were grouped into seven clusters with cluster IV and V being largest with nine genotypes followed by eight genotypes in cluster I. The random distribution of genotypes indicated absence of parallelism between geographical diversity and genetic diversity.

Kumar *et al.* (2015), studied genetic diversity among 68 genotypes of American cotton using Mahalanobis D^2 statistic and genotypes were grouped into 8 clusters by employing Euclidean's method. Based on inter cluster distances cluster I and cluster VI were found to be most divergent followed by cluster V and cluster VI, cluster I and cluster VIII and cluster II and cluster VI.

The use of diverse genotypes included in these clusters is advocated in crossing programme to evolve high heterotic hybrids and for taping the good transgressive segregants in segregating generations.

Saeed *et al.* (2015), studied genetic diversity in 159 upland cotton genotypes for quality and morphological traits based on 11 quantitative and qualitative characters. The genotypes grouped in to six clusters. The genotypes in cluster I, II, and III comprised of genotypes with better earliness and fiber quality traits. Cluster IV was characterized by genotypes having less attack of CLCuD, higher GOT% and somehow good quality of fiber traits. Cluster VI was represented by genotypes having good plant height, sympodial branches per plant and fiber fineness.

Ullah *et al* (2015), studied genetic diversity in nine different upland cotton cultivars for yield and related attributes. He reported that genetic variances of the studied parameters were higher in comparison to variance of environment and highly heritable in broad sense.

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).

Raju (2005) used PCA to estimate genetic divergence in 80 genotypes of upland cotton. First five principal components, which had a cumulative variation 74.48%, formed the basis for divergence of genotypes.

Rajamani and Rao (2009) assessed 63 genotypes of upland cotton using principal component analysis and identified five principal components which showed Eigen values more than one and they together explained 93.91% of the variability.

Srinivasulu (2009) carried out genetic divergence analysis with 60 genotypes of upland cotton using principal component analysis and identified six principal components which explained 83.89% variability in upland cotton.

Lakshmi *et al.* (2009) assessed 72 genotypes using principal component analysis. Seven principal components were identified out of which first five principal components explained 76.5% of variability in cotton.

Venkateswarulu *et al.* (2010b) collected 50 genotypes of upland cotton from different research centers across the country and carried out PCA based on 16 characters. PCA identified six principal components which explained 77.41% variability in upland cotton.

Asha *et al.* (2013) studied genetic diversity in 40 cotton genotypes for 15 yield and yield contributing characters. In PCA, first seven principal components with Eigen value more than one contributed 87.98 per cent towards the total variability. PC₁ alone contributed 22.27 per cent variability towards the total variability.

Haritha and Ahamed (2013) studied genetic diversity in 40 genotypes of cotton for 21 morpho physiological characters. In PCA, first eight principal components with Eigen value more than one contributed 78.35 per cent towards the total variability. PC₁ contributed maximum towards variability (24.28%).

Tulasi *et al.* (2014) studied principal component analysis with 40 genotypes of cotton based on 15 quantitative characters in upland cotton. The first five principal components with Eigen value more than one contributed 78.35 per cent towards the total variability with PC₁ alone shown 38.73 per cent of variability towards the total variability.

Baloch *et al.* (2015a) studied genetic diversity analysis in 26 genetically modified cotton (*Gossypium hirsutum* L.) genotypes by using cluster analysis and principal component analysis. Reported that cluster I consisted of 9 genotypes which were considered as high yielding genotypes and first three principal components accounted 99% of the total variability.

Latif *et al.* (2015) estimated genetic divergence in 60 cotton (*Gossypium hirsutum* L.) genotypes using principal component analysis and identified that out of eight principal components (PCs), three PCs depicted more than one Eigen value. First two principal components PC₁ and PC₂ explained 47.57% and 16.78% of variation respectively with 63.36% cumulative variation among all attributes. In PC₁ sympodial branches, number of bolls per plant, boll weight and yield per plant depicted more contribution towards total variation. PC₂ was more associated with plant height and seed index attributes.

Liaquat *et al.* (2015a) studied genetic divergence of morphological and fiber traits in 75 upland cotton genotypes. PCA revealed significant difference between genotypes and the first four components with Eigen values greater than 1 contributed 66.68% of the total variability among the genotypes. PC₁ and PC₂ possessed 25.85% and 18.54% of the total variation

Liaquat *et al.* (2015b) investigated 100 lines of cotton using principal component analysis. In principal component analysis (PCA) four PCs with Eigen value > 1 contributed 60.423% of the variation amongst the investigated lines. The first PC and second PC explained 20.16% and 15.14% of the total variation, respectively.

Saeed *et al.* (2015) studied genetic diversity in 159 genotypes of upland cotton for quality and morphological traits using principal component analysis and cluster analysis. In PCA, five principal components with Eigen value more than one contributed 65% towards the total variability. The first two principal components contributed almost 34.1% in total variation. By using cluster analysis 159 exotic genotypes grouped into 6 clusters, of which cluster IV comprised of 46 genotypes, characterized by genotypes having less attack of CLCuD, higher GOT% and somehow good quality of fibers.

Shakeel *et al.* (2015) studied genetic diversity in fifty upland cotton genotypes for quality and yield related traits using principal component analysis and linkage cluster analysis. Out of ten, the first four PCs with Eigen value more than one contributed 64.8% variability among the cotton accessions. In PC₁ and PC₃ the genotypes possess good yield and fiber traits whereas in PC₂ the genotypes have desired yield components.

Talib *et al.* (2015) studied genetic diversity in 50 upland cotton genotypes based on 11 quantitative traits using principal component analysis and cluster analysis. Out of ten, four PCs exhibited more than 1 Eigen value. The PC₁ have 23.8%, PC₂ showed 16.8%, PC₃ exhibited 12.3% and PC₄ exhibited 11.9% variability among the genotypes for the traits under study. They concluded that variety performance of cotton germplasm did not necessarily depend on the geographical origin or even pedigree relationship. Varieties that display high phenotypic similarity need not be genetically similar because the environment can manipulate phenotypic expression.

Table 2.1. Review of literature on genetic variability in cotton (*G. hirsutum* L.)

S.No.	Character	Wider genetic variability	Narrow genetic variability
1.	Plant height (cm)	Neelam <i>et al.</i> (2002) Laxman and Ganesh (2003) Patnaik <i>et al.</i> (2004) Neelima <i>et al.</i> (2005) Tuteja <i>et al.</i> (2006) Sarada <i>et al.</i> (2010) Hafiz <i>et al.</i> (2013) Dhivya <i>et al.</i> (2014) Abbas <i>et al.</i> (2014) Khan <i>et al.</i> (2015) Narendra (2015)	Deshpande and Baig (2003) Kaushik and Kapoor (2006) Pratap (2006) Kale <i>et al.</i> (2007) Rao (2008) Neelima <i>et al.</i> (2008) Rajanna (2010) Kulkarni <i>et al.</i> (2011) Farooq <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Ahsan <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015a) Ahsan <i>et al.</i> (2015b) Dahiphale <i>et al.</i> (2015) Rajamani <i>et al.</i> (2015)
2	Days to 50% flowering	Ahuja and Tuteja (2000) Laxman and Ganesh (2003) Neelima <i>et al.</i> (2005)	Neelam <i>et al.</i> (2002) Altaher and Singh (2003a) Narisireddy and Ratnakumari (2004) Raju (2005) Kaushik and Kapoor (2006) Pratap (2006) Neelima <i>et al.</i> (2008) Rajanna (2010) Sarada <i>et al.</i> (2010) Kulkarni <i>et al.</i> (2011) Venkatesh (2012) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Narendra (2015)
3	No. of monopodia plant ⁻¹	Kaushik <i>et al.</i> (2003) Sivaprasad (2003) Raju (2005) Kaushik and Kapoor (2006)	Ahuja and Tuteja (2000) Gururajan (2000) Girase and Mehetre (2002) Erande <i>et al.</i> (2014)

S.No	Character	Wider genetic variability	Narrow genetic variability
3	No. of monopodia plant ⁻¹	Tuteja <i>et al.</i> (2006) Verma <i>et al.</i> (2006) Neelima <i>et al.</i> (2008) Rao (2008) Rajanna (2010) Kishore <i>et al.</i> (2011) Kulkarni <i>et al.</i> (2011) Mohan (2011) Hafiz <i>et al.</i> (2013) Khan <i>et al.</i> (2015) Dahiphale <i>et al.</i> (2015) Rajamani <i>et al.</i> (2015)	
4	No. of sympodia plant ⁻¹	Gururajan (2000) Neelam <i>et al.</i> (2002) Deshpande and Baig (2003) Tuteja <i>et al.</i> (2003) Kaushik and Kapoor (2006) Tuteja <i>et al.</i> (2006) Neelima <i>et al.</i> (2008) Kulkarni <i>et al.</i> (2011) Santhoshkumar <i>et al.</i> (2012) Hafiz <i>et al.</i> (2013) Vineela <i>et al.</i> (2013) Abbas <i>et al.</i> (2014) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015) Narendra (2015)	Girase and Mehetre (2002) Laxman and Ganesh (2003) Vinodhana <i>et al.</i> (2013) Farooq <i>et al.</i> (2014) Rajamani <i>et al.</i> (2015)
5	No. of bolls plant ⁻¹	Sivaprasad (2003) Gururajan and Sundar (2004) Narisireddy and Ratnakumari (2004) Neelima <i>et al.</i> (2005) Kaushik and Kapoor (2006) Pratap (2006) Tuteja <i>et al.</i> (2006) Neelima <i>et al.</i> (2008)	Girase and Mehetre (2002) Pratap (2006) Hafiz <i>et al.</i> (2013)

S.No.	Character	Wider genetic variability	Narrow genetic variability
5	No. of bolls plant ⁻¹	Bazi (2011) Kishore <i>et al.</i> (2011) Mohan (2011) Santhoshkumar <i>et al.</i> (2012) Vinodhana <i>et al.</i> (2013) Abbas <i>et al.</i> (2014) Ahsan <i>et al.</i> (2014) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015a) Ahsan <i>et al.</i> (2015b) Khan <i>et al.</i> (2015) Narendra (2015)	
6	Boll weight (g)	Kaushik <i>et al.</i> (2003) Laxman and Ganesh (2003) Muthuswamy <i>et al.</i> (2003) Gururajan and Sundar (2004) Sivaprasad <i>et al.</i> (2004) Tuteja <i>et al.</i> (2006) Kulkarni <i>et al.</i> (2011) Mohan (2011) Abbas <i>et al.</i> (2014)	Reddy (2001) Altaher and Singh (2003a) Neelima <i>et al.</i> (2008) Rajanna (2010) Bazi (2011) Vinodhana <i>et al.</i> (2013) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015a)
7	Ginning out turn (%)	Muthuswamy <i>et al.</i> (2003) Laxman and Ganesh (2003) Tuteja <i>et al.</i> (2003) Patnaik <i>et al.</i> (2004) Neelima <i>et al.</i> (2005) Tuteja <i>et al.</i> (2006) Naqib <i>et al.</i> (2010)	Rao and Reddy (2001) Neelima (2002) Muraleedhar (2005) Kaushik and Kapoor (2006) Neelima <i>et al.</i> (2008) Rao (2008) Mahantesh (2009) Rajanna (2010) Sarada <i>et al.</i> (2010) Mohan (2011) Vinodhana <i>et al.</i> (2013) Divya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014)

S.No.	Character	Wider genetic variabilit	Narrow genetic variability
7	Ginning out turn (%)		Ahsan <i>et al.</i> (2015a) Khan <i>et al.</i> (2015) Rajamani <i>et al.</i> (2015)
8	Seed index (g)	Muthuswamy <i>et al.</i> (2003) Sivaprasad (2003) Gururajan and Sundar (2004) Kumar (2004) Patnaik <i>et al.</i> (2004) Kaushik and Kapoor (2006) Kishore <i>et al.</i> (2011) Dhivya <i>et al.</i> (2014) Khan <i>et al.</i> (2015) Narendra (2015)	Rao and Reddy (2001) Neelam <i>et al.</i> (2002) Altaher and Singh (2003a) Laxman and Ganesh (2003) Neelima <i>et al.</i> (2008) Mahantesh (2009) Srinivasulu (2009) Rajanna (2010) Vinodhana <i>et al.</i> (2013) Ahsan <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015b) Dahiphale <i>et al.</i> (2015)
9	Lint index (g)	Laxman and Ganesh (2003) Muthuswamy <i>et al.</i> (2003) Sivaprasad (2003) Gururajan and Sundar (2004) Patnaik <i>et al.</i> (2004) Neelima <i>et al.</i> (2005) Kaushik and Kapoor (2006) Kishore <i>et al.</i> (2011) Kulkarni <i>et al.</i> (2011) Ahsan <i>et al.</i> (2014) Dhivya <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015a) Ahsan <i>et al.</i> (2015b) Khan <i>et al.</i> (2015)	Rao and Reddy (2001) Altaher and Singh (2003a) Neelima <i>et al.</i> (2008) Naqib <i>et al.</i> (2010) Rajanna (2010) Vinodhana <i>et al.</i> (2013)
10	2.5 % span length (mm)	Muthuswamy <i>et al.</i> (2003) Gururajan and Sundar (2004) Naphade <i>et al.</i> (2004) Patnaik <i>et al.</i> (2004) Kale <i>et al.</i> (2007)	Altaher and Singh (2003a) Neelima <i>et al.</i> (2005) Kaushik and Kapoor (2006) Pratap (2006) Tuteja <i>et al.</i> (2006)

S.No.	Character	Wider genetic variabilit	Narrow genetic variability
10	2.5 % span length (mm)		Verma <i>et al.</i> (2006) Rao <i>et al.</i> (2008) Neelima <i>et al.</i> (2008) Srinivasulu (2009) Rajanna (2010) Sarada <i>et al.</i> (2010) Kishore <i>et al.</i> (2011) Mohan (2011) Vinodhana <i>et al.</i> (2013) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Narendra (2015) Rajamani <i>et al.</i> (2015)
11	Micronaire (10 ⁻⁶ g/inch)	Rao and Reddy (2001) Neelam <i>et al.</i> (2002) Muthuswamy <i>et al.</i> (2003) Naphade <i>et al.</i> (2004) Patnaik <i>et al.</i> (2004) Neelima <i>et al.</i> (2005) Kulkarni <i>et al.</i> (2011)	Reddy (2001) Neelima (2002) Altaher and Singh (2003a) Kaushik and Kapoor (2006) Neelima <i>et al.</i> (2008) Srinivasulu (2009) Rajanna (2010) Sarada <i>et al.</i> (2010) Vinodhana <i>et al.</i> (2013) Khan <i>et al.</i> (2015) Narendra (2015) Rajamani <i>et al.</i> (2015)
12	Bundle strength (g/tex)	Muthuswamy <i>et al.</i> (2003) Gururajan and Sundar (2004) Naphade <i>et al.</i> (2004) Patnaik <i>et al.</i> (2004) Neelima <i>et al.</i> (2005) Kulkarni <i>et al.</i> (2011) Abbas <i>et al.</i> (2014)	Rao and Reddy (2001) Girase and Mehetre (2002) Neelam <i>et al.</i> (2002) Altaher and Singh (2003a) Rao (2008) Srinivasulu (2009) Rajanna (2010) Sarada <i>et al.</i> (2010) Bazi (2011) Rajamani <i>et al.</i> (2015)
13	Uniformity ratio	Patnaik <i>et al.</i> (2004) Neelima <i>et al.</i> (2005)	Muraleedhar (2005) Pratap (2006) Neelima <i>et al.</i> (2008) Rao (2008)

S.No.	Character	Wider genetic variability	Narrow genetic variability
13	Uniformity ratio		Srinivasulu (2009) Rajanna (2010) Sarada <i>et al.</i> (2010) Kishore <i>et al.</i> (2011) Bazi (2011) Mohan (2011) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015) Rajamani <i>et al.</i> (2015)
14	Seed cotton yield plant ⁻¹ (g)	Kaushik and Kapoor (2006) Pratap (2006) Verma <i>et al.</i> (2006) Naqib <i>et al.</i> (2010) Sarada <i>et al.</i> (2010) Kishore <i>et al.</i> (2011) Kulkarni <i>et al.</i> (2011) Mohan (2011) Santhoshkumar <i>et al.</i> (2012) Vinodhana <i>et al.</i> (2013) Ahsan <i>et al.</i> (2014) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015a) Ahsan <i>et al.</i> (2015b) Dahiphale <i>et al.</i> (2015) Khan <i>et al.</i> (2015) Narendra (2015) Rajamani <i>et al.</i> (2015)	Mahantesh (2009) Rajanna (2010) Bazi (2011)
15	Lint yield plant ⁻¹ (g)	Deshpande and Baig (2003) Patnaik <i>et al.</i> (2004) Pratap (2006) Patil (2010) Rajanna (2010) Erande <i>et al.</i> (2014) Dahiphale <i>et al.</i> (2015)	

Chapter V

SUMMARY AND CONCLUSIONS

The present investigation was carried out during *kharif* 2015-16 at Regional Agricultural Research Station, Lam farm, Guntur, Andhra Pradesh with 50 genotypes of cotton (*G. hirsutum* L.).

The mean, genetic variability, heritability, genetic advance as per cent of mean, genetic divergence, character association and the magnitude of direct and indirect effects of yield component traits on seed cotton yield were studied for 15 characters viz., plant height (cm), days to 50% flowering, number of monopodia, 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, seed cotton yield per plant (g) and lint yield per plant (g).

The analysis of variance revealed significant differences among the genotypes for all the characters studied indicating the presence of diverse material in the present study.

The genotypic coefficients of variation for all the characters studied were lesser than the phenotypic coefficients of variation indicating the interaction of genotypes with environment. Moderate to high variability and high heritability coupled with high genetic advance as per cent of mean was observed for plant height, boll weight and micronaire indicating the predominance of additive gene action and hence, direct phenotypic selection may be useful with respect to these traits.

High heritability coupled with moderate genetic advance was observed in case of days to 50% flowering, seed index, lint index and 2.5% span length revealing the role of additive and non additive gene action. The other traits viz., no. of monopodia per plant, seed cotton yield per plant and lint yield per plant showed moderate to high heritability and high genetic advance indicating the

operation of additive gene action. No. of sympodia per plant, number of bolls per plant, ginning out turn, bundle strength and uniformity ratio showed moderate to high heritability and moderate to low genetic advance indicating the operation of non additive gene action. It might be exploited through heterosis breeding, cyclic hybridization, biparental mating and diallel selective mating system.

Correlation study indicated that plant height, number of sympodia per plant, no. of bolls per plant, boll weight, ginning out turn, seed index, lint index, micronaire and lint yield per plant had positive significant association with seed cotton yield per plant.

The path analysis indicated that as plant height, number of sympodia per plant, no. of bolls per plant, boll weight, ginning out turn, seed index, lint index, micronaire and lint yield per plant showed positive and significant correlation, direct selection based on these attributes may be helpful in evolving high yielding varieties of upland cotton.

The results of multivariate analysis indicated the presence of considerable genetic divergence among the 50 genotypes studied. The 50 genotypes were grouped into 8 clusters using Tocher's method in D^2 analysis.

By Mahalanobis's D^2 statistic, it could be inferred that seed index, days to 50% flowering, boll weight, 2.5% span length and micronaire contributed maximum towards genetic divergence. Based on intra-and inter-cluster distance among the groups, it is suggested to make crosses between the genotypes of cluster VI (ARBH 1402) and cluster VII (HYPS 152), between genotypes of cluster I (SSGR 105) and cluster VIII (L 788), between the genotypes of cluster I (SSGR 105) and cluster IV (L 799), between the genotypes of cluster V (GJHV 497) and cluster VIII (L 788) after confirming their general combining ability.

Principal component analysis identified six principal components (PCs), which contributed 81.99 per cent of cumulative variance. The significant factors loaded in PC1 towards maximum genetic divergence were seed cotton yield per plant, bundle strength, lint index, micronaire, number of bolls per plant, number of sympodia per plant, plant height and uniformity ratio. 2D and 3D graphs

showed wide divergence between L 788, MCU 5, HYPS 152, GISV 267, TSH 0499, SSGR 105, ARBH1402 and HS 294 signifying their usefulness in cotton breeding to develop high heterotic hybrids.

The genotypes L 788, HS 294, MCU 5, HYPS 152 and GISV 267 showed maximum inter-cluster distance in Mahalanobis D^2 analysis, principal component analysis and cluster analysis and also have better *per se* performance in sympodia per plant, number of bolls per plant, boll weight, seed index, lint index and quality characters . So they can be exploited for the development of heterotic hybrids in future breeding programmes.

Table 2.3. Review of literature on association of component characters with seed cotton yield in cotton (*G. hirsutum* L.)

S. No.	Character	Association	S/NS	Reference
1	Plant height (cm)	Positive	S	Kaushik and Kapoor (2006) Rao (2008) Khan <i>et al.</i> (2009) Kishore <i>et al.</i> (2011) Rajanna <i>et al.</i> (2011) Tulasi <i>et al.</i> (2012) Rao and Gopinath (2013) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a) Asha <i>et al.</i> (2015) Ulla <i>et al.</i> (2015)
			NS	Murthy (1997) Khan <i>et al.</i> (2015)
		Negative	S	Reddy (2001) Pratap <i>et al.</i> (2007) Dahiphale <i>et al.</i> (2015)
			NS	Kaushik <i>et al.</i> (2003) Raju (2005) Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Farooq <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013)
		Positive	S	Tuteja <i>et al.</i> (2006) Lakshmi <i>et al.</i> (2012) Ranjan <i>et al.</i> (2014)
			NS	Kaushik and Kapoor (2006) Kale <i>et al.</i> (2007) Erande <i>et al.</i> (2014)
2	Days to 50% flowering	Negative	S	Neelima <i>et al.</i> (2005) Chandrashekhar <i>et al.</i> (2016)
			NS	Annapurve <i>et al.</i> (2007) Rao (2008) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Kumar <i>et al.</i> (2014)

S. No.	Character	Association	S/NS	Reference
3	No. of monopodia plant ⁻¹	Positive	S	Mahantesh (2009) Mohan (2011) Tulasi <i>et al.</i> (2012) Rao and Gopinath (2013) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a) Dahiphale <i>et al.</i> (2015) Reddy <i>et al.</i> (2015)
			NS	Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Kishore <i>et al.</i> (2011) Rajanna <i>et al.</i> (2011) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Batool <i>et al.</i> (2010)
			NS	Rao (2008) Venkateswarlu <i>et al.</i> (2010a), Farooq <i>et al.</i> (2013) Farooq <i>et al.</i> (2014)
4	No. of sympodia plant ⁻¹	Positive	S	Vijayalaxmi <i>et al.</i> (2008) Batool <i>et al.</i> (2010) Ekinci <i>et al.</i> (2010) Patnaik and Sial (2010) Salahuddin <i>et al.</i> (2010) Mohan (2011) Rajanna <i>et al.</i> (2011) Tulasi <i>et al.</i> (2012) Rao and Gopinath (2013) Erande <i>et al.</i> (2014) Asha <i>et al.</i> (2015) Baloch <i>et al.</i> (2015b) Dahipale <i>et al.</i> (2015) Khan <i>et al.</i> (2015)
			NS	Neelam <i>et al.</i> (2002) Pradeep and Sumalini (2005) Raju (2005) Kishore <i>et al.</i> (2011) Farooq <i>et al.</i> (2014)
		Negative	NS	Rao (2008) Farooq <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013)

S. No	Character	Association	S/NS	Reference
5	No. of bolls plant ⁻¹	Positive	S	Khan <i>et al.</i> (2009) Rasheed <i>et al.</i> (2009) Makhdoom <i>et al.</i> (2010) Patnaik and Sial (2010) Salahuddin <i>et al.</i> (2010) Kishore <i>et al.</i> (2011) Mohan (2011) Lakshmi <i>et al.</i> (2012) Imran <i>et al.</i> (2012) Tulasi <i>et al.</i> (2012) Rao and Gopinath (2013) Vinodhana <i>et al.</i> (2013) Ahsan <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a) Ahsan <i>et al.</i> (2015a) Asha <i>et al.</i> (2015) Baloch <i>et al.</i> (2015b) Reddy <i>et al.</i> (2015) Ullah <i>et al.</i> (2015) Chandrashekhar <i>et al.</i> (2016)
			NS	Pradeep and Sumalini (2005) Annapurve <i>et al.</i> (2007)
		Negative	NS	Farooq <i>et al.</i> (2013)
6	Boll weight (g)	Positive	S	Khan <i>et al.</i> (2009) Rasheed <i>et al.</i> (2009) Batoool <i>et al.</i> (2010) Salahuddin <i>et al.</i> (2010) Kishore <i>et al.</i> (2011) Mohan (2011) Tulasi <i>et al.</i> (2012) Rao and Gopinath (2013) Ahsan <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a) Ahsan <i>et al.</i> (2015a) Asha <i>et al.</i> (2015) Baloch <i>et al.</i> (2015b) Khan <i>et al.</i> (2015) Reddy <i>et al.</i> (2015) Ullah <i>et al.</i> (2015) Chandrashekhar <i>et al.</i> (2016)

S. No	Character	Association	S/NS	Reference
6	Boll weight (g)	Positive	NS	Kaushik <i>et al.</i> (2003) Vijayalaxmi <i>et al.</i> (2008) Vinodhana <i>et al.</i> (2013) Farooq <i>et al.</i> (2014)
		Negative	S	Gururajan (2000) Rao <i>et al.</i> (2001)
			NS	Farooq <i>et al.</i> (2013)
7	Ginning out-turn (%)	Positive	S	Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Naqib <i>et al.</i> (2010) Salahuddin <i>et al.</i> (2010) Tulasi <i>et al.</i> (2012) Farooq <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Dahiphale <i>et al.</i> (2015)
			NS	Rao <i>et al.</i> (2001) Neelam <i>et al.</i> (2002) Rao (2008) Rajanna <i>et al.</i> (2011) Khan <i>et al.</i> (2015)
		Negative	S	Venkateswarlu <i>et al.</i> (2010a) Mohan (2011)
			NS	Vijayalaxmi <i>et al.</i> (2008) Kishore <i>et al.</i> (2011) Farooq <i>et al.</i> (2013) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a)
8	Seed index (g)	Positive	S	Sambamurthy <i>et al.</i> (2006) Mahantesh (2009) Kumar <i>et al.</i> (2010) Mohan (2011) Tulasi <i>et al.</i> (2012) Rao and Gopinath (2013) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a)
			NS	Kaushik and Kapoor (2006) Rao (2008) Naqib <i>et al.</i> (2010) Kishore <i>et al.</i> (2011) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	NS	Ladole and Meshram (2000) Rao <i>et al.</i> (2001) Mandloi <i>et al.</i> (2003) Raju (2005) Rajanna <i>et al.</i> (2011)

S. No.	Character	Association	S/NS	Reference
9	Lint index (g)	Positive	S	Sivaprasad (2003) Sambamurthy <i>et al.</i> (2006) Naqib <i>et al.</i> (2010) Salahuddin <i>et al.</i> (2010) Tulasi <i>et al.</i> (2012) Rao and Gopinath (2013) Kumar <i>et al.</i> (2014)
			NS	Rao (2008) Mohan (2011) Rajanna <i>et al.</i> (2011) Erande <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a) Khan <i>et al.</i> (2015)
		Negative	S	Venkateswarlu <i>et al.</i> (2010a) Imran <i>et al.</i> (2012)
			NS	Mandloi <i>et al.</i> (2003) Kaushik and Kapoor (2006) Kishore <i>et al.</i> (2011) Vinodhana <i>et al.</i> (2013)
10	2.5% span length (mm)	Positive	S	Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)Asha <i>et al.</i> (2015) Dahiphale <i>et al.</i> (2015) Reddy <i>et al.</i> (2015) Chandrashekhar <i>et al.</i> (2016)
			NS	Neelima (2002) Mandloi <i>et al.</i> (2003) Kumar <i>et al.</i> (2010) Vinodhana <i>et al.</i> (2013)
		Negative	S	Gururajan and Sundar (2004) Venkateswarlu <i>et al.</i> (2010a) Kishore <i>et al.</i> (2011) Mohan (2011)
			NS	Kale <i>et al.</i> (2007) Rao (2008) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Farooq <i>et al.</i> (2013)

S. No	Character	Association	S/NS	Reference
11	Micronaire (10 ⁻⁶ g/inch)	Positive	S	Azhar <i>et al.</i> (2004) Raju (2005) Neelima <i>et al.</i> (2005) Sambamurthy <i>et al.</i> (2006) Kumar and Ravikesavan (2008) Venkateswarlu <i>et al.</i> (2010a) Khan <i>et al.</i> (2015) Chandrashekhara <i>et al.</i> (2016)
		Negative	S	Rajanna <i>et al.</i> (2011) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
			NS	Kumar <i>et al.</i> (2010) Mohan (2011) Farooq <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013)
12	Bundle strength (g/tex)	Positive	S	Muhammad <i>et al.</i> (2003) Azhar <i>et al.</i> (2004) Kumar <i>et al.</i> (2010) Kumar <i>et al.</i> (2014) Asha <i>et al.</i> (2015) Reddy <i>et al.</i> (2015)
			NS	Neelam <i>et al.</i> (2002) Neelima (2002) Mandloi <i>et al.</i> (2003) Kumar <i>et al.</i> (2010) Bazi (2011) Mohan (2011)
		Negative	S	Vinodhana <i>et al.</i> (2013) Farooq <i>et al.</i> (2013)
13	Uniformity ratio	Positive	S	Sivaprasad (2003) Neelima <i>et al.</i> (2005) Khan <i>et al.</i> (2015)
			NS	Neelima (2002) Raju (2005)
		Negative	S	Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014)
			NS	Tuteja <i>et al.</i> (2005) Kishore <i>et al.</i> (2011) Mohan (2011) Rajanna <i>et al.</i> (2011) Kumar <i>et al.</i> (2014)

S. No	Character	Association	S/NS	Reference
14	Lint yield plant ⁻¹ (g)	Positive	S	Deshpande and Baig (2003) Mandloi <i>et al.</i> (2003) Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Lakshmi <i>et al.</i> (2012) Erande <i>et al.</i> (2014) Dahiphale <i>et al.</i> (2015) Reddy <i>et al.</i> (2015)

Note: S: Significant NS: Non-significant

Table 2.4. Review of literature on association among component characters of seed cotton yield in cotton (*G. hirsutum* L.)

S.No.	Character	Association	S/NS	Reference
I.Plant height (cm) with				
1.	Days to 50% flowering	Positive	S	Erande <i>et al.</i> (2014)
			NS	Sangeetha (1998)
		Negative	S	Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011)
			NS	Sakthi <i>et al.</i> (2007) Rao (2008)
2.	No. of monopodia plant ⁻¹	Positive	S	Kaushik and Kapoor (2006) Tulasi <i>et al.</i> (2012) Hafiz <i>et al.</i> (2013) Rajamani <i>et al.</i> (2013) Rao and Gopinath (2013) Abbas <i>et al.</i> (2014) Chitti <i>et al.</i> (2014) Saeed <i>et al.</i> (2015) Liaqat <i>et al.</i> (2015a)
			NS	Rao (2008) Kumar <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
			S	Ranjan <i>et al.</i> (2014a)
			NS	Pradeep and Sumalini (2005) Kale <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014)
3.	No. of sympodia plant ⁻¹	Positive	S	Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Hafiz <i>et al.</i> (2013) Rao and Gopinath (2013) Vinodhana <i>et al.</i> (2013) Abbas <i>et al.</i> (2014) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Liaqat <i>et al.</i> (2015a) Majeedano <i>et al.</i> (2014) Saeed <i>et al.</i> (2015)

S.No.	Character	Association	S/NS	Reference
	No. of sympodia plant ⁻¹	Positive	NS	Kale <i>et al.</i> (2007) Rao (2008) Khan <i>et al.</i> (2015)
4.	No. of bolls plant ⁻¹	Positive	S	Kaushik and Kapoor (2006) Rajanna <i>et al.</i> (2011) Tulasi <i>et al.</i> (2012) Hafiz <i>et al.</i> (2013) Rao and Gopinath (2013) Vinodhana <i>et al.</i> (2013) Abbas <i>et al.</i> (2014) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Majeedano <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a) Dahiphale <i>et al.</i> (2015)
			NS	Sangeetha (1998) Annapurve <i>et al.</i> (2007) Khan <i>et al.</i> (2015)
		Negative	NS	Sakthi <i>et al.</i> (2007)
5.	Boll weight (g)	Positive	S	Tulasi <i>et al.</i> (2012) Rajamani <i>et al.</i> (2013) Farooq <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a)
			NS	Pradeep and Sumalini (2005) Annapurve <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
			S	Chitti <i>et al.</i> (2014)
			NS	Sakthi <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011)
6.	Ginning out-turn (%)	Positive	S	Farooq <i>et al.</i> (2014) Dahiphale <i>et al.</i> (2015)
			NS	Kale <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Tulasi <i>et al.</i> (2012)

S.No.	Character	Association	S/NS	Reference
6.	Ginning out-turn (%)	Negative	S	Tyagi (1994)
			NS	Annapurve <i>et al.</i> (2007) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a) Saeed <i>et al.</i> (2015)
7.	Seed index (g)	Positive	S	Rajanna <i>et al.</i> (2011) Tulasi <i>et al.</i> (2012) Rao and Gopinath (2013) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014)
			NS	Kale <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Ranjan <i>et al.</i> (2014a) Khan <i>et al.</i> (2015)
		Negative	S	Pratap <i>et al.</i> (2007) Kumar <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015a)
			NS	Rajamani <i>et al.</i> (2013) Chitti <i>et al.</i> (2014)
8.	Lint index (g)	Positive	S	Rajanna <i>et al.</i> (2011) Tulasi <i>et al.</i> (2012) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a)
			NS	Vijayalaxmi <i>et al.</i> (2008) Khan <i>et al.</i> (2015)
		Negative	NS	Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014)
9.	2.5% span length (mm)	Positive	S	Muthu <i>et al.</i> (2004) Kumar <i>et al.</i> (2014)
			NS	Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Hafiz <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014)
		Negative	S	Rajamani <i>et al.</i> (2013)
			NS	Kaushik and Kapoor (2006)

S.No.	Character	Association	S/NS	Reference
10.	Micronaire value (10 ⁻⁶ g/inch)	Positive	S	Abbas <i>et al.</i> (2014) Liaqat <i>et al.</i> (2015a)
			NS	Vijayalaxmi <i>et al.</i> (2008) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Rajanna <i>et al.</i> (2011)
			NS	Sakthi <i>et al.</i> (2007) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
11.	Bundle strength (g/tex)	Positive	S	Vijayalaxmi <i>et al.</i> (2008) Kumar <i>et al.</i> (2014) Liaqat <i>et al.</i> (2015a)
			NS	Kowsalya and Raveendran (1996) Rajanna <i>et al.</i> (2011) Vinodhana <i>et al.</i> (2013)
		Negative	NS	Sangeetha (1998) Sakthi <i>et al.</i> (2007) Rajamani <i>et al.</i> (2013)
12.	Uniformity Ratio	Positive	NS	Rao (2008) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Sakthi <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011)
			NS	Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
13.	Seed cotton yield plant ⁻¹ (g)	Positive	S	Tulasi <i>et al.</i> (2012) Rao and Gopinath (2013) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Majeedano <i>et al.</i> (2014)
			NS	Khan <i>et al.</i> (2015)
		Negative	S	Chitti <i>et al.</i> (2014)
14.	Lint yield plant ⁻¹ (g)	Positive	S	Samanc and Ozkaynak (2000) Rajanna <i>et al.</i> (2011)
			NS	Erande <i>et al.</i> (2014)
		Negative	NS	Rao (2008) Vijayalaxmi <i>et al.</i> (2008)
II. Days to 50% flowering with				
1.	No. of monopodia plant ⁻¹	Positive	S	Muraleedhar (2005) Kaushik and Kapoor (2006) Vijayalaxmi <i>et al.</i> (2008) Ranjan <i>et al.</i> (2014a)

S.No	Character	Association	S/NS	Reference
1.	No. of monopodia plant ⁻¹	Positive	S	Kumar <i>et al.</i> (2014)
			NS	Ladole and Meshram (2000) Reddy (2001)
		Negative	S	Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
			NS	Neelam <i>et al.</i> (2002) Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007)
2.	No. of sympodia plant ⁻¹	Positive	S	Ladole and Meshram (2000) Muraleedhar (2005)
			NS	Basha (1997) Erande <i>et al.</i> (2014)
		Negative	S	Altaher and Singh (2003b) Raju (2005) Vijayalaxmi <i>et al.</i> (2008)
			NS	Kaushik and Kapoor (2006) Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
3.	No. of bolls plant ⁻¹	Positive	S	Muraleedhar (2005) Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a)
			NS	Kaushik and Kapoor (2006) Kale <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011) Kumar <i>et al.</i> (2014)
		Negative	S	Reddy (2001)
			NS	Raju (2005) Annapurve <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007) Rajamani <i>et al.</i> (2013)
4.	Boll weight (g)	Positive	S	Altaher and Singh (2003b) Sivaprasad (2003) Ranjan <i>et al.</i> (2014a)
			NS	Erande <i>et al.</i> (2014)
		Negative	S	Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
			NS	Neelima (2002)

S.No.	Character	Association	S/NS	Reference
4.	Boll weight (g)	Negative	NS	Annapurve <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007)
5.	Ginning out turn (%)	Positive	S	Neelam <i>et al.</i> (2002) Raju (2005)
			NS	Kaushik and Kapoor (2006) Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014)
		Negative	S	Pratap <i>et al.</i> (2007)
			NS	Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
6.	Seed index (g)	Positive	S	Raju (2005) Erande <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a)
			NS	Kale <i>et al.</i> (2007) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
		Negative	S	Muraleedhar (2005) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011)
			NS	Neelam <i>et al.</i> (2002) Kaushik and Kapoor (2006)
7.	Lint index (g)	Positive	S	Raju (2005) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a)
			NS	Basha (1997) Neelam <i>et al.</i> (2002)
		Negative	S	Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011)
			NS	Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014)
8.	2.5% span length (mm)	Positive	S	Neelima (2002)
			NS	Raju (2005)
		Negative	NS	Kaushik and Kapoor (2006) Sakthi <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
9.	Micronaire value (10 ⁻⁶ g/inch)	Positive	S	Pratap <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011)
			NS	Sangeetha (1998) Sakthi <i>et al.</i> (2007)

S.No.	Character	Association	S/NS	Reference
9.	Micronaire value (10 ⁻⁶ g/inch)	Negative	S	Altaher and Singh (2003b) Muraleedhar (2005) Vijayalaxmi <i>et al.</i> (2008)
			NS	Neelam <i>et al.</i> (2002) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
10.	Bundle strength (g/tex)	Positive	S	Sivaprasad (2003) Vijayalaxmi <i>et al.</i> (2008)
			NS	Neelam <i>et al.</i> (2002)
		Negative	S	Altaher and Singh (2003b) Raju (2005)
			NS	Sakthi <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
11.	Uniformity ratio	Positive	S	Neelima (2002) Neelima <i>et al.</i> (2005)
			NS	Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014)
		Negative	S	Raju (2005) Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Kumar <i>et al.</i> (2014)
			NS	Neelima (2002) Neelima <i>et al.</i> (2005)
12.	Lint yield plant ⁻¹ (g)	Positive	S	Patel <i>et al.</i> (2013)
			NS	Erande <i>et al.</i> (2014)
		Negative	S	Pratap <i>et al.</i> (2007) Rao (2008)
			NS	Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011)
III. No. of monopodia plant ⁻¹ with				
1.	No. of sympodia plant ⁻¹	Positive	S	Mohan (2011) Rajanna <i>et al.</i> (2011) Abbas <i>et al.</i> (2014) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Dahiphale <i>et al.</i> (2015) Liaqat <i>et al.</i> (2015a)
			NS	Hafiz <i>et al.</i> (2013) Rajamani <i>et al.</i> (2013) Khan <i>et al.</i> (2015)

S.No.	Character	Association	S/NS	Reference
1.	No. of sympodia plant ⁻¹	Negative	S	Verma <i>et al.</i> (2006) Vijayalaxmi <i>et al.</i> (2008) Farooq <i>et al.</i> (2014)
			NS	Neelam <i>et al.</i> (2002) Pradeep and Sumalini (2005)
2.	No. of bolls plant ⁻¹	Positive	S	Verma <i>et al.</i> (2006) Vijayalaxmi <i>et al.</i> (2008) Kishore <i>et al.</i> (2011) Mohan (2011) Hafiz <i>et al.</i> (2013) Rajamani <i>et al.</i> (2013) Abbas <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
			NS	Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011) Patel <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Farooq <i>et al.</i> (2014)
			NS	Reddy (2001)
		Positive	S	Basha (1997)
			NS	Reddy (2001) Neelima (2002) Tulasi <i>et al.</i> (2012) Rajamani <i>et al.</i> (2013) Rao and Gopinath (2013) Abbas <i>et al.</i> (2014) Chitti <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a)
3.	Boll weight (g)	Negative	S	Pratap <i>et al.</i> (2007) Kumar <i>et al.</i> (2014)
			NS	Annapurve <i>et al.</i> (2007) Rao (2008) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Farooq <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
4.	Ginning out-turn (%)	Positive	S	Pratap <i>et al.</i> (2007) Annapurve <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Tulasi <i>et al.</i> (2012) Abbas <i>et al.</i> (2014)

S.No.	Character	Association	S/NS	Reference
4.	Ginning out-turn (%)	Positive	S	Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a)
			NS	Neelima (2002) Kale <i>et al.</i> (2007) Rao (2008) Farooq <i>et al.</i> (2014) Chitti <i>et al.</i> (2014)
		Negative	S	Mohan (2011)
			NS	Neelam <i>et al.</i> (2002) Rajamani <i>et al.</i> (2013) Khan <i>et al.</i> (2015)
5.	Seed index (g)	Positive	S	Mahantesh (2009) Mohan (2011) Tulasi <i>et al.</i> (2012) Rao and Gopinath (2013) Kumar <i>et al.</i> (2014)
			NS	Neelima (2002) Rajanna <i>et al.</i> (2011)
		Negative	S	Vijayalaxmi <i>et al.</i> (2008)
			NS	Kale <i>et al.</i> (2007) Rajamani <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a) Khan <i>et al.</i> (2015)
6.	Lint index (g)	Positive	S	Rao and Gopinath (2013) Ranjan <i>et al.</i> (2014a)
			NS	Neelima (2002) Tulasi <i>et al.</i> (2012) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
		Negative	NS	Raju (2005) Kale <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
7.	2.5% span length (mm)	Positive	S	Sivaprasad (2003) Mohan (2011) Hafiz <i>et al.</i> (2013)

S.No.	Character	Association	S/NS	Reference
7.	2.5% span length (mm)	Positive	NS	Neelam <i>et al.</i> (2002) Kale <i>et al.</i> (2007) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
		Negative	S	Rao (2008) Abbas <i>et al.</i> (2014)
			NS	Verma <i>et al.</i> (2006) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
8.	Micronaire value (10 ⁻⁶ g/inch)	Positive	S	Liaqat <i>et al.</i> (2015a)
			NS	Neelima (2002) Rao (2008) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
		Negative	S	Muraleedhar (2005) Vijayalaxmi <i>et al.</i> (2008) Mahantesh (2009)
			NS	Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
9.	Bundle strength (g/tex)	Positive	S	Muraleedhar (2005) Mohan (2011)
			NS	Neelam <i>et al.</i> (2002) Neelima (2002) Vijayalaxmi <i>et al.</i> (2008) Kumar <i>et al.</i> (2014)
		Negative	NS	Reddy (2001) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
10.	Uniformity ratio	Positive	NS	Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Khan <i>et al.</i> (2015)
		Negative	S	Vijayalaxmi <i>et al.</i> (2008) Mahantesh (2009)
			NS	Neelima (2002) Erand <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
11.	Seed cotton yield plant ⁻¹ (g)	Positive	S	Chitti <i>et al.</i> (2014)
			NS	Khan <i>et al.</i> (2015)
		Negative	NS	Farooq <i>et al.</i> (2014)
12.	Lint yield plant ⁻¹ (g)	Positive	S	Rajanna <i>et al.</i> (2011) Patel <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Dahiphale <i>et al.</i> (2015)

S.No.	Character	Association	S/NS	Reference
IV. No. of sympodia plant⁻¹ with				
1.	No. of bolls plant ⁻¹	Positive	S	Rajanna <i>et al.</i> (2011) Salahuddin <i>et al.</i> (2010) Mohan (2011) Hafiz <i>et al.</i> (2013) Patel <i>et al.</i> (2013) Rao and Gopinath (2013) Rajamani <i>et al.</i> (2013) Abbas <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Majeedano <i>et al.</i> (2014)
			NS	Pradeep and Sumalini (2005) Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	NS	Raju (2005) Vijayalaxmi <i>et al.</i> (2008)
2.	Boll weight (g)	Positive	S	Sakthi <i>et al.</i> (2007) Salahuddin <i>et al.</i> (2010) Mohan (2011) Tulasi <i>et al.</i> (2012) Abbas <i>et al.</i> (2014) Majeedano <i>et al.</i> (2014)
			NS	Rao (2008) Vijayalaxmi <i>et al.</i> (2008) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Pratap <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011) Vinodhana <i>et al.</i> (2013)
			NS	Pradeep and Sumalini (2005) Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Chitti <i>et al.</i> (2014)
3.	Ginning out turn (%)	Positive	S	Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Mohan (2011) Tulasi <i>et al.</i> (2012) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Liaqat <i>et al.</i> (2015a)

S.No.	Character	Association	S/NS	Reference
3.	Ginning out turn (%)	Positive	NS	Neelima <i>et al.</i> (2005) Sakthi <i>et al.</i> (2007) Rao (2008)
		Negative	S	Altaher and Singh (2003b) Abbas <i>et al.</i> (2014) Chitti <i>et al.</i> (2014)
			NS	Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Vinodhana <i>et al.</i> (2013) Rajamani <i>et al.</i> (2013) Khan <i>et al.</i> (2015)
4.	Seed index (g)	Positive	S	Muthu <i>et al.</i> (2004) Neelima <i>et al.</i> (2005) Mahantesh (2009) Mohan (2011) Rajanna <i>et al.</i> (2011) Tulasi <i>et al.</i> (2012)
			NS	Rao (2008) Vijayalaxmi <i>et al.</i> (2008) Vinodhana <i>et al.</i> (2013) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Muthuswamy and Vivekanandan (2004) Muraleedhar (2005)
			NS	Kale <i>et al.</i> (2007) Chitti <i>et al.</i> (2014)
5.	Lint index (g)	Positive	S	Neelam <i>et al.</i> (2002) Neelima (2002) Muthu <i>et al.</i> (2004) Raju (2005) Neelima <i>et al.</i> (2005) Sakthi <i>et al.</i> (2007) Mahantesh (2009) Tulasi <i>et al.</i> (2012)
			NS	Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Khan <i>et al.</i> (2015)
		Negative	S	Muraleedhar (2005) Venkateswarlu <i>et al.</i> (2010a) Chitti <i>et al.</i> (2014)
			NS	Rao <i>et al.</i> (2001)

S.No.	Character	Association	S/NS	Reference
5.	Lint index (g)	Negative	NS	Erande <i>et al.</i> (2014)
6.	2.5% Span length (mm)	Positive	S	Neelam <i>et al.</i> (2002) Sakthi <i>et al.</i> (2007) Mohan (2011) Vinodhana <i>et al.</i> (2013)
			NS	Verma <i>et al.</i> (2006)
		Negative	S	Raju (2005) Kale <i>et al.</i> (2007) Rao (2008) Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014)
			NS	Muraleedhar (2005) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
7.	Micronaire value (10 ⁻⁶ g/inch)	Positive	S	Raju (2005) Vijayalaxmi <i>et al.</i> (2008) Mohan (2011) Liaqat <i>et al.</i> (2015a)
			NS	Neelam <i>et al.</i> (2002) Sakthi <i>et al.</i> (2007) Khan <i>et al.</i> (2015)
		Negative	S	Rajanna <i>et al.</i> (2011) Abbas <i>et al.</i> (2014)
			NS	Vinodhana <i>et al.</i> (2013) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014)
8.	Bundle strength (g/tex)	Positive	S	Altaher and Singh (2003b) Muthu <i>et al.</i> (2004) Mohan (2011) Rajanna <i>et al.</i> (2011)
			NS	Sakthi <i>et al.</i> (2007) Rao (2008) Vinodhana <i>et al.</i> (2013)
		Negative	NS	Raju (2005) Vijayalaxmi <i>et al.</i> (2008) Rajamani <i>et al.</i> (2013)
9.	Uniformity ratio	Positive	S	Vijayalaxmi <i>et al.</i> (2008) Mohan (2011)
			NS	Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Rao (2008) Venkateswarlu <i>et al.</i> (2010a)

S.No	Character	Association	S/NS	Reference
10.	Seed cotton yield plant ⁻¹ (g)	Positive	S	Majeedano <i>et al.</i> (2014)
11.	Lint yield plant ⁻¹ (g)	Positive	S	Pratap <i>et al.</i> (2007) Rao (2008) Rajanna <i>et al.</i> (2011) Patel <i>et al.</i> (2013) Erande <i>et al.</i> (2014)
			NS	Vijayalaxmi <i>et al.</i> (2008)
V. No. of bolls plant ⁻¹ with				
1.	Boll weight (g)	Positive	S	Neelima (2002) Altaher and Singh (2003b) Neelima <i>et al.</i> (2005) Sakthi <i>et al.</i> (2007) Salahuddin <i>et al.</i> (2010) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Majeedano <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a)
			NS	Rao (2008) Rajamani <i>et al.</i> (2013) Khan <i>et al.</i> (2015)
		Negative	S	Rajanna <i>et al.</i> (2011) Kumar <i>et al.</i> (2014)
			NS	Kale <i>et al.</i> (2007) Vinodhana <i>et al.</i> (2013)
2.	Ginning out-turn (%)	Positive	S	Muthu <i>et al.</i> (2004) Pratap <i>et al.</i> (2007) Salahuddin <i>et al.</i> (2010) Abbas <i>et al.</i> (2014)
			NS	Kale <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajamani <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a) Khan <i>et al.</i> (2015)
		Negative	S	Venkateswarlu <i>et al.</i> (2010a) Mohan (2011) Vinodhana <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
			NS	Sangeetha (1998) Rajanna <i>et al.</i> (2011)

S.No.	Character	Association	S/NS	Reference
3.	Seed index (g)	Positive	S	Neelima <i>et al.</i> (2005) Mahantesh (2009) Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014)
			NS	Reddy (2001) Ranjan <i>et al.</i> (2014a) Khan <i>et al.</i> (2015)
		Negative	S	Vijayalaxmi <i>et al.</i> (2008) Mohan (2011) Kumar <i>et al.</i> (2014) Dahiphale <i>et al.</i> (2015)
			NS	Rao (2008) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
4.	Lint index (g)	Positive	S	Muthu <i>et al.</i> (2004) Neelima <i>et al.</i> (2005) Chitti <i>et al.</i> (2014)
			NS	Sakthi <i>et al.</i> (2007) Mahantesh (2009) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a) Khan <i>et al.</i> (2015)
		Negative	S	Vijayalaxmi <i>et al.</i> (2008) Venkateswarlu <i>et al.</i> (2010a) Mohan (2011) Kumar <i>et al.</i> (2014)
			NS	Rao (2008) Rajanna <i>et al.</i> (2011) Vinodhana <i>et al.</i> (2013)
5.	2.5% Span length (mm)	Positive	S	Mohan (2011) Hafiz <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Abbas <i>et al.</i> (2014)
			NS	Sakthi <i>et al.</i> (2007) Rao (2008) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)

S.No.	Character	Association	S/NS	Reference
5.	2.5% Span length (mm)	Negative	S	Tyagi (1994) Muraleedhar (2005)
			NS	Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011)
6.	Micronaire value (10 ⁻⁶ g/inch)	Positive	S	Muthu <i>et al.</i> (2004) Raju (2005) Sakthi <i>et al.</i> (2007) Rao (2008) Venkateswarlu <i>et al.</i> (2010a)
			NS	Rao <i>et al.</i> (2001) Neelam <i>et al.</i> (2002) Khan <i>et al.</i> (2015)
		Negative	S	Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Mohan (2011) Vinodhana <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
			NS	Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014)
7.	Bundle strength (g/tex)	Positive	S	Altaher and Singh (2003b) Muthu <i>et al.</i> (2004) Kumar <i>et al.</i> (2014)
			NS	Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Vinodhana <i>et al.</i> (2013)
		Negative	S	Sangeetha (1998) Abbas <i>et al.</i> (2014)
			NS	Raju (2005) Rao (2008)
8.	Uniformity ratio	Positive	S	Muthu <i>et al.</i> (2004)
			NS	Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
		Negative	S	Vijayalaxmi <i>et al.</i> (2008) Mohan (2011)
			NS	Neelima (2002) Sakthi <i>et al.</i> (2007) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Khan <i>et al.</i> (2015)

S.No.	Character	Associatio	S/NS	Reference
9.	Seed cotton yield p (g)	Positive	S	Tulasi <i>et al.</i> (2012) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Majeedano <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
10.	Lint yield plant ⁻¹ (g)	Positive	S	Pratap <i>et al.</i> (2007) Rao (2008) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011)
			NS	Erande <i>et al.</i> (2014)
VI. Boll weight (g) with				
1.	Ginning out-turn (%)	Positive	S	Muthuswamy and Vivekanandan (2004) Raju (2005) Mohan (2011) Chitti <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
			NS	Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Abbas <i>et al.</i> (2014)
			NS	Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Ranjan <i>et al.</i> (2014a)
2.	Seed index (g)	Positive	S	Neelima <i>et al.</i> (2005) Rasheed <i>et al.</i> (2009) Venkateswarlu <i>et al.</i> (2010a) Rajanna <i>et al.</i> (2011) Mohan (2011) Rajamani <i>et al.</i> (2013) Rao and Gopinath (2013) Vinodhana <i>et al.</i> (2013) Ranjan <i>et al.</i> (2014a) Kumar <i>et al.</i> (2014)
			NS	Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Rao (2008)
			NS	Chitti <i>et al.</i> (2014)

S.No.	Character	Association	S/NS	Reference
3.	Lint index (g)	Positive	S	Vijayalaxmi <i>et al.</i> (2008) Venkateswarlu <i>et al.</i> (2010a) Rajanna <i>et al.</i> (2011) Mohan (2011) Rajamani <i>et al.</i> (2013) Rao and Gopinath (2013) Vinodhana <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
			NS	Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015) Ranjan <i>et al.</i> (2014a)
4.	2.5% Span length (mm)	Positive	S	Sivaprasad (2003) Verma <i>et al.</i> (2006) Vijayalaxmi <i>et al.</i> (2008) Abbas <i>et al.</i> (2014)
			NS	Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
		Negative	S	Mohan (2011)
			NS	Neelima (2002)
5.	Micronaire value (10 ⁻⁶ g/inch)	Positive	S	Tyagi (1994) Vinodhana <i>et al.</i> (2013) Abbas <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
			NS	Sakthi <i>et al.</i> (2007) Rao (2008) Khan <i>et al.</i> (2015)
		Negative	S	Rao <i>et al.</i> (2001) Neelima (2002) Erande <i>et al.</i> (2014)
			NS	Vijayalaxmi <i>et al.</i> (2008) Rajamani <i>et al.</i> (2013)
6.	Bundle strength (g/tex)	Positive	S	Muraleedhar (2005) Rao (2008) Mahantesh (2009) Rajamani <i>et al.</i> (2013) Abbas <i>et al.</i> (2014) Liaqat <i>et al.</i> (2015a)
			NS	Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008)

S.No	Character	Association	S/NS	Reference
6.	Bundle strength (g/tex)	Negative	S	Rao <i>et al.</i> (2001) Mohan (2011) Vinodhana <i>et al.</i> (2013)
			NS	Rajanna <i>et al.</i> (2011) Kumar <i>et al.</i> (2014)
7.	Uniformity ratio	Positive	NS	Rajanna <i>et al.</i> (2011) Khan <i>et al.</i> (2015)
		Negative	S	Neelima (2002) Muraleedhar (2005) Rajamani <i>et al.</i> (2013)
			NS	Sakthi <i>et al.</i> (2007) Rao (2008) Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014)
8.	Seed cotton yield plant ⁻¹ (g)	Positive	S	Tulasi <i>et al.</i> (2012) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Majeedano <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
			NS	Farooq <i>et al.</i> (2014)
9.	Lint yield plant ⁻¹ (g)	Positive	S	Dedaniya and Pethani (1994) Rao (2008) Rajanna <i>et al.</i> (2011) Erande <i>et al.</i> (2014)
			NS	Patel <i>et al.</i> (2013)
VII. Ginning out-turn (%) with				
1.	Seed index (g)	Positive	S	Neelima (2002) Altaher and Singh (2003b)
			NS	Rao <i>et al.</i> (2001) Kale <i>et al.</i> (2007) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014)
		Negative	S	Mohan (2011) Rajanna <i>et al.</i> (2011) Rao and Gopinath (2013) Kumar <i>et al.</i> (2014)
			NS	Chitti <i>et al.</i> (2014) Khan <i>et al.</i> (2015)

S.No	Character	Association	S/NS	Reference
2.	Lint index (g)	Positive	S	Muthu <i>et al.</i> (2004) Raju (2005) Pratap <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rasheed <i>et al.</i> (2009) Mohan (2011) Rajanna <i>et al.</i> (2011) Chitti <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
			NS	Rao <i>et al.</i> (2001) Neelam <i>et al.</i> (2002) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
3.	2.5% span length (mm)	Positive	S	Sivaprasad (2003) Kale <i>et al.</i> (2007) Dahiphale <i>et al.</i> (2015)
			NS	Reddy (2001) Neelima (2002) Rajamani <i>et al.</i> (2013)
		Negative	S	Muthu <i>et al.</i> (2004) Sakthi <i>et al.</i> (2007) Mahantesh (2009) Mohan (2011) Abbas <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
			NS	Neelam <i>et al.</i> (2002) Kale <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Erande <i>et al.</i> (2014)
4.	Micronaire value (10 ⁻⁶ g/inch)	Positive	S	Rao <i>et al.</i> (2001) Muthu <i>et al.</i> (2004) Mohan (2011)
			NS	Rao (2008) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Khan <i>et al.</i> (2015)

S.No.	Character	Association	S/NS	Reference
4.	Micronaire value (10 ⁻⁶ g/inch)	Negative	S	Vijayalaxmi <i>et al.</i> (2008)
			NS	Mandloi <i>et al.</i> (2003) Raju (2005)
5.	Bundle strength (g/tex)	Positive	S	Mandloi <i>et al.</i> (2003) Sambamurthy <i>et al.</i> (2006) Rao (2008)
			NS	Neelima (2002) Vijayalaxmi <i>et al.</i> (2008)
		Negative	S	Neelam <i>et al.</i> (2002) Mahantesh (2009) Mohan (2011) Vinodhana <i>et al.</i> (2013) Abbas <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Liaqat <i>et al.</i> (2015a)
			NS	Sakthi <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
6.	Uniformity ratio	Positive	S	Sakthi <i>et al.</i> (2007) Mohan (2011) Kumar <i>et al.</i> (2014)
			NS	Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Altaher and Singh (2003b)
			NS	Vijayalaxmi <i>et al.</i> (2008) Anadan (2009)
7.	Lint yield plant ⁻¹ (g)	Positive	S	Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rao (2008) Rajanna <i>et al.</i> (2011) Patel <i>et al.</i> (2013) Dahiphale <i>et al.</i> (2015)
			NS	Dedaniya and Pethani (1994) Mandloi <i>et al.</i> (2003) Erande <i>et al.</i> (2014)

S. No.	Character	Association	S/NS	Reference
VIII. Seed index (g) with				
1.	Lint index (g)	Positive	S	Mahantesh (2009) Rasheed <i>et al.</i> (2009) Venkateswarlu <i>et al.</i> (2010a) Rajanna <i>et al.</i> (2011) Mohan (2011) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014a) Liaqat <i>et al.</i> (2015a)
			NS	Neelam <i>et al.</i> (2002) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
2.	2.5% span length (mm)	Positive	S	Vijayalaxmi <i>et al.</i> (2008) Mohan (2011) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Kumar <i>et al.</i> (2014) Liaqat <i>et al.</i> (2015a)
			NS	Neelam <i>et al.</i> (2002)
		Negative	S	Kale <i>et al.</i> (2007)
			NS	Neelima (2002) Mandloi <i>et al.</i> (2003) Erande <i>et al.</i> (2014)
3.	Micronaire value (10 ⁻⁶ g/inch)	Positive	S	Rao (2008) Vijayalaxmi <i>et al.</i> (2008) Rajamani <i>et al.</i> (2013)
			NS	Neelam <i>et al.</i> (2002) Neelima (2002) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Rajanna <i>et al.</i> (2011) Mohan (2011) Kumar <i>et al.</i> (2014) Liaqat <i>et al.</i> (2015a)
			NS	Vinodhana <i>et al.</i> (2013)

S. No.	Character	Association	S/NS	Reference
4.	Bundle strength (g/tex)	Positive	S	Muthu <i>et al.</i> (2004) Mohan (2011) Vinodhana <i>et al.</i> (2013) Kumar <i>et al.</i> (2014) Liaqat <i>et al.</i> (2015a)
			NS	Neelam <i>et al.</i> (2002) Neelima (2002) Altaher and Singh (2003b)
		Negative	S	Rao <i>et al.</i> (2001) Rajanna <i>et al.</i> (2011)
			NS	Rao (2008) Vijayalaxmi <i>et al.</i> (2008) Rajamani <i>et al.</i> (2013)
5.	Uniformity ratio	Positive	NS	Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Neelima (2002) Muraleedhar (2005) Rajanna <i>et al.</i> (2011) Kumar <i>et al.</i> (2014)
			NS	Rao (2008) Vijayalaxmi <i>et al.</i> (2008) Rajamani <i>et al.</i> (2013)
6.	Seed cotton yield plant ⁻¹ (g)	Positive	NS	Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	NS	Chitti <i>et al.</i> (2014)
7.	Lint yield plant ⁻¹ (g)	Positive	NS	Rao (2008) Erande <i>et al.</i> (2014)
		Negative	NS	Mandloi <i>et al.</i> (2003) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011)
IX. Lint index (g) with				
1.	2.5% spanlength (mm)	Positive	S	Muthu <i>et al.</i> (2004) Sambamurthy <i>et al.</i> (2006) Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
			NS	Rajanna <i>et al.</i> (2011) Erande <i>et al.</i> (2014)

S. No	Character	Association	S/NS	Reference
1.	2.5% spanlength (mm)	Negative	S	Mohan (2011)
			NS	Neelima (2002) Mandloi <i>et al.</i> (2003) Vinodhana <i>et al.</i> (2013)
2.	Micronaire value (10 ⁻⁶ g/inch)	Positive	S	Neelam <i>et al.</i> (2002) Rao (2008) Rajamani <i>et al.</i> (2013)
			NS	Sakthi <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Mandloi <i>et al.</i> (2003) Mahantesh (2009) Kumar <i>et al.</i> (2014) Liaqat <i>et al.</i> (2015a)
			NS	Rao <i>et al.</i> (2001)
3.	Bundle strength (g/tex)	Positive	S	Muthu <i>et al.</i> (2004) Sambamurthy <i>et al.</i> (2006)
			NS	Neelima (2002) Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008)
		Negative	S	Vinodhana <i>et al.</i> (2013)
			NS	Reddy (2001) Neelam <i>et al.</i> (2002) Mandloi <i>et al.</i> (2003) Raju (2005) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
4.	Uniformity ratio	Positive	S	Mohan (2011)
			NS	Raju (2005) Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Muthu <i>et al.</i> (2004) Sakthi <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011)

S.No.	Character	Association	S/NS	Reference
4.	Uniformity ratio	Negative	NS	Sangeetha (1998) Neelima (2002) Rao (2008) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
5.	Seed cotton yield plant ⁻¹ (g)	Positive	S	Chitti <i>et al.</i> (2014)
			NS	Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
6.	Lint yield plant ⁻¹ (g)	Positive	S	Pratap <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011)
			NS	Rao (2008) Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014)
		Negative	S	Muthu <i>et al.</i> (2004) Mandloi <i>et al.</i> (2003)
X. 2.5% span length with				
1.	Micronaire value (10 ⁻⁶ g/inch)	Positive	S	Mandloi <i>et al.</i> (2003) Muthuswamy and Vivekanandan (2004)
		Negative	S	Raju (2005) Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Venkateswarlu <i>et al.</i> (2010a) Mohan (2011) Rajanna <i>et al.</i> (2011) Rao ana Gopinath (2013) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
			NS	Neelima (2002) Sakthi <i>et al.</i> (2007) Rao (2008)
2.	Bundle strength (g/tex)	Positive	S	Rathore <i>et al.</i> (2004) Raju (2005) Tuteja <i>et al.</i> (2005) Vijayalaxmi <i>et al.</i> (2008) Mohan (2011) Rajanna <i>et al.</i> (2011) Rao and Gopinath (2013) Vinodhana <i>et al.</i> (2013)

S. No	Character	Association	S/NS	Reference		
2.	Bundle strength (g/tex)	Positive	S	Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014) Chandrashekhar <i>et al.</i> (2016)		
			NS	Reddy (2001) Neelima (2002)		
		Negative	S	Rao <i>et al.</i> (2001)		
3.	Uniformity ratio	Positive	S	Sivaprasad (2003)		
			NS	Neelima (2002)		
		Negative	S	Raju (2005) Pratap <i>et al.</i> (2007) Rao (2008) Vijayalaxmi <i>et al.</i> (2008) Venkateswarlu <i>et al.</i> (2010a) Mohan (2011) Rajanna <i>et al.</i> (2011) Rao and Gopinath (2013) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014) Chandrashekhar <i>et al.</i> (2016)		
				NS	Muthu <i>et al.</i> (2004) Tuteja <i>et al.</i> (2005) Erande <i>et al.</i> (2014)	
4.	Lint yield plant ⁻¹ (g)	Positive	NS	Dedaniya and Pethani (1994) Mandloi <i>et al.</i> (2003) Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014)		
				Negative	NS	Rao (2008)
						S
		XI. Micronaire value with				
1.	Bundle strength (g/tex)	Positive	S	Neelima (2002) Abbas <i>et al.</i> (2014)		
			NS	Raju(2005) Rao (2008) Vijayalaxmi <i>et al.</i> (2008) Mahantesh (2009) Mohan (2011) Vinodhana <i>et al.</i> (2013)		

S. No.	Character	Association	S/NS	Reference		
1.	Bundle strength (g/tex)	Negative	S	Kumar <i>et al.</i> (2014)		
			NS	Neelam <i>et al.</i> (2002) Tuteja <i>et al.</i> (2005) Rajanna <i>et al.</i> (2011) Chandrashekhar <i>et al.</i> (2016)		
2.	Uniformity ratio	Positive	S	Rathore <i>et al.</i> (2004) Raju(2005) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Rao ana Gopinath (2013) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)		
			NS	Muthu <i>et al.</i> (2004) Khan <i>et al.</i> (2015)		
		Negative	S	Tuteja <i>et al.</i> (2005)		
			NS	Sangeetha (1998) Neelima (2002)		
		3.	Lint yield plant ⁻¹ (g)	Positive	S	Rao (2008)
					NS	Mandloi <i>et al.</i> (2003)
Negative	S			Rajanna <i>et al.</i> (2011) Erande <i>et al.</i> (2014)		
	NS			Dedaniya and Pethani (1994)		
XII. Bundle strength (g/tex) with						
1.	Uniformity ratio	Positive	S	Rajan (1997)		
		Negative	S	Tuteja <i>et al.</i> (2005) Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)		
			NS	Neelima (2002)		
			2.	Lint yield plant ⁻¹ (g)	Positive	S
Negative	S	Mandloi <i>et al.</i> (2003)				
	NS	Rao (2008) Rajanna <i>et al.</i> (2011)				
XIII. Uniformity ratio with						
1.	Micronaire value	Positive	S	Chandrashekhar <i>et al.</i> (2016)		
2.	Lint yield plant ⁻¹ (g)	Positive	S	Rajanna <i>et al.</i> (2011)		
		Negative	NS	Dedaniya and Pethani (1994) Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014)		

Note: S: Significant

NS: Non-significant

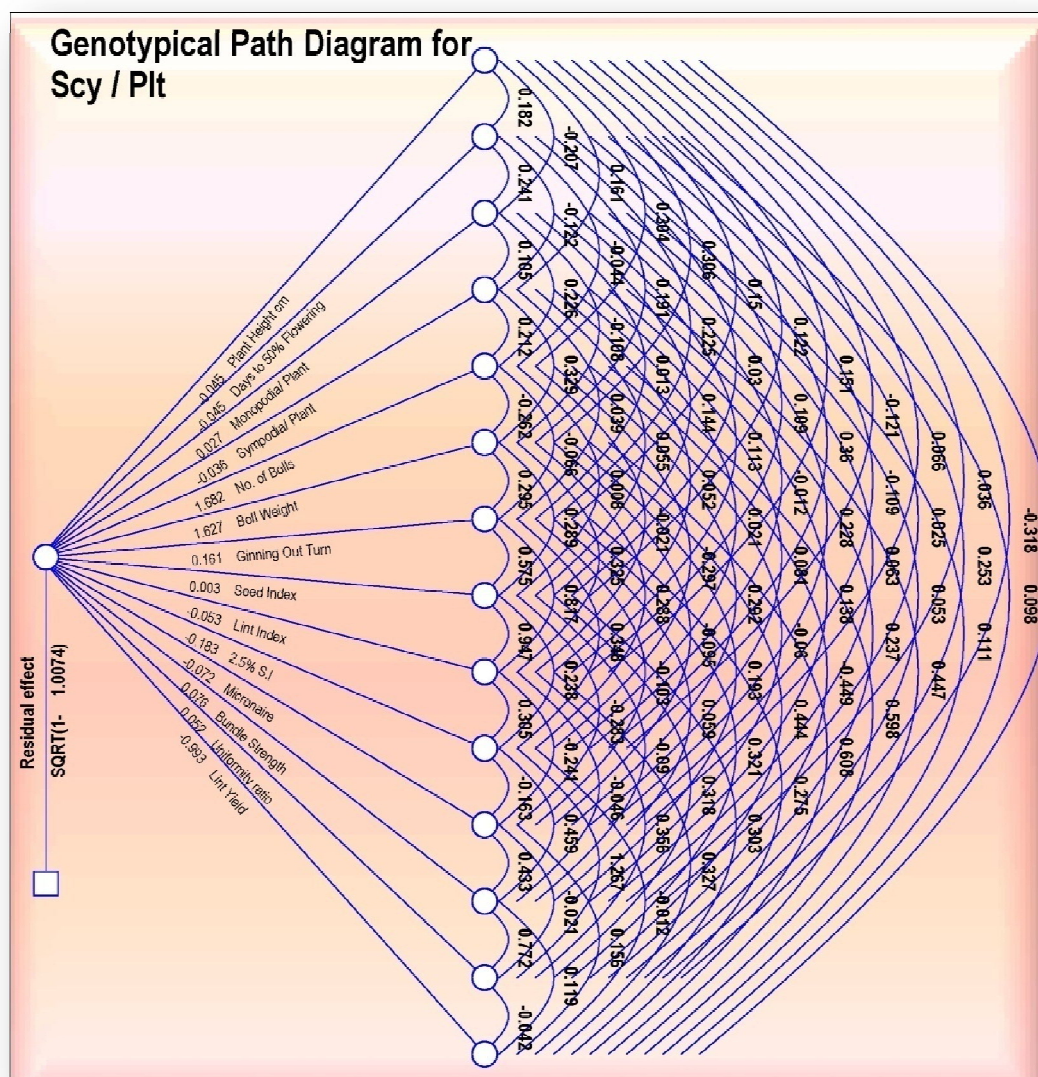


Fig. 4.2. Genotypic path diagram showing cause and effect relationship of yield components with seed cotton yield per plant in cotton (*G. hirsutum* L.)

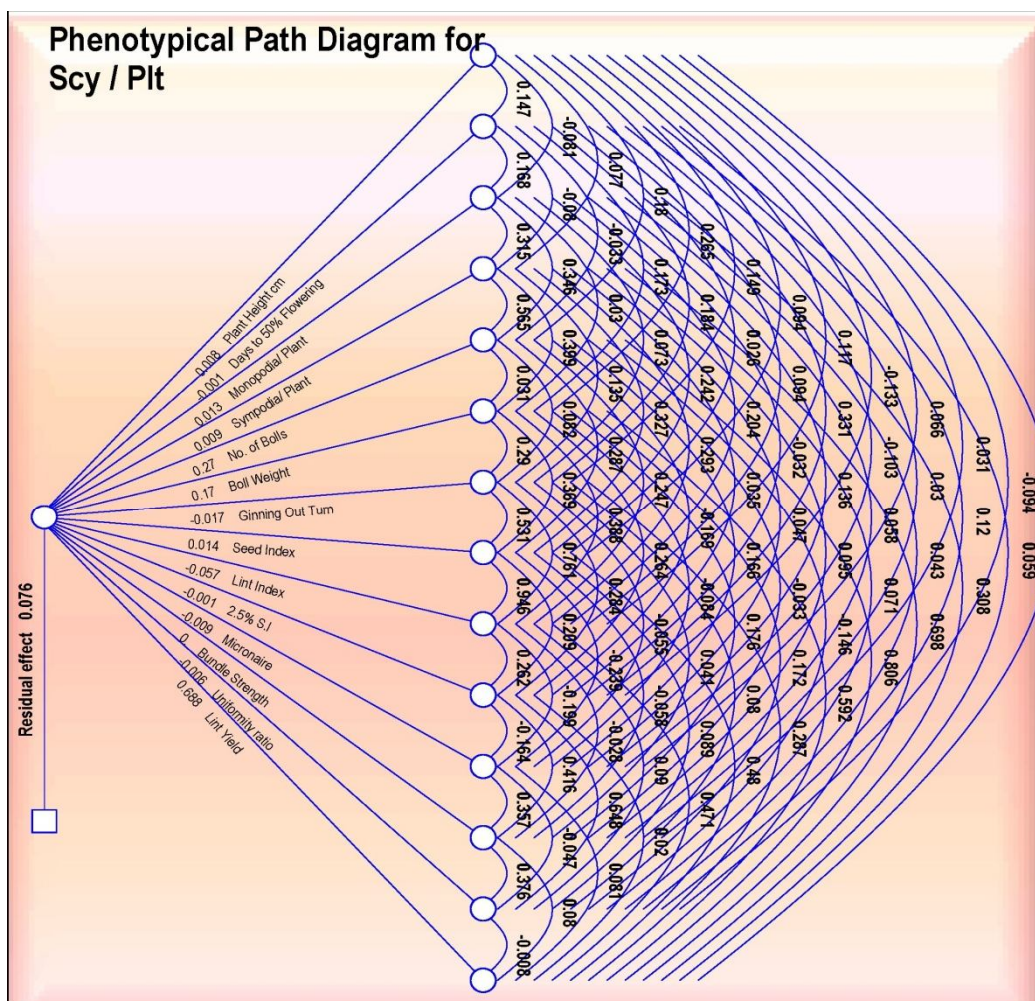


Fig. 4.1. Phenotypic path diagram showing cause and effect relationship of yield components with seed cotton yield per plant in cotton (*G. hirsutum* L.)

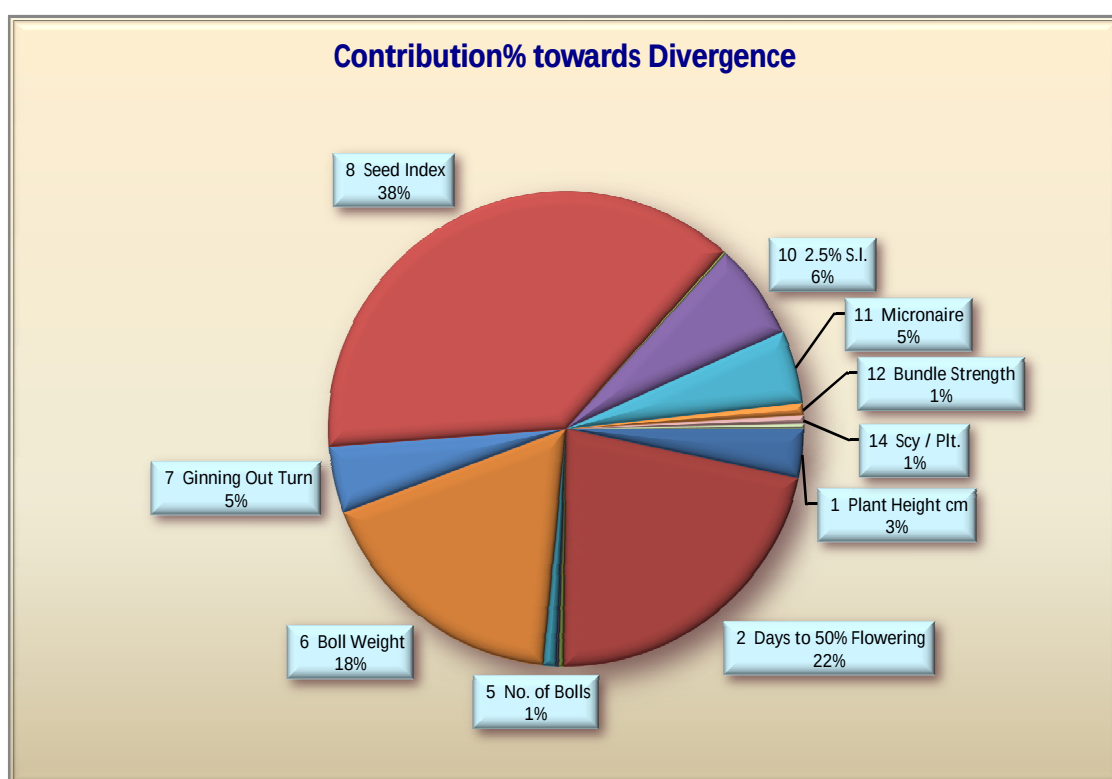


Fig. 4.3. Contribution of different characters towards genetic divergence in 50 cotton (*G. hirsutum* L.) genotypes

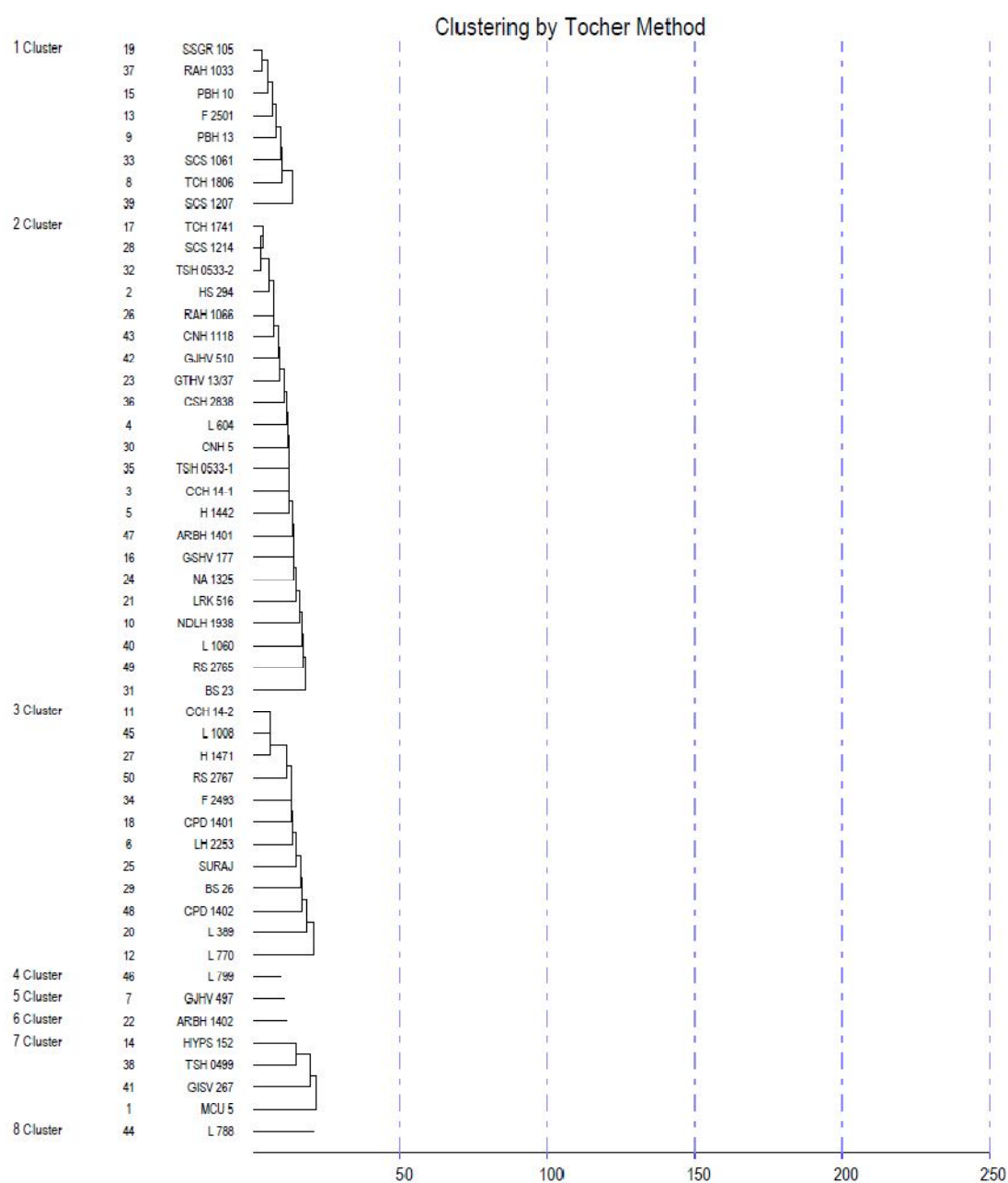


Fig. 4.4. Dendrogram showing relationship among 50 cotton (*G. hirsutum* L.) genotypes in eight clusters based on Mahalanobis D^2 values

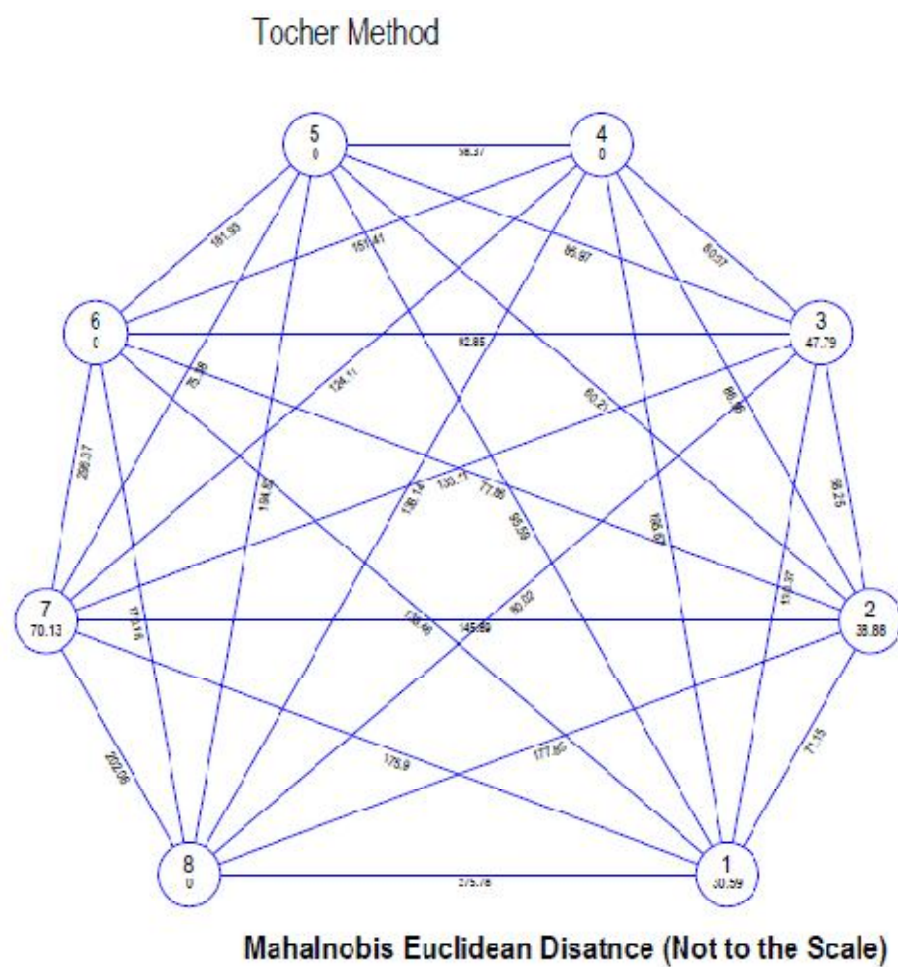


Fig. 4.5. Intra- and inter-cluster distance of 50 cotton (*G. hirsutum* L.) genotypes in 8 clusters based on Euclidean distance

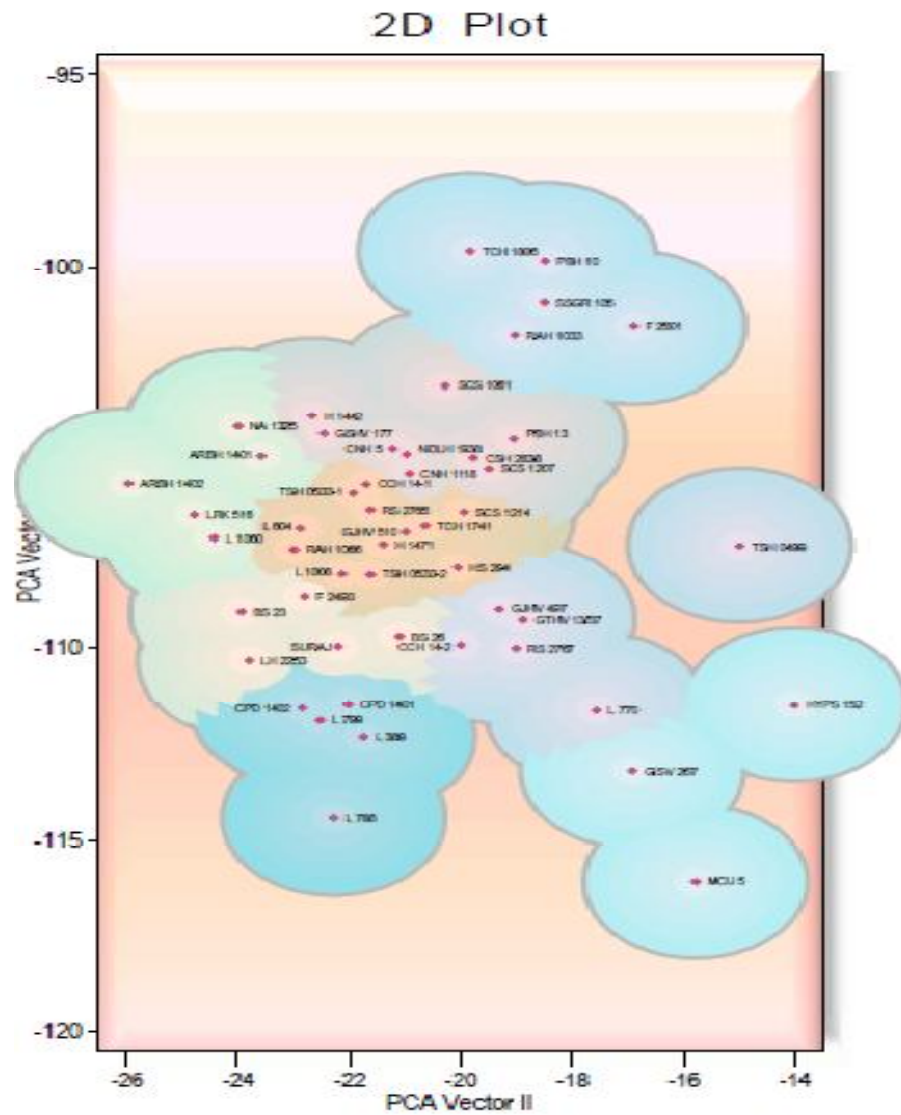


Fig. 4.6. Two dimensional graph showing relative position of 50 cotton (*G. hirsutum* L.) genotypes based on PCA scores

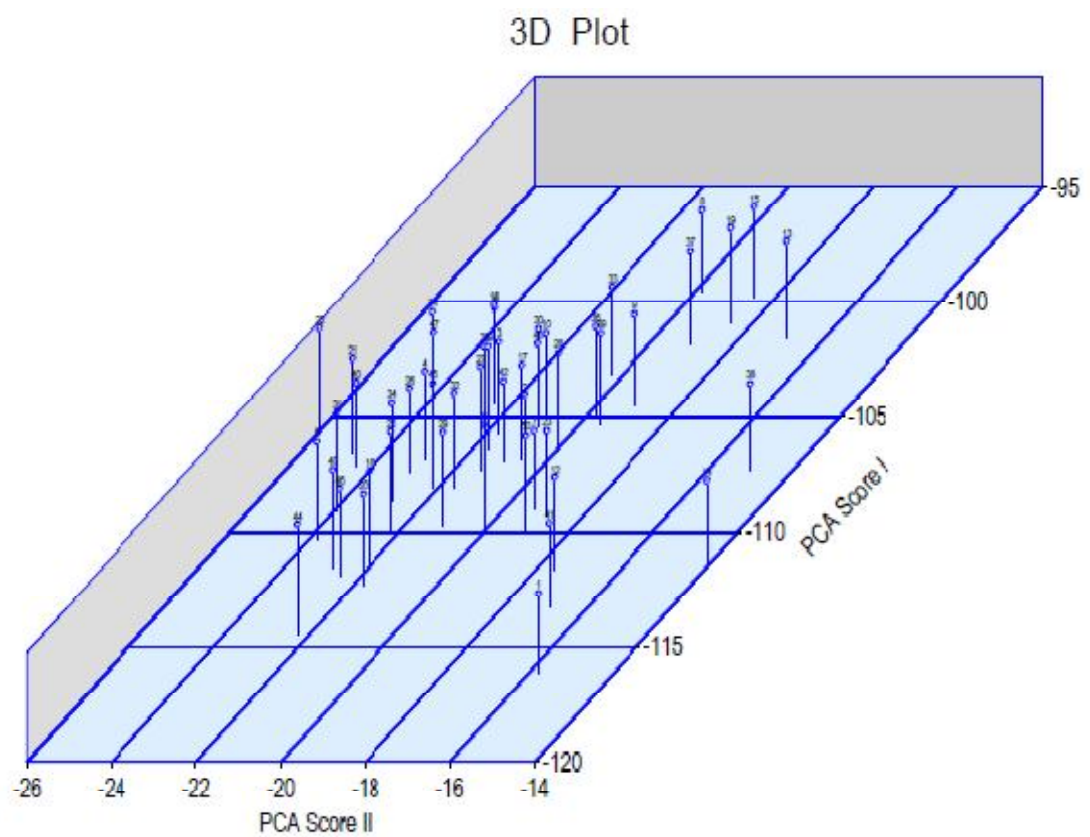


Fig. 4.7. Three dimensional graph showing relative position of 50 cotton (*G. hirsutum* L.) genotypes based on PCA scores

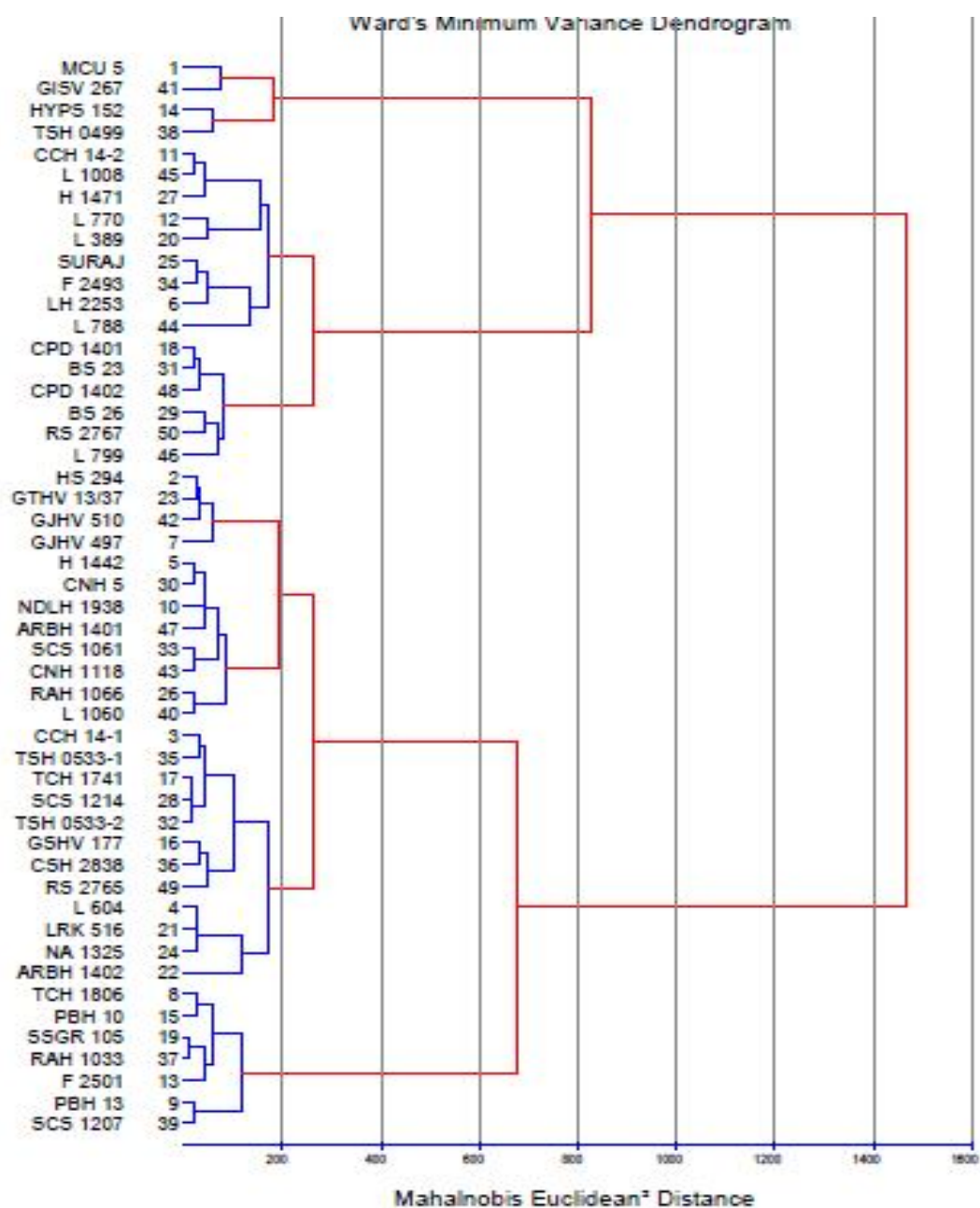


Fig. 4.8. Dendrogram showing relationship among 50 cotton (*G. hirsutum* L.) genotypes in eight clusters based on Mahalanobis Euclidean² distance

