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

By
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B.Sc. (Ag.)

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

**MASTER OF SCIENCE IN AGRICULTURE
(GENETICS AND PLANT BREEDING)**

CHAIRPERSON: Dr. Y. SATISH

DEPARTMENT OF GENETICS AND PLANT BREEDING

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2015

CERTIFICATE

Mr. PRADEEP SEEPANA has satisfactorily prosecuted the course of research and that thesis entitled **"GENETIC DIVERGENCE IN UPLAND COTTON** (*Gossypium hirsutum* L.)**"** submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that neither the thesis nor its part thereof has been previously submitted by him for a degree of any university.

Date:

(Y.SATISH)
Chairperson
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CERTIFICATE

This is to certify that thesis entitled **"GENETIC DIVERGENCE IN UPLAND COTTON** (*Gossypium hirsutum* L.)**"** submitted in partial fulfilment of the requirements for the degree of 'Master of science in Agriculture' in the major field of **Genetics and Plant Breeding** of the Acharya N. G. Ranga Agricultural University, Hyderabad, is a record of the bonafide original research work carried out by **Mr. PRADEEP SEEPANA** under our guidance and supervision.

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

Thesis approved by the student's advisory committee

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Place:

Date: **(PRADEEP SEEPANA)**

DECLARATION

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

Place: **(PRADEEP SEEPANA)**

Date: **I. D. No. BAM-13-14**

LIST OF SYMBOLS AND ABBREVIATIONS

%	:	Per cent
*	:	Significance at 5% level
**	:	Significance at 1% level
/ or $^{-1}$	:	Per
AICRP	:	All India Coordinated Research Project
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
et al.,	:	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.e.,	:	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
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

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ABSTRACT

Name of the Author : **S. PRADEEP**

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

Faculty : **AGRICULTURE**

Major Field of study : **GENETICS AND PLANT BREEDING**

Major Advisor : **Dr. Y. SATISH**

University : **ACHARYA N.G. RANGA AGRICULTURAL UNIVERSITY**

Year of submission : **2015**

The present investigation was carried out during *Kharif,* 2014-15 at Regional Agricultural Research Station, Lam farm, Guntur, Andhra Pradesh to characterize 60 genotypes of cotton (*Gossypium hirsutum* L.), 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, 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 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, number of monopodia per plant, number of bolls per plant, lint index, seed cotton yield per plant and lint yield per plant indicating the predominance of additive gene action and hence, direct phenotypic selection may be useful with respect to these traits.

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

The path analysis indicated that plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, ginning out turn, seed index, lint index 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.

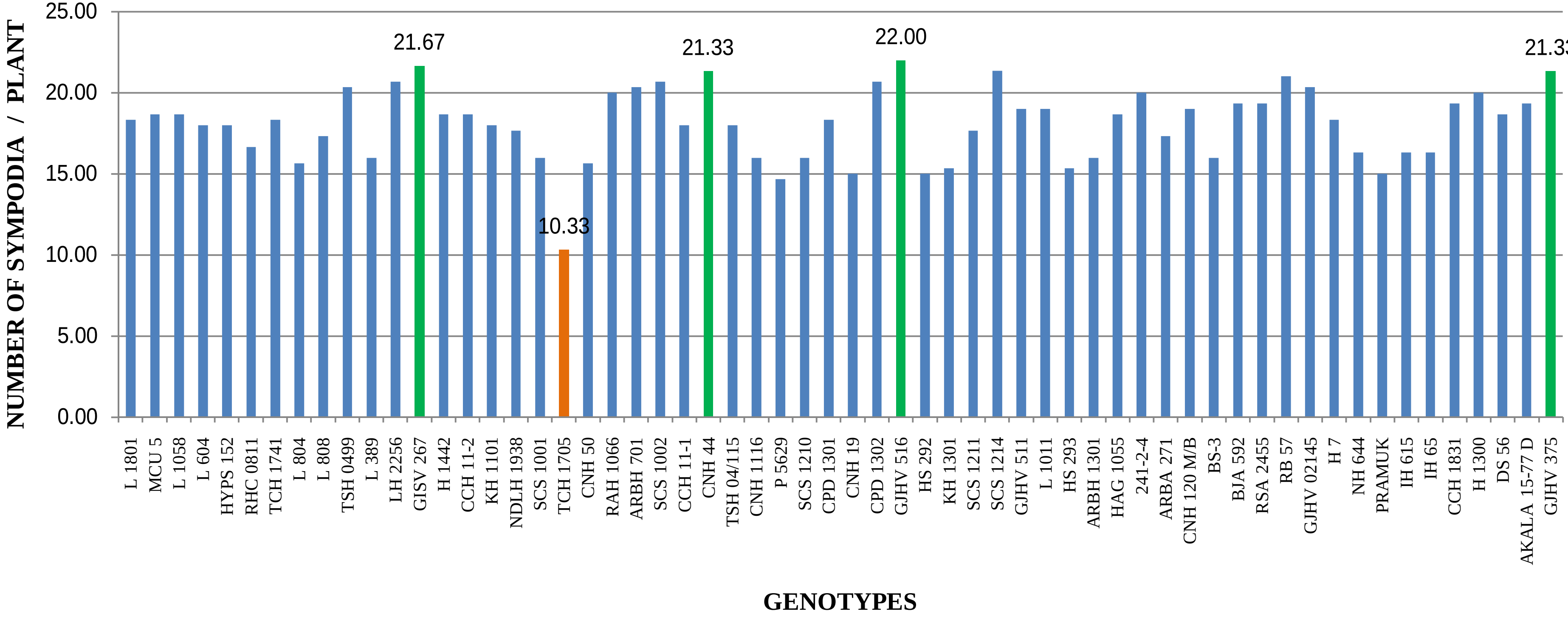
The results of multivariate analysis indicated the presence of considerable genetic divergence among the 60 genotypes studied. The 60 genotypes were grouped into 11 clusters in case of D^2 analysis indicating that the genetic diversity and geographical diversity were not related.

By Mahalanobi's D^2 statistic, it could be inferred that 2.5% span length, seed index, days to 50% flowering, micronaire, number of monopodia per plant and bundle strength 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 IX (HYPS 152) and cluster X (IH 65), between genotypes of cluster IX (HYPS 152) and cluster XI (L 389), between the genotypes of cluster VII (TCH 1705) and cluster XI (L 389), between the genotypes of cluster VIII (GISV 267) and cluster X (IH 65) after confirming their general combining ability.

Principal component analysis identified seven principal components (PCs), which contributed 78.696 per cent of cumulative variance. The significant factors loaded in PC1 towards maximum genetic divergence were plant height, ginning out turn, lint yield per plant, number of bolls per plant, 2.5% span length, seed index, lint index, number of monopodia per plant, days to 50% flowering, seed cotton yield per plant, number of sympodia per plant and boll weight. 2D and 3D graphs showed wide divergence between GISV 267, MCU 5, HYPS 152, TCH 1741, CNH 120 M/B, LH 2256 and IH 65 signifying their usefulness in cotton breeding to develop high heterotic hybrids.

The genotypes HYPS 152, GISV 267, MCU 5, L 389 and TCH 1741 showed maximum inter-cluster distance in Mahalanobi's D^2 analysis, principal component 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.

CONTENTS



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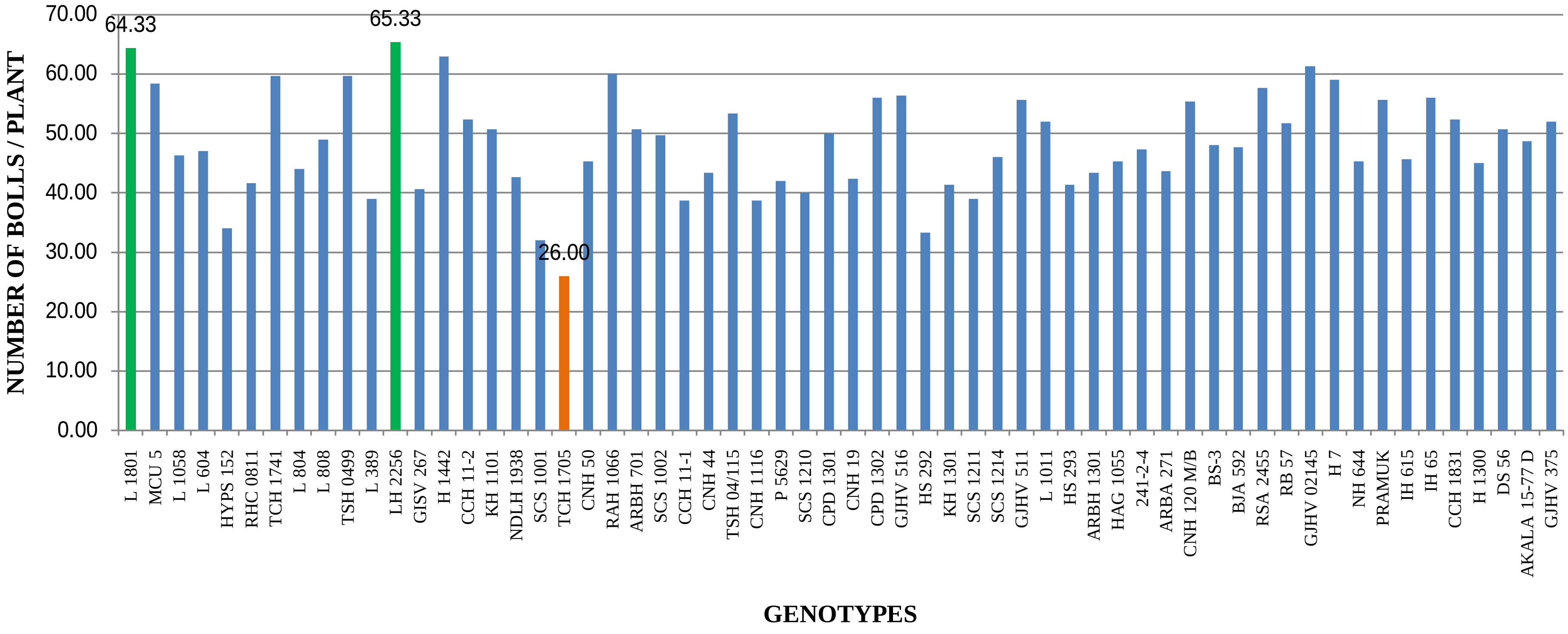

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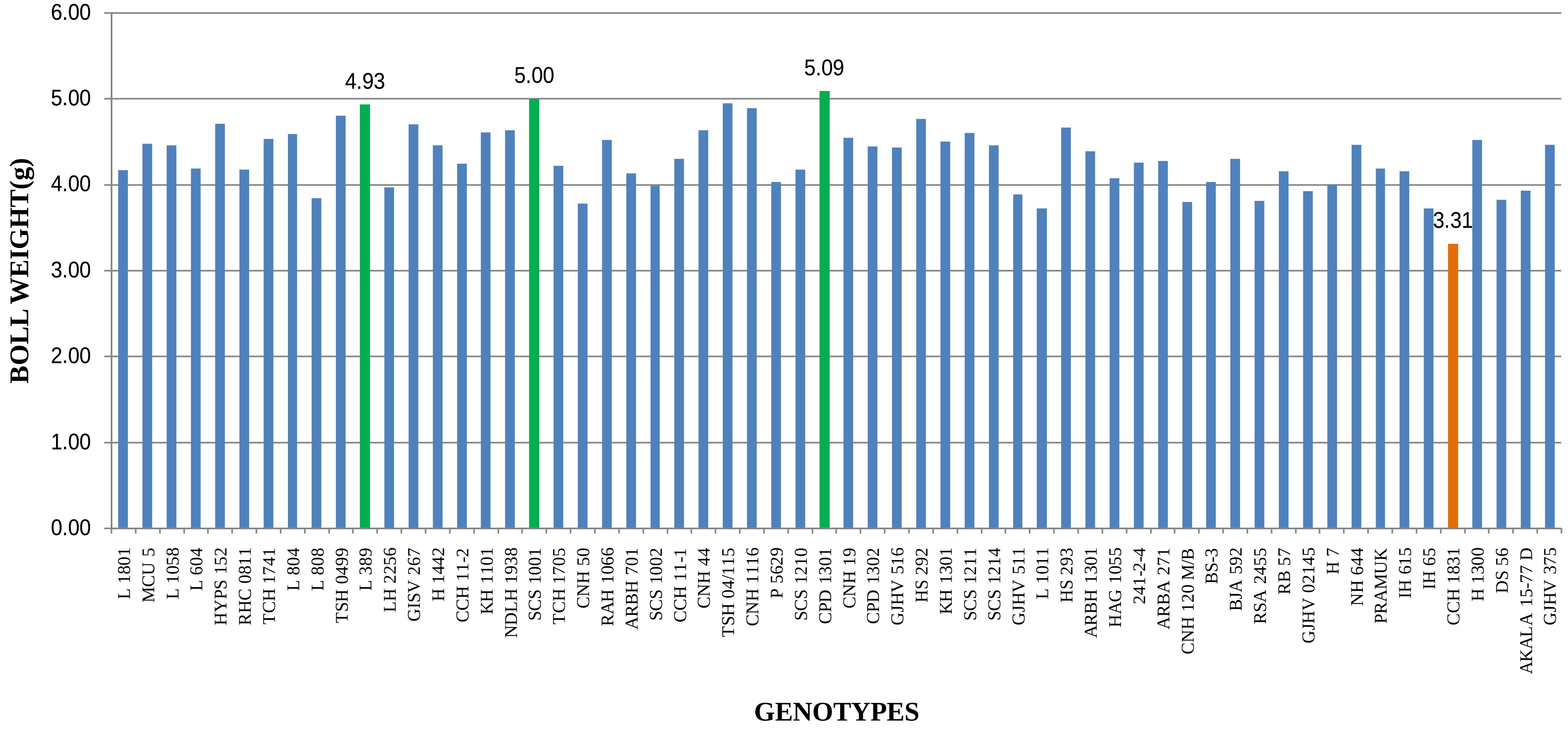

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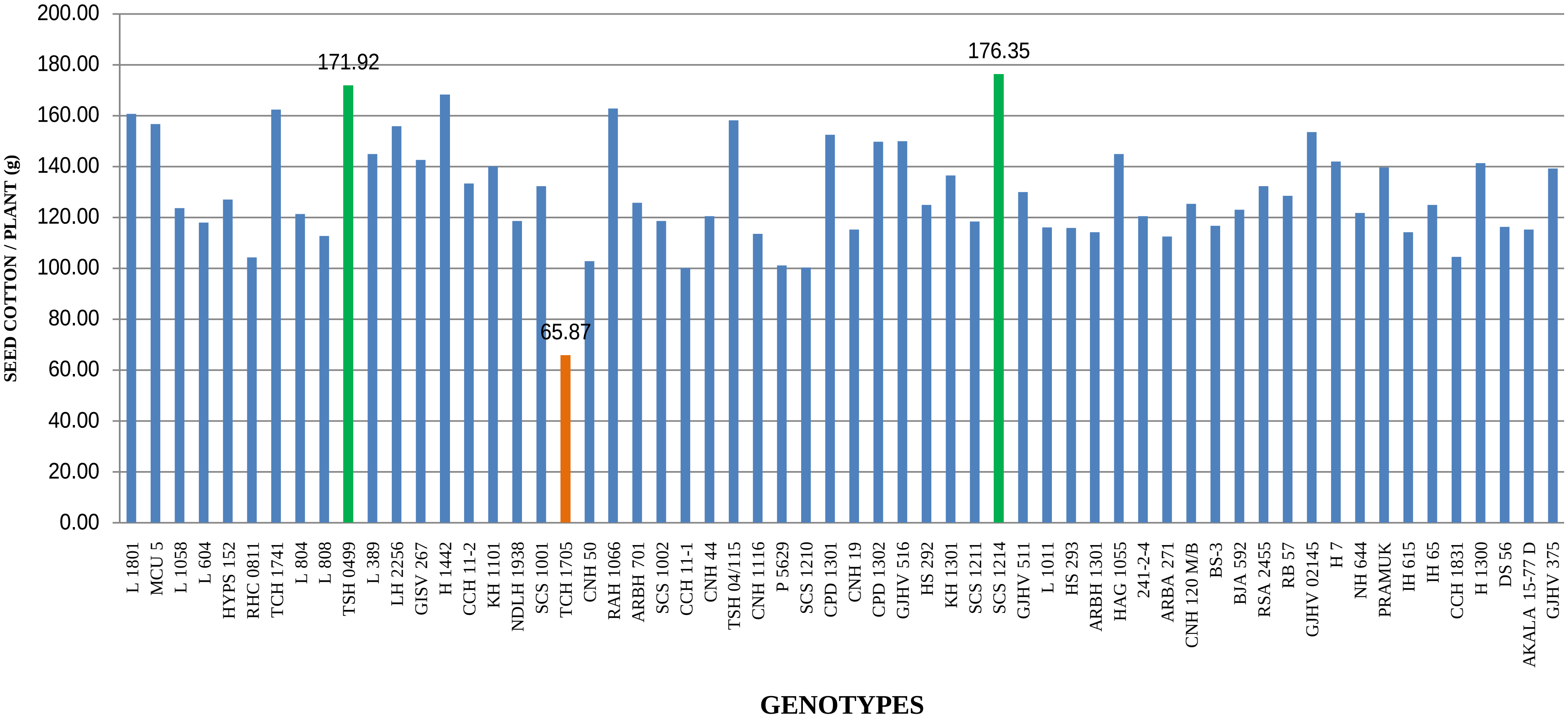

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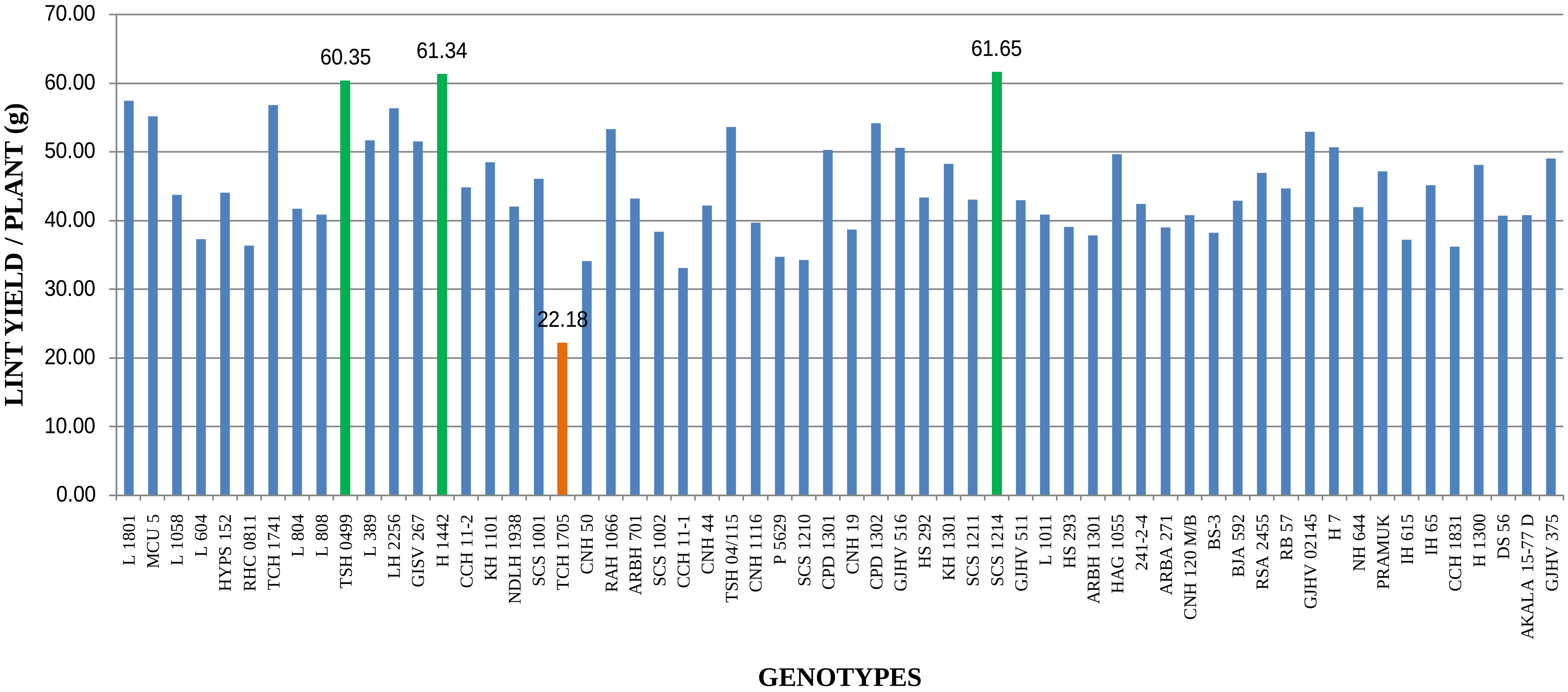

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Chapter I

INTRODUCTION

Cotton (*Gossypium hirsutum* L.), is the most important fibre crop and back bone of textile industry of India. It is the king of apparel fibres, since times immemorial popularly called as "White gold" and has played a pivotal role in the history and civilization of mankind. It alone accounts for 70 per cent of total fibre utilization in textile sector with approximately 38 per cent of the country's export. India has a pride 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 family Malvaceae and genus *Gossypium*, consisting about 50 species. Of these, commercial cotton fiber is produced from only four species viz., *Gossypium hirsutum L.* (n=26, AAD_1D_1), *Gossypium barbadense L.* (n=26, AAD_2D_2), *Gossypium arboreum* L. (n=13, A_1A_1) and *Gossypium herbaceum L.* (n=13, A_2A_2). The former two are tetraploids and known as new world cottons, the later two are diploids and known as old world or Desi or Asiatic cottons.

Among four linted cotton species, upland cotton (*Gossypium hirsutum* L.) 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 12.655 million hectares and production of 40.0 million bales of cotton. Average productivity in India is 537 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 0.736 million hectares with an annual production of 2.11 million bales (170kg each) and productivity of 624 kg ha^{-1} lint (AICRP, Annual Report, 2014-15).

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

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

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

1. To assess the genetic diversity among the American cotton (G. *hirsutum* L.) genotypes

2. To assess the variability, genetic advance, heritability for seed cotton yield and fibre quality traits

3. To assess the character association, direct and indirect effects of yield component traits and fibre quality traits on seed cotton yield

Chapter III

MATERIALS AND METHODS

The present investigation entitled, "Genetic divergence in upland cotton (*Gossypium hirsutum* L.)" was taken up during *Kharif*, 2014-15 at Regional Agricultural Research Station, Lam Farm, Guntur, Andhra Pradesh. The site of the experiment is situated at $16^0 2'$ North and $80^0 3'$ East longitude at a height of 31.5 m above mean sea level. The soils are black cotton type with clay texture.

3.1 MATERIALS

The experimental material used in the present study consisted of 60 genotypes of cotton (*Gossypium hirsutum* L.), which were obtained from different cotton research centers across the country. The information on source of these 60 genotypes is presented in Table 3.1.

3.2 METHODS

3.2.1 Experimental Technique

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

Table 3.2. Experimental details of the present investigation

Location	**Regional Agricultural Research Station, Lam Farm, Guntur, Andhra Pradesh**
Season	*Kharif*, 2014-15
Entries	60 Genotypes of cotton (*Gossypium hirsutum* L.)
Design	Randomized complete block design
Replications	3
Plot size	1 row of 6 m length
Spacing	105 cm between rows and 60 cm within rows
Fertilizers	120 N kg : 60 P_2O_5 kg : 40 K_2O kg ha^{-1}
Plant protection	Need based plant protection measures were taken up against pest and diseases.

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

S. No.	NAME OF THE GENOTYPE	SOURCE
1	L 1801	ANGRAU, Lam
2	MCU 5	TNAU, Coimbotore
3	L 1508	ANGRAU, Lam
4	L 604	ANGRAU, Lam
5	HYPS 152	AICCIP.
6	RHC 0811	MPKV, Rahuri
7	TCH 1741	TNAU, Coimbotore
8	L 804	ANGRAU, Lam
9	L 808	ANGRAU, Lam
10	TSH 0499	TNAU, Srivalliputtur
11	L 389	ANGRAU, Lam
12	LH 2256	PAU, Ludhiana
13	GISV 267	NAU, Surat
14	H 1442	CCSHAU, Hissar
15	CCH 11-2	CICR, Coimbotore
16	KH 1101	JNKVV, Khandwa.
17	NDLH 1938	ANGRAU, Nandyal
18	SCS 1001	UAS, Siriguppa.
19	TCH 1705	TNAU, Coimbotore
20	CNH 50	CICR, Nagpur
21	RAH 1066	RAU, Sriganganagar
22	ARBH 701	UAS, Arabhavi
23	SCS1002	UAS, Siriguppa.
24	CCH 11-1	CICR, Coimbotore
25	CNH 44	CICR, Nagpur
26	TSH 04/115	TNAU, Srivalliputtur
27	CNH 1116	CICR, Nagpur
28	P 5629	IARI, New Delhi.
29	SCS 1210	UAS, Siriguppa.
30	CPD 1301	UAS, Dharwad
31	CNH 19	CICR, Nagpur

32	CPD 1302	UAS, Dharwad
33	GJHV 516	JAU, Junagarh
34	HS 292	CCSHAU, Sirsa
35	KH 1301	JNKVV, Khandwa
36	SCS 1211	UAS, Siriguppa.
37	SCS 1214	UAS, Siriguppa.
38	GJHV 511	JAU, Junagarh
39	L 1011	ANGRAU, Lam
40	HS 293	CCSHAU, Sirsa
41	ARBH 1301	UAS, Arabhavi
42	HAG 1055	UAS, Hagari.
43	241-2-4	AICCIP.
44	ARBH 271	UAS, Arabhavi
45	CNH 120 M/B	CICR, Nagpur
46	BS-3	OUAT, Bhavanipatna
47	BJA 592	AICCIP.
48	RSA 2455	AICCIP.
49	RB 57	ARS, Banswara
50	GJHV 02145	JAU, Junagarh
51	H 7	CCSHAU, Hissar
52	NH 644	MAU, Nanded
53	PRAMUK	AICCIP.
54	IH 615	RVSKVV, Indore
55	IH 65	RVSKVV, Indore
56	CCH 1831	CICR, Coimbotore
57	H 1300	CCSHAU, Hissar
58	DS 56	AICCIP.
59	AKALA 15-77D	AICCIP.
60	GJHV 375	JAU, Junagarh

3.2.2 Recording Observations

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

3.2.2.1 Plant height (cm)

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 zig zag 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 20 bolls per plot.

3.2.2.7 Ginning-out turn (%)

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

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

3.2.2.8 Seed index (g)

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

3.2.2.9 Lint index (g)

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

3.2.2.10 2.5% span length (mm)

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

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

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

3.2.2.12 Bundle strength (g/tex)

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

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

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

Where,

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

μ = General mean

b_i = Effect of i^{th} block

t_j = Effect of j^{th} genotype

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

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

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

Where, r = Number of replications

t = Number of genotypes

df = Degrees of freedom

SS = Sum of squares

MSS = Mean sum of squares

σ^2_e = Error variance

σ^2_g = Variance due to genotypes

σ^2_r = Variance due to replications

M_r = Mean squares due to replications

M_t = Mean squares due to treatments

M_e = Mean squares due to error

3.3.2 Estimation of Genetic Parameters

1. Coefficient of Variation

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

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

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

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

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

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

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

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

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

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

3. Genetic advance (GA)

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

GA = k x σ_p x h^2 (b)

GA = Genetic advance

k = selection intensity which accounts to a constant value 2.06 at 5%

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

σ_p = Phenotypic standard deviation

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

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

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

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

3.3.3 Correlation studies

Analysis of covariance

Analysis of covariance was computed by following procedure.

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

Where,

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

μ = General mean

t_i = True effect of i^{th} treatment

b_j = True effect of j^{th} block

b_{yx} = Tegression coefficient of y on x

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

e_{ij} = Random error

The structure of analysis of covariance is as follows

Source	**df**	**SS_y**	**SS_x**	**SP_{xy}**	**MSS_y**	**MSS_x**	**MSP_{xy}**
Replications	(r-1)	RSS_Y	RSS_X	RSP_{XY}	RMS_Y	RMS_X	MSP_r
Genotypes	(t-1)	TSS_Y	TSS_X	TSP_{XY}	TMS_Y	RMS_X	MSP_t
Error	(r-1)(t-1)	ESS_Y	ESS_X	ESP_{XY}	EMS_Y	RMS_X	MSP_e

Where,

df = Degrees of freedom

SP = Sum of products

SS = Sum of squares

MSP = Mean sum of products

MSS = Mean sum of squares

r = Number of replications

t = Number of genotypes

Genotypic covariance $(X_i.X_j)g$ = (RMSP – EMSP) / r

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

RMSP = Mean sum of products of genotypes

EMSP = Error mean sum of products = environmental covariance

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

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

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

e_ie_j = Environmental covariance between i^{th} and j^{th} characters

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

Phenotypic coefficients of correlation (r_p)

$$r(x_i.x_j)_p = \frac{Cov(x_i.x_j)p}{(V(x_i)\,p \times V(x_j)\,p)^{1/2}}$$

Genotypic coefficient of correlation (r_g)

$$r(x_i.x_j)_g = \frac{Cov(x_i.x_j)g}{(V(x_i)\,g \times V(x_j)\,g)^{1/2}}$$

Where,

$r\,(x_i.x_j)_g$ = Genotypic correlation between i^{th} and j^{th} characters

COV $(x_i.x_j)_g$ = Genotypic covariance between i^{th} and j^{th}characters

$V(x_i)_g$ = Genotype variance of i^{th} character

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

r $(x_i.x_j)_g$ = Phenotypic correlation between i^{th} and j^{th} characters

COV $(x_i.x_j)_p$ = Phenotypic covariance between i^{th} and j^{th}characters

$V(X_i)_p$ = Phenotype variance of i^{th} character

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

3.3.3.1 Test of significance

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

3.3.4 Path Coefficient Analysis

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

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

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

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

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

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

Where,

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

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

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

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

A **C** **B**

$$\begin{bmatrix} r_{1y} \\ r_{2y} \\ . \\ . \\ r_{ky} \end{bmatrix} = \begin{bmatrix} 1 & r_{12} & r_{13} & . & . & . & r_{1k} \\ r_{21} & 1 & r_{23} & . & . & . & r_{2k} \\ . & . & . & . & . & . & . \\ . & . & . & . & . & . & . \\ r_{k1} & r_{k2} & r_{k3} & . & . & . & 1 \end{bmatrix} \begin{bmatrix} P_{1y} \\ P_{2y} \\ . \\ . \\ P_{ky} \end{bmatrix}$$

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

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

Then direct effects were calculated as follows,

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

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

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

3.3.4.1 Residual effect

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

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

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

3.3.5 Genetic Divergence

3.3.5.1 Mahalanobi's D^2 analysis

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

3.3.5.1.1 Test of significance

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

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

Where,

$\wedge$ = Wilk's criterion

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

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

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

Where,

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

n = degrees of freedom for error + varieties

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

P = Number of variables or characters (16)

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

e = 2.7183

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

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

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

Transformation of correlated variables

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

3.3.5.1.2 Computation of D^2 values

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

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

Where,

Y_i^t is uncorrelated mean value of 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 (16) degrees of freedom where p (16) is the number of characters considered. The tabulated value of χ^2 at 5 per cent level of significance for 16 degrees of freedom being 26.29 which is lower than calculated values of D^2 in most cases clearly shows that most of D^2 values are significant.

3.3.5.1.4 Contribution of individual characters towards divergence

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

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

Where,

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

M = All possible combinations of number of genotypes considered.

3.3.5.1.5 Grouping of genotypes into various clusters

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

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

3.3.5.1.6 Average intra- cluster distance

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

3.3.5.1.7 Average inter- cluster distance

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

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

Where,

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

3.3.5.2 Principal component analysis and cluster analysis

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

3.3.5.2.1 Eigen values and eigen vectors

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

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

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

The principal components were identified by the following procedure.

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

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

Where,

A_{ij} are found such that Y_j is uncorrelated Y_1, $Y_{2},$……..Y_{j-1} the j^{th} largest variance. The A_{ij} are the elements of the normalized eigen vector associated with largest j^{th} eigen value. The variance of the j^{th} principal component of the λ_j and the total system variance trace (S) = $\lambda_1+\lambda_2 +\ldots+ \lambda_p$. The importance of the j^{th} principal component is given by

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

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

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

Where,

S_i is the standard deviation of X_i.

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

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

Where,

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

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

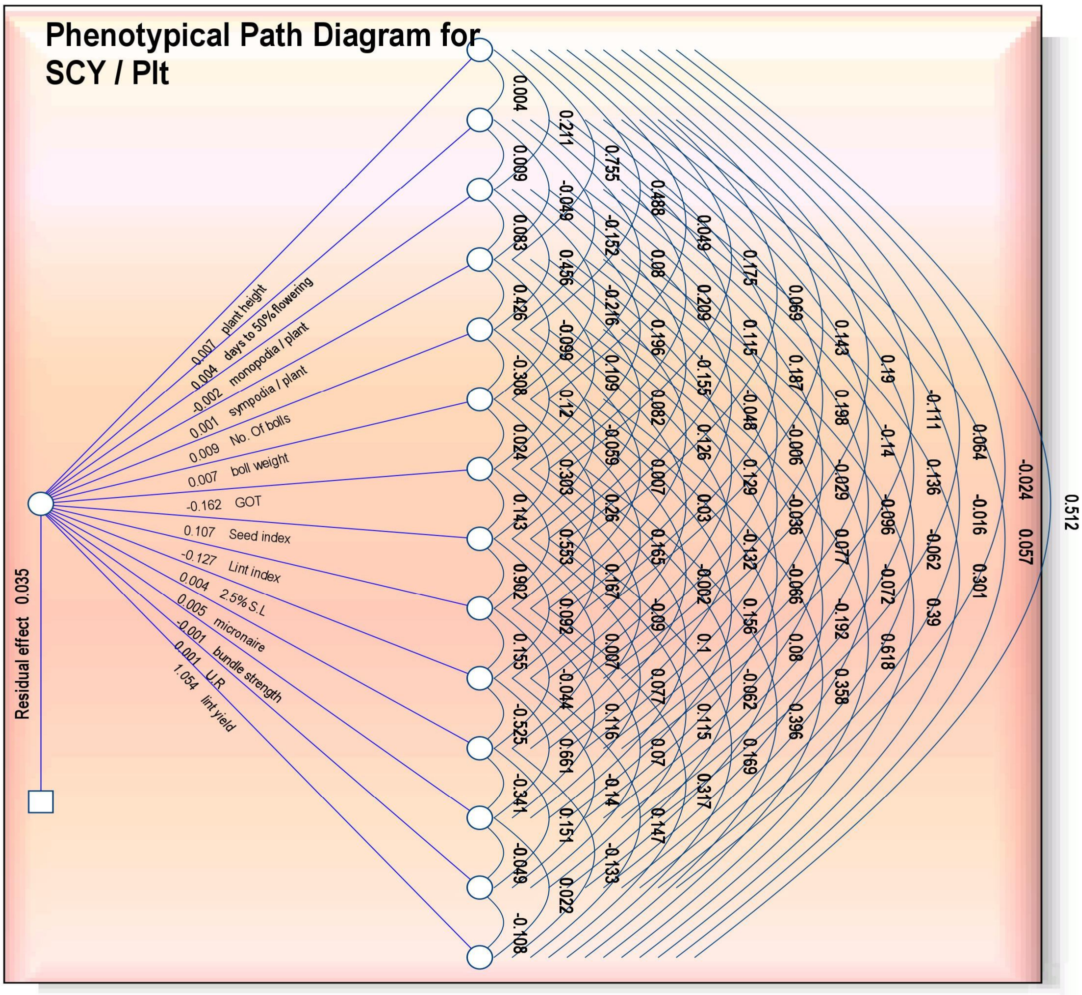

Fig. 4.6. Phenotypic path diagram showing cause and effect relationship of yield components with seed cotton yield per plant in cotton (*Gossypium hirsutum* L.)

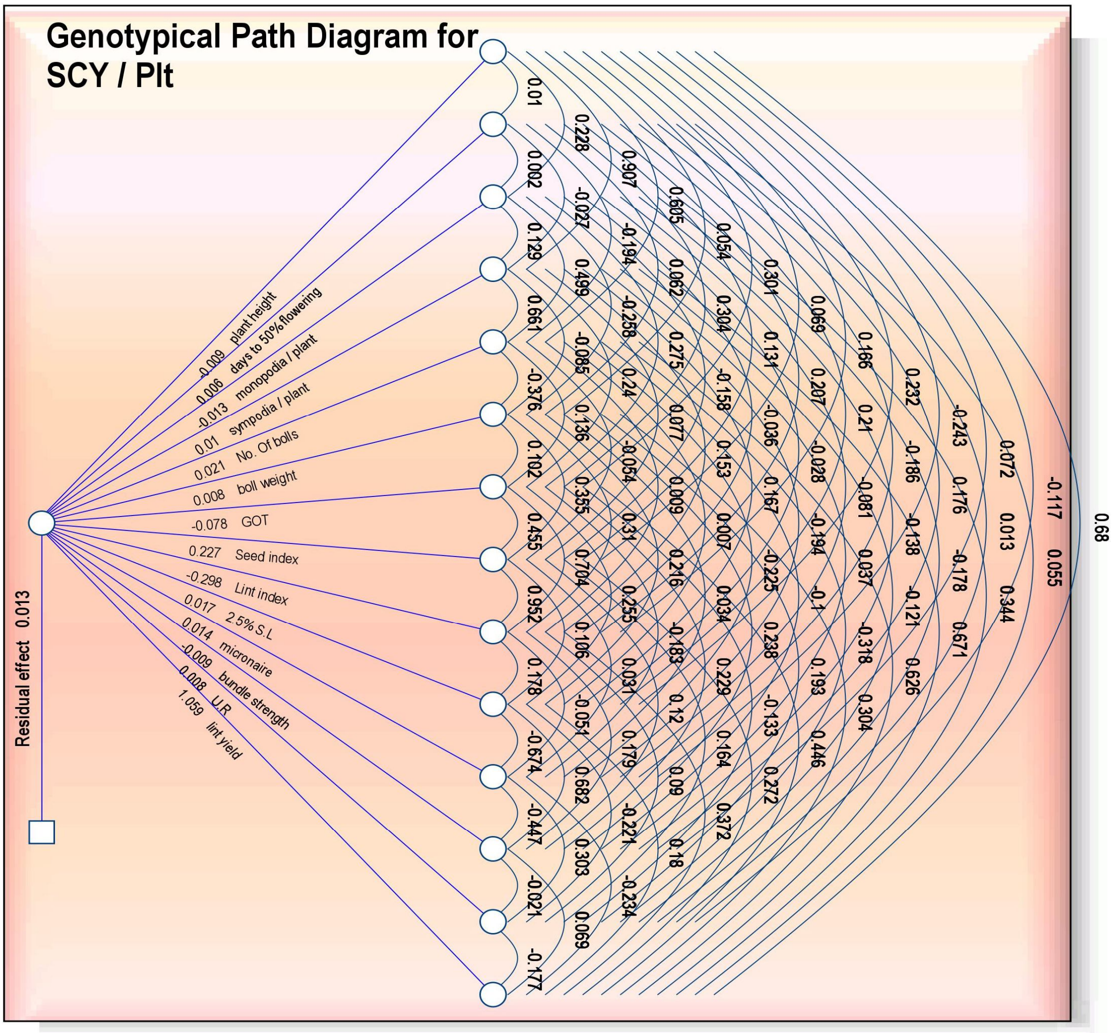

Fig. 4.7. Genotypic path diagram showing cause and effect relationship of yield components with seed cotton yield per plant in cotton (*Gossypium hirsutum* L.)

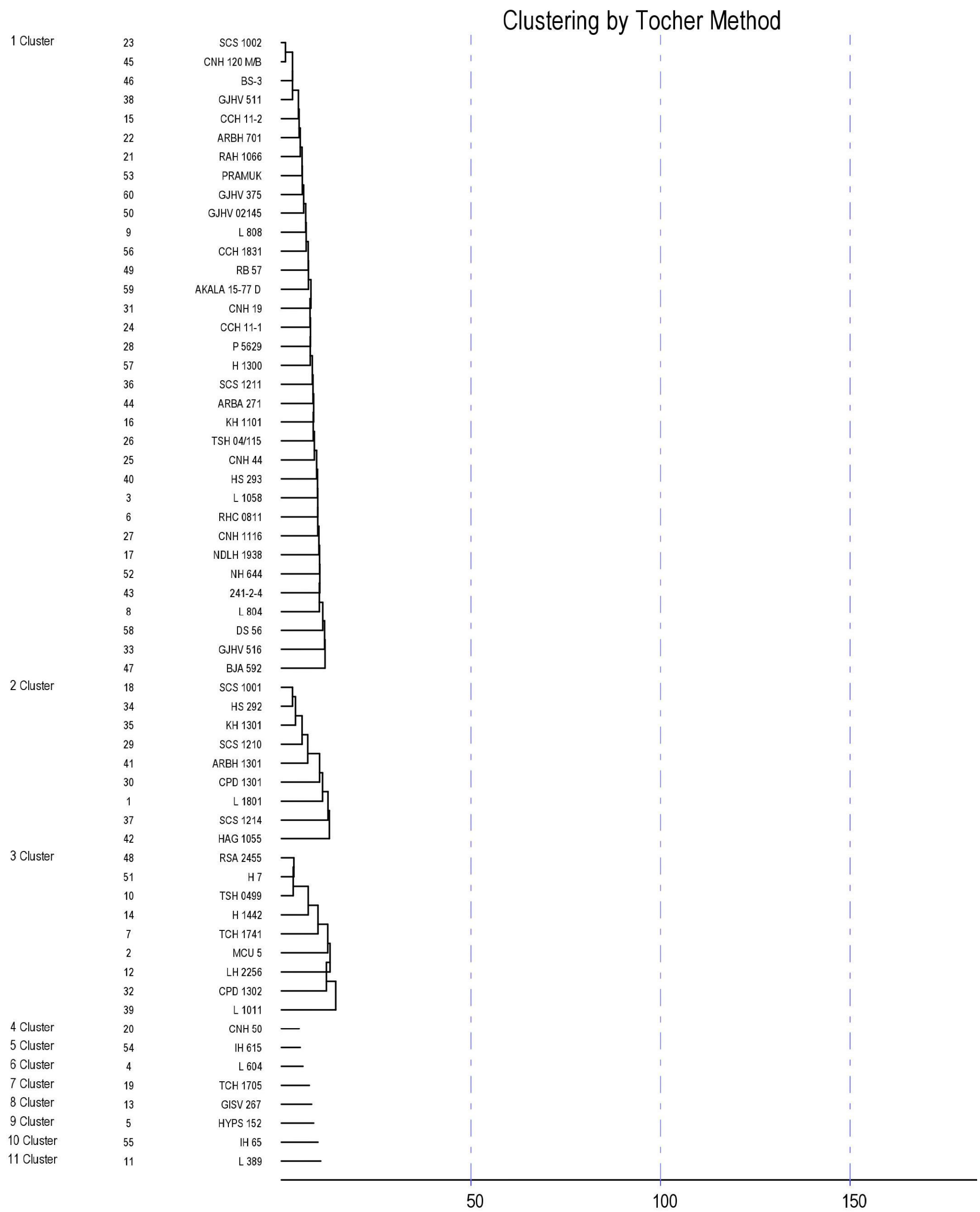

Fig. 4.8. Dendrogram showing relationship among 60 cotton (*Gossypium hirsutum* L.) genotypes in eight clusters based on Mahalanobis' D^2 values

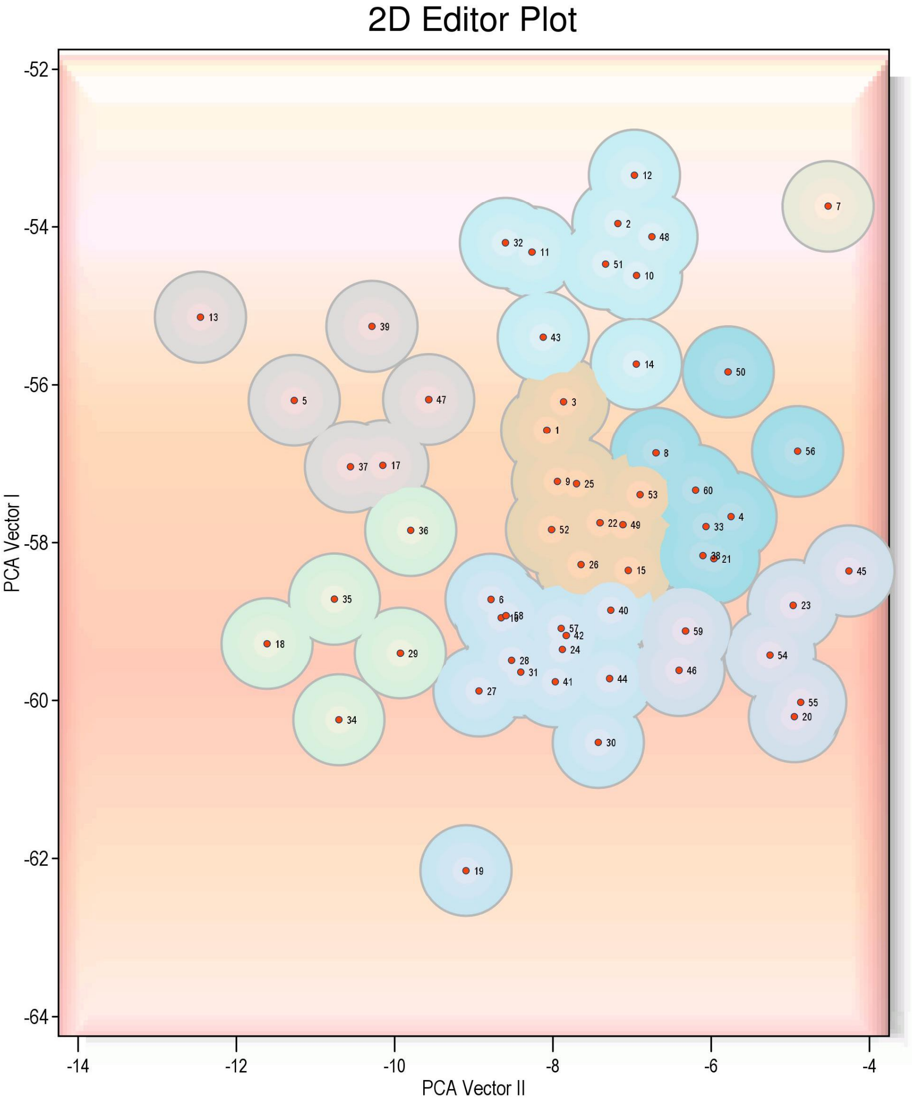

Fig. 4.10. Two dimensional graph showing relative position of 60 cotton (*Gossypium hirsutum* L.) **genotypes based on PCA scores**

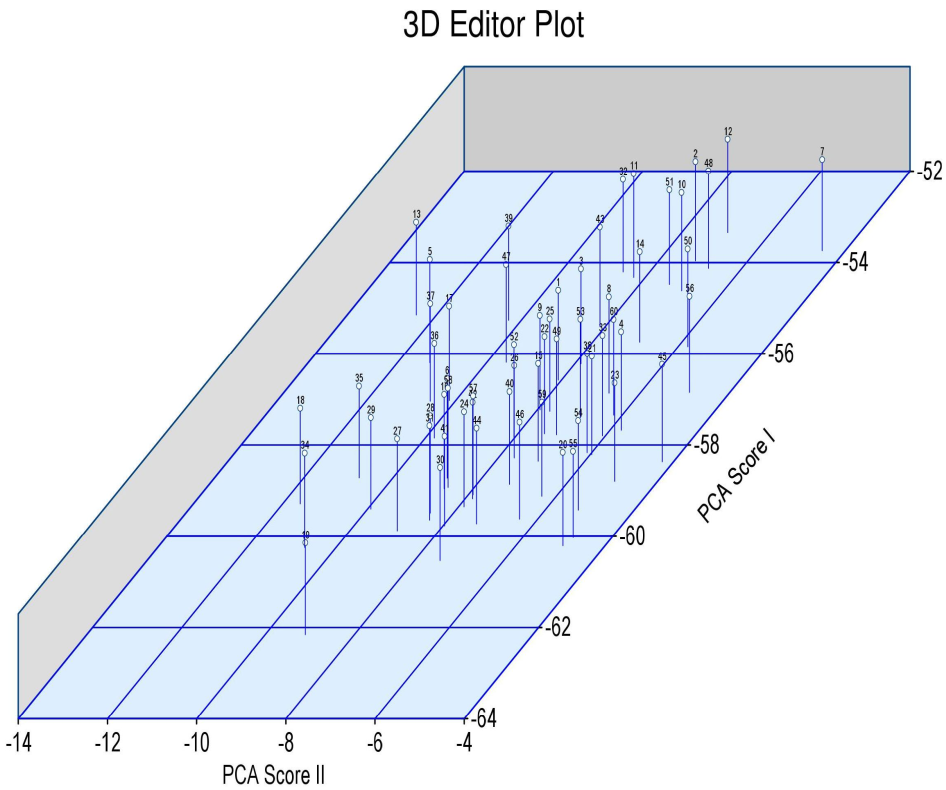

Fig. 4.11. Three dimensional graph showing relative position of 60 cotton (*Gossypium hirsutum* L.) genotypes based on PCA scores

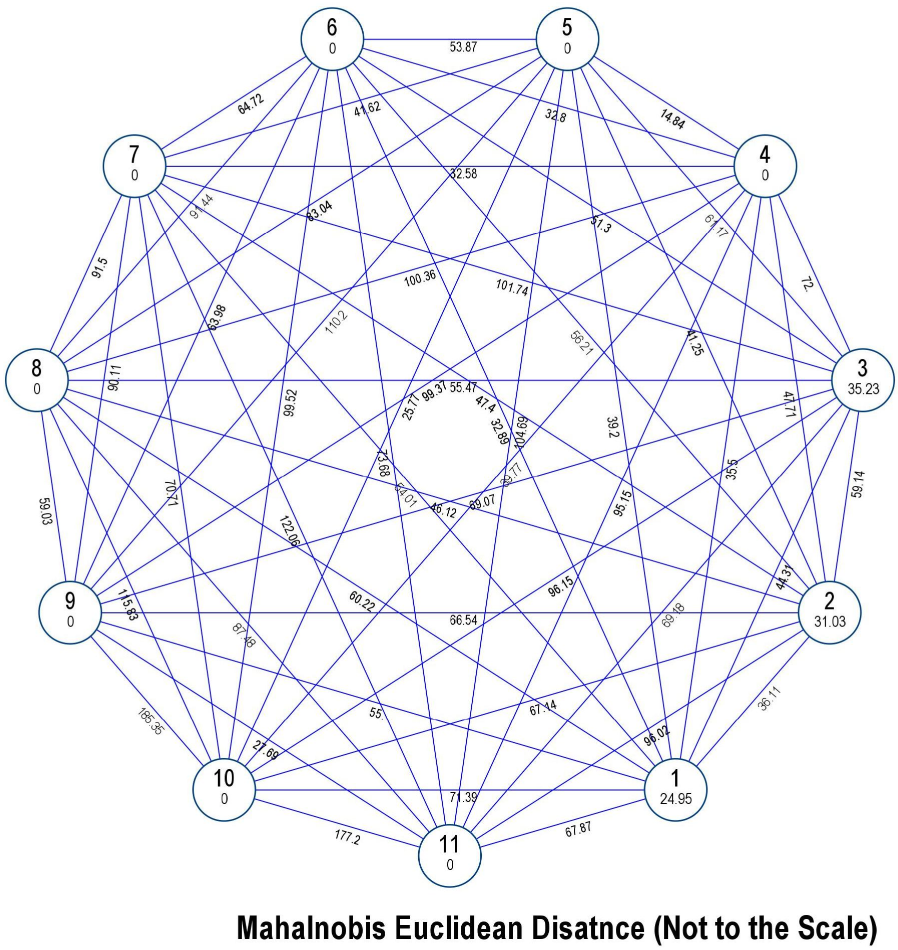

Fig. 4.9. Intra-and inter-cluster distance of 60 cotton (*Gossypium hirsutum* L) in 11 clusters based on Euclidean ^{2} distance

Table 4.2. Analysis of variance for yield and yield components in cotton (*Gossypium hirsutum* L .)

Source	d.f.	Plant height(cm)	Days to 50% flowering	No. of monopodia / plant	No. of sympodia / plant	No. of bolls / plant	Boll weight (g)	Ginning-out-turn (%)	Seed index (g)
Mean squares									
Replications	2	28.950	2.839	0.150	11.717	2.822	0.150	0.260	0.595
Varieties	59	694.778**	56.625**	1.412**	15.060**	211.626**	0.407**	3.827**	3.195**
Error	118	59.396	3.217	0.076	3.485	14.568	0.055	0.840	0.257

Source	d.f.	Lint index (g)	2.5% span length (mm)	Micronaire (10^{-6} g/in)	Bundle strength (g/tex)	Uniformity ratio	Seed cotton yield / plant (g)	Lint yield /plant (g)
Mean squares								
Replications	2	0.082	0.158	0.041	0.464	0.422	95.276	15.698
Varieties	59	1.352**	12.892**	0.542**	5.571**	3.540**	1328.144**	180.939**
Error	118	0.056	0.549	0.056	0.514	1.405	160.984	21.902

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

Table 4.1. Mean performance of 60 genotypes of cotton (*Gossypium hirsutum* L.) for 15 characters

S.No.	Genotype	Plant height (cm)	Days to 50% flowering	No. of monopodia/ plant	No. of sympodia/ plant	No. of bolls/ plant	Boll weight (g)	Ginning out turn (%)	Seed index (g)
1	L 1801	117.33	62.00	2.23	18.33	64.33	4.17	35.73	11.09
2	MCU 5	119.00	62.67	2.27	19.00	58.33	4.47	35.23	9.95
3	L 1058	129.67	68.67	3.10	18.67	46.33	4.47	35.37	9.72
4	L 604	121.67	61.00	1.33	18.00	47.00	4.20	**31.60**	8.58
5	HYPS 152	120.67	71.00	0.90	18.00	34.00	4.70	34.70	10.57
6	RHC 0811	112.00	68.67	1.33	16.67	41.67	4.20	34.90	9.13
7	TCH 1741	151.67	60.33	**4.47**	18.33	59.67	4.53	34.93	9.38
8	L 804	108.33	60.33	2.00	15.67	44.00	4.60	34.37	9.05
9	L 808	118.67	68.33	2.63	17.33	49.00	3.83	36.23	9.63
10	TSH 0499	143.33	70.67	2.80	20.33	59.67	4.80	35.07	9.23
11	L 389	126.67	70.33	1.87	16.00	39.00	4.93	35.63	9.73
12	LH 2256	132.00	59.67	2.00	20.67	**65.33**	3.97	36.10	11.37
13	GISV 267	141.33	71.67	2.10	21.67	40.67	4.70	36.10	**12.56**
14	H 1442	136.00	64.67	2.80	18.33	63.00	4.47	**36.43**	9.55
15	CCH 11-2	119.00	70.00	2.10	18.67	52.33	4.23	33.67	9.76
16	KH 1101	124.00	62.00	1.23	18.00	50.67	4.60	34.63	10.25
17	NDLH 1938	113.67	67.67	1.63	17.33	42.67	4.63	35.47	11.03
18	SCS 1001	108.33	69.67	1.23	16.00	32.00	5.00	34.83	10.69
19	TCH 1705	**69.67**	68.00	1.57	**10.33**	**26.00**	4.20	33.67	8.87
20	CNH 50	95.00	60.00	1.93	15.67	45.33	3.80	33.17	8.46
21	RAH 1066	128.00	68.00	2.33	20.00	60.00	4.53	32.70	9.82
22	ARBH 701	135.67	69.33	1.90	20.33	50.67	4.13	34.33	10.07
23	SCS 1002	134.00	59.00	1.67	20.67	49.67	4.00	32.37	8.50
24	CCH 11-1	114.00	69.00	1.87	18.00	38.67	4.30	33.10	9.48
25	CNH 44	145.67	61.00	2.43	21.33	43.33	4.63	35.00	9.99
26	TSH 04/115	116.67	64.67	2.00	18.00	53.33	4.97	33.90	11.36
27	CNH 1116	112.67	61.67	1.57	16.00	38.67	4.90	34.97	10.05
28	P 5629	104.33	70.33	1.53	14.67	42.00	4.03	34.37	8.86
29	SCS 1210	110.00	71.33	1.83	16.00	40.00	4.17	34.20	11.59
30	CPD 1301	124.33	61.00	1.10	18.33	50.00	**5.07**	32.97	10.67

Contd………

S.No.	Genotype	Plant height (cm)	Days to 50% flowering	No. of monopodia/ Plant	No. of sympodia/ plant	No. of bolls/ plant	Boll weight (g)	Ginning out turn (%)	Seed index (g)
31	CNH 19	105.33	67.67	1.87	15.00	42.33	4.53	33.57	9.81
32	CPD 1302	142.33	63.67	2.03	20.67	56.00	4.43	36.17	11.75
33	GJHV 516	**154.00**	61.00	0.93	**22.00**	56.33	4.43	33.73	9.13
34	HS 292	103.33	63.33	**0.80**	15.00	33.33	4.77	34.73	10.98
35	KH 1301	102.33	67.67	2.27	14.67	41.33	4.50	35.40	10.40
36	SCS 1211	129.00	68.33	1.70	17.67	39.00	4.60	36.37	9.79
37	SCS 1214	133.00	66.67	1.83	21.33	46.00	4.43	34.93	10.41
38	GJHV 511	121.33	67.33	2.00	19.00	55.67	3.90	33.03	8.90
39	L 1011	130.00	70.33	1.77	19.00	52.00	3.73	35.23	12.25
40	HS 293	129.67	59.00	1.27	15.33	41.33	4.67	33.73	10.78
41	ARBH 1301	100.00	60.67	2.00	16.00	43.33	4.40	33.10	11.76
42	HAG 1055	120.67	67.67	2.90	18.67	45.33	4.07	34.23	**8.18**
43	241-2-4	127.33	67.33	1.77	20.00	47.33	4.27	35.20	10.09
44	ARBA 271	112.33	**57.67**	1.47	17.33	43.67	4.27	34.63	8.90
45	CNH 120 M/B	136.67	58.67	2.23	19.00	55.33	3.77	32.53	8.38
46	BS-3	106.33	64.67	2.00	16.00	48.00	4.03	32.73	8.49
47	BJA 592	128.67	69.67	1.43	19.33	47.67	4.30	34.90	10.14
48	RSA 2455	127.33	70.00	3.27	19.33	57.67	3.83	35.43	9.42
49	RB 57	135.67	60.00	1.10	21.00	51.67	4.13	34.77	10.13
50	GJHV 02145	135.33	66.33	2.43	20.33	61.33	3.93	34.40	10.10
51	H 7	142.00	69.33	3.17	18.33	59.00	4.00	35.70	10.10
52	NH 644	108.00	59.33	2.10	16.33	45.33	4.47	34.43	10.50
53	PRAMUK	121.33	70.33	2.17	15.00	55.67	4.20	33.73	9.09
54	IH 615	103.67	59.67	2.80	16.33	45.67	4.17	32.60	10.50
55	IH 65	107.33	63.00	3.47	16.33	56.00	3.73	36.13	8.69
56	CCH 1831	129.33	59.33	2.40	19.33	52.33	**3.33**	34.67	9.25
57	H 1300	133.67	66.67	1.57	20.00	45.00	4.53	34.03	8.27
58	DS 56	123.67	**72.00**	0.90	18.67	50.67	3.80	35.00	9.72
59	AKALA 15-77 D	112.00	60.00	1.90	19.33	48.67	3.93	35.47	8.74
60	GJHV 375	138.00	68.33	2.30	21.33	52.00	4.47	35.20	8.80
	Mean	122.22	65.31	1.99	18.07	48.37	4.31	34.53	9.87
	C.V. %	6.31	2.75	13.81	10.33	7.89	5.42	2.65	5.14
	C.D. (5%)	12.46	2.90	0.45	3.02	6.17	0.38	1.48	0.82

Contd………

S.No.	Genotype	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)	Lint yield per plant (g)
1	L 1801	6.17	27.60	4.60	22.05	48.00	160.63	57.40
2	MCU 5	5.41	**33.80**	**3.27**	24.23	47.33	156.59	55.16
3	L 1058	5.32	30.83	4.50	22.41	48.33	123.64	43.74
4	L 604	**3.96**	28.13	3.37	23.09	46.00	117.92	37.28
5	HYPS 152	5.62	33.37	3.80	23.35	47.33	126.97	44.13
6	RHC 0811	4.90	31.53	4.70	22.78	47.33	104.13	36.33
7	TCH 1741	5.02	29.93	4.17	22.25	46.67	162.42	56.74
8	L 804	4.75	30.77	3.47	23.03	46.67	121.31	41.73
9	L 808	5.48	27.90	4.30	20.88	48.67	112.63	40.81
10	TSH 0499	5.00	29.33	3.50	22.42	48.00	171.92	60.22
11	L 389	5.39	32.27	3.40	19.11	47.00	144.86	51.63
12	LH 2256	6.43	29.33	3.70	21.55	45.67	155.80	56.17
13	GISV 267	**7.09**	28.23	4.53	21.70	49.00	142.60	51.48
14	H 1442	5.48	25.83	4.20	21.49	47.67	168.30	61.30
15	CCH 11-2	4.96	27.93	4.47	20.27	48.67	133.17	44.86
16	KH 1101	5.43	27.50	4.53	22.82	49.00	140.08	48.49
17	NDLH 1938	6.06	30.63	4.23	23.38	47.33	118.54	42.03
18	SCS 1001	5.72	27.60	4.43	21.76	48.00	132.16	46.06
19	TCH 1705	4.50	26.50	4.53	21.46	47.67	**65.87**	**22.16**
20	CNH 50	4.20	25.70	4.57	19.09	46.00	102.67	34.09
21	RAH 1066	4.77	28.23	4.53	20.58	47.33	162.83	53.23
22	ARBH 701	5.26	27.60	4.57	20.20	48.67	125.77	43.13
23	SCS 1002	4.06	27.70	4.47	20.78	**49.33**	118.53	38.37
24	CCH 11-1	4.69	26.97	4.40	21.65	47.67	99.99	33.11
25	CNH 44	5.38	28.77	4.73	22.87	48.33	120.44	42.12
26	TSH 04/115	5.82	26.93	4.43	20.45	47.67	158.20	53.64
27	CNH 1116	5.41	28.27	4.83	22.32	**49.33**	113.53	39.66
28	P 5629	4.64	27.37	4.00	22.19	48.33	101.04	34.73
29	SCS 1210	6.02	25.70	4.60	20.82	49.00	100.23	34.27
30	CPD 1301	5.26	25.60	4.90	20.63	47.67	152.37	50.23

Contd.........

S.No.	Genotype	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)	Lint yield per plant (g)
31	CNH 19	4.96	28.83	4.77	22.14	48.00	115.23	38.68
32	CPD 1302	6.66	29.13	4.40	21.06	47.00	149.67	54.14
33	GJHV 516	4.65	28.27	4.53	21.30	47.67	149.92	50.62
34	HS 292	5.83	26.87	4.60	20.55	49.00	124.92	43.36
35	KH 1301	5.69	27.37	4.47	22.92	48.00	136.33	48.22
36	SCS 1211	5.60	27.30	4.27	21.62	48.33	118.36	43.04
37	SCS 1214	5.57	28.07	4.57	21.89	48.00	**176.35**	**61.81**
38	GJHV 511	4.39	28.40	4.23	21.51	48.00	129.93	42.90
39	L 1011	6.65	29.93	4.20	23.55	46.33	115.93	40.87
40	HS 293	5.48	26.73	4.60	20.27	47.33	115.80	39.02
41	ARBH 1301	5.82	26.90	4.67	21.12	49.00	114.13	37.81
42	HAG 1055	4.26	26.37	4.67	21.34	48.00	144.88	49.47
43	241-2-4	5.47	31.27	3.53	22.94	47.00	120.48	42.41
44	ARBA 271	4.72	28.77	4.57	22.45	**49.33**	112.37	38.89
45	CNH 120 M/B	4.03	27.43	4.57	20.62	49.00	125.33	40.78
46	BS-3	4.14	27.43	4.27	21.42	**49.33**	116.56	38.11
47	BJA 592	5.43	30.77	3.77	**25.15**	46.00	122.86	42.91
48	RSA 2455	5.16	31.30	3.53	23.19	47.33	132.28	47.05
49	RB 57	5.40	26.87	4.20	20.96	48.33	128.36	44.62
50	GJHV 02145	5.30	27.80	4.13	19.51	46.67	153.57	52.79
51	H 7	5.60	29.17	4.03	22.20	48.33	141.84	50.76
52	NH 644	5.51	31.27	4.60	23.30	47.67	121.65	41.91
53	PRAMUK	4.62	30.23	4.50	22.20	45.33	139.61	47.08
54	IH 615	5.07	25.50	4.67	19.03	47.00	114.07	37.15
55	IH 65	4.91	**21.80**	**5.13**	**17.71**	46.67	124.80	45.09
56	CCH 1831	4.90	28.00	4.07	20.25	47.67	104.37	36.08
57	H 1300	4.25	27.93	4.73	22.47	46.67	141.24	48.27
58	DS 56	5.22	26.70	4.47	20.61	47.67	116.22	40.63
59	AKALA 15-77 D	4.79	27.80	4.83	21.44	**45.00**	115.08	40.84
60	GJHV 375	4.77	27.33	4.70	20.37	**45.00**	139.07	49.06
	Mean	5.22	28.32	4.33	21.61	47.64	129.61	44.81
	C.V. %	4.53	2.62	5.47	3.32	2.49	9.79	10.44
	C.D. (5%)	0.38	1.20	0.38	1.16	1.92	20.52	7.57

Table 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 (*Gossypium hirsutum* L.)

S.No.	Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance as per cent of mean
			Minimum	Maximum	PCV (%)	GCV (%)		
1	Plant height (cm)	122.22	69.67	154.00	13.47	11.91	78.1	21.68
2	Days to 50% flowering	65.31	57.67	72.00	7.02	6.46	84.7	12.25
3	No. of monopodia/plant	1.99	0.80	4.47	36.22	33.48	85.5	63.76
4	No. of sympodia /plant	18.07	10.33	22.00	15.00	10.87	52.5	16.23
5	No. of bolls/plant	48.37	26.00	65.33	18.52	16.76	81.8	31.23
6	Boll weight (g)	4.31	3.33	5.07	9.62	7.95	68.2	13.53
7	Ginning out-turn (%)	34.53	31.60	36.43	3.92	2.89	54.3	4.39
8	Seed index (g)	9.87	8.18	12.56	11.26	10.02	79.2	18.37
9	Lint index (g)	5.22	3.96	7.09	13.39	12.60	88.6	24.42
10	2.5% Span length (mm)	28.32	21.80	33.80	7.63	7.16	88.2	13.86
11	Micronaire (10^{-6}g/in)	4.33	3.27	5.13	10.78	9.28	74.2	16.47
12	Bundle strength (g/tex)	21.61	17.71	25.15	6.86	6.01	76.7	10.84
13	Uniformity ratio	47.64	45.00	49.33	3.05	1.77	33.6	2.12
14	Seed cotton yield/plant (g)	129.61	65.87	176.35	18.10	15.22	70.7	26.37
15	Lint yield/plant (g)	44.81	22.16	61.81	19.32	16.25	70.8	28.16

PCV = Phenotypic coefficient of variation GCV = Genotypic coefficient of variation

Table 4.4. Phenotypic (above diagonal) and genotypic (below diagonal) correlations among 15 characters in 60 cotton (*Gossypium hirsutum* L.) **genotypes**

Character	Plant height (cm)	Days to 50% flowering	No. of monopodia /plant	No. of sympodia/ plant	No. of bolls /plant	Boll weight (g)	Ginning out-turn(%)	Seed index	Lint index (g)	2.5% span-length (mm)	Micronaire (10^{-6}g/in)	Bundle strength (g/tex)	Uniformity ratio	Seed cotton yield /plant (g)	Lint yield /plant (g)
Plant height(cm)	--	0.0036	0.2106 **	0.7546 **	0.4884 **	0.0487	0.1754 *	0.0689	0.1432	0.1903 *	-0.1106	0.0636	-0.0239	0.5126 **	0.5120 **
Days to 50% flowering	0.0096	--	0.0093	-0.0486	-0.1522 *	0.0797	0.2088 **	0.1146	0.1873 *	0.1980 **	-0.1399	0.1356	-0.0156	0.0179	0.0569
No. of monopodia /plant	0.2285**	0.0022	--	0.0828	0.4559 **	-0.2159 **	0.1955 **	-0.1548 *	-0.0481	-0.0063	-0.0290	-0.0961	-0.0620	0.2772 **	0.3008 **
No. of sympodia/plant	0.9074**	-0.0270	0.1290	--	0.4264 **	-0.0993	0.1093	0.0822	0.1256	0.1292	-0.0360	0.0769	-0.0720	0.3950 **	0.3896 **
No. of bolls/plant	0.6053**	-0.1944**	0.4985**	0.6613**	--	-0.3084 **	0.1201	-0.0589	0.0067	0.0302	-0.1321	-0.0659	-0.1916 **	0.6328 **	0.6175 **
Boll weight (g)	0.0538	0.0618	-0.2575**	-0.0854	-0.3757**	--	0.0241	0.3030 **	0.2600 **	0.1645 *	-0.0015	0.1556 *	0.0803	0.3782**	0.3577 **
Ginning outturn (%)	0.3015**	0.3038**	0.2753**	0.2400**	0.1363	0.1016	--	0.1426	0.5526 **	0.1669 *	-0.0901	0.1005	-0.0617	0.2041 **	0.3964 **
Seed index (g)	0.0686	0.1308	-0.1577*	0.0770	-0.0537	0.3553**	0.4552**	--	0.9019 **	0.0916	0.0075	0.0768	0.1147	0.1515 *	0.1692 *
Lint index (g)	0.1660*	0.2069**	-0.0360	0.1532*	0.0094	0.3101**	0.7041**	0.9516**	--	0.1552 *	-0.0441	0.1165	0.0702	0.2184 **	0.3167 **
2.5%span length (mm)	0.2319**	0.2098**	-0.0282	0.1671*	0.0068	0.2160**	0.2546*	0.1060	0.1775*	--	-0.5249 **	0.6606 **	-0.1399	0.1227	0.1473 *
Micronaire(10^{-6} g/in)	-0.2426**	-0.1859*	-0.0811	-0.1935**	-0.2247**	0.0336	-0.1829*	0.0306	-0.0506	-0.6739**	--	-0.3409 **	0.1512 *	-0.1183	-0.1328
Bundle strength (g/tex)	0.0715	0.1762*	-0.1383	0.0368	-0.1004	0.2381**	0.2288**	0.1196	0.1794*	0.6819**	-0.4470**	--	-0.0487	0.0017	0.0218
Uniformity ratio	-0.1174	0.0127	-0.1785*	-0.1206	-0.3183**	0.1927**	-0.1325	0.1643*	0.0898	-0.2213**	0.3032**	-0.0213	--	-0.1014	-0.1084
Seed cotton yield/plant(g)	0.6727**	0.0037	0.3105**	0.6763**	0.6441**	0.3088**	0.2889**	0.2041**	0.2638**	0.1455*	-0.2073**	0.0284	-0.1608*	--	0.9790 **
Lint yield/plant (g)	0.6802**	0.0547	0.3442**	0.6711**	0.6259**	0.3040**	0.4462**	0.2724**	0.3723**	0.1802*	-0.2340**	0.0692	-0.1772*	0.9854**	--

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

Table 4.5. Direct and indirect effects (phenotypic) of yield components on seed cotton yield per plant in 60 genotypes of cotton (*Gossypium hirsutum* L.)

Character	Plant height (cm)	Days to 50% flowering	No. of mono-podia /plant	No. of sympodia /plant	No. of bolls /plant	Boll weight (g)	Ginning out-turn (%)	Seed index (g)	Lint index (g)	2.5% span-length (mm)	Micro-naire (10^{-6}g/in)	Bundle strength (g/tex)	Unifor-mity ratio	Lint yield /plant (g)
Plant height (cm)	**0.0071**	0.0000	0.0015	0.0054	0.0035	0.0003	0.0012	0.0005	0.0010	0.0014	-0.0008	0.0005	-0.0002	0.0036
Days to 50% flowering	0.0000	**0.0041**	0.0000	-0.0002	-0.0006	0.0003	0.0009	0.0005	0.0008	0.0008	-0.0006	0.0006	-0.0001	0.0002
No. of monopodia /plant	-0.0004	0.0000	**-0.0017**	-0.0001	-0.0008	0.0004	-0.0003	0.0003	0.0001	0.0000	0.0000	0.0002	0.0001	-0.0005
No. of sympodia/plant	0.0007	0.0000	0.0001	**0.0009**	0.0004	-0.0001	0.0001	0.0001	0.0001	0.0001	0.0000	0.0001	-0.0001	0.0004
No. of bolls/plant	0.0043	-0.0013	0.0040	0.0038	**0.0088**	-0.0027	0.0011	-0.0005	0.0001	0.0003	-0.0012	-0.0006	-0.0017	0.0054
Boll weight (g)	0.0003	0.0005	-0.0015	-0.0007	-0.0021	**0.0068**	0.0002	0.0021	0.0018	0.0011	0.0000	0.0011	0.0005	0.0024
Ginning out-turn (%)	-0.0284	-0.0338	-0.0317	-0.0177	-0.0195	-0.0039	**-0.1620**	-0.0231	-0.0895	-0.0270	0.0146	-0.0163	0.0100	-0.0642
Seed index (g)	0.0074	0.0123	-0.0166	0.0088	-0.0063	0.0326	0.0153	**0.1074**	0.0969	0.0098	0.0008	0.0083	0.0123	0.0182
Lint index (g)	-0.0182	-0.0238	0.0061	-0.0159	-0.0009	-0.0330	-0.0701	-0.1144	**-0.1269**	-0.0197	0.0056	-0.0148	-0.0089	-0.0402
2.5%Span length (mm)	0.0008	0.0009	0.0000	0.0006	0.0001	0.0007	0.0007	0.0004	0.0007	**0.0043**	-0.0023	0.0028	-0.0006	0.0006
Micronaire (10^{-6}g/in)	-0.0005	-0.0007	-0.0001	-0.0002	-0.0006	0.0000	-0.0004	0.0000	-0.0002	-0.0026	**0.0049**	-0.0017	0.0007	-0.0006
Bundle strength (g/tex)	-0.0001	-0.0002	0.0001	-0.0001	0.0001	-0.0002	-0.0001	-0.0001	-0.0002	-0.0009	0.0004	**-0.0013**	0.0001	0.0000
Uniformity ratio	0.0000	0.0000	0.0000	0.0000	-0.0001	0.0000	0.0000	0.0001	0.0000	-0.0001	0.0001	0.0000	**0.0006**	-0.0001
Lint yield/plant (g)	0.5396	0.0599	0.3170	0.4106	0.6508	0.3770	0.4177	0.1783	0.3338	0.1552	-0.1400	0.0230	-0.1143	**1.0538**
Correlation with seed cotton yield	0.5126**	0.0179	0.2772**	0.3950**	0.6328**	0.3782**	0.2041**	0.1515*	0.2184**	0.1227	-0.1183	0.0017	-0.1014	0.9790**

*** Significant at 5% level, ** Significant at 1% level, Residual effect = 0.0347, Bold and diagonal values indicate direct effects**

Table 4.6. Direct and indirect effects (genotypic) of yield components on seed cotton yield per plant in 60 genotypes of cotton (*Gossypium hirsutum* L.)

Character	Plant height (cm)	Days to 50% flowering	No. of monopodia /plant	No. of sympodia /plant	No. of bolls /plant	Boll weight (g)	Ginning out-turn (%)	Seed index (g)	Lint index (g)	2.5% span length (mm)	Micronaire (10^{-6} g/in)	Bundle strength (g/tex)	Uniformity ratio	Lint yield /plant (g)
Plant height (cm)	**-0.0090**	-0.0001	-0.0021	-0.0081	-0.0054	-0.0005	-0.0027	-0.0006	-0.0015	-0.0021	0.0022	-0.0006	0.0011	-0.0061
Days to 50% flowering	0.0001	**0.0056**	0.0000	-0.0002	-0.0011	0.0003	0.0017	0.0007	0.0012	0.0012	-0.0010	0.0010	0.0001	0.0003
No. of monopodia /plant	-0.0031	0.0000	**-0.0134**	-0.0017	-0.0067	0.0035	-0.0037	0.0021	0.0005	0.0004	0.0011	0.0019	0.0024	-0.0046
No. of sympodia/plant	0.0093	-0.0003	0.0013	**0.0103**	0.0068	-0.0009	0.0025	0.0008	0.0016	0.0017	-0.0020	0.0004	-0.0012	0.0069
No. of bolls/plant	0.0126	-0.0040	0.0103	0.0137	**0.0208**	-0.0078	0.0028	-0.0011	0.0002	0.0001	-0.0047	-0.0021	-0.0066	0.0130
Boll weight (g)	0.0004	0.0005	-0.0021	-0.0007	-0.0030	**0.0081**	0.0008	0.0029	0.0025	0.0017	0.0003	0.0019	0.0016	0.0025
Ginning out-turn (%)	-0.0234	-0.0236	-0.0213	-0.0186	-0.0106	-0.0079	**-0.0775**	-0.0353	-0.0546	-0.0197	0.0142	-0.0177	0.0103	-0.0346
Seed index (g)	0.0156	0.0297	-0.0358	0.0175	-0.0122	0.0806	0.1032	**0.2268**	0.2158	0.0240	0.0069	0.0271	0.0373	0.0618
Lint index (g)	-0.0494	-0.0616	0.0107	-0.0456	-0.0028	-0.0923	-0.2096	-0.2833	**-0.2977**	-0.0528	0.0151	-0.0534	-0.0267	-0.1108
2.5%Spanlength (mm)	0.0039	0.0036	-0.0005	0.0028	0.0001	0.0037	0.0043	0.0018	0.0030	**0.0169**	-0.0114	0.0115	-0.0037	0.0030
Micronaire (10^{-6} g/in)	-0.0033	-0.0025	-0.0011	-0.0026	-0.0031	0.0005	-0.0025	0.0004	-0.0007	-0.0092	**0.0136**	-0.0061	0.0041	-0.0032
Bundle strength (g/tex)	-0.0006	-0.0015	0.0012	-0.0003	0.0009	-0.0020	-0.0020	-0.0010	-0.0015	-0.0058	0.0038	**-0.0085**	0.0002	-0.0006
Uniformity ratio	-0.0010	0.0001	-0.0015	-0.0010	-0.0026	0.0016	-0.0011	0.0014	0.0007	-0.0018	0.0025	-0.0002	**0.0083**	-0.0015
Lint yield/plant (g)	0.7205	0.0579	0.3646	0.7109	0.6630	0.3220	0.4727	0.2886	0.3944	0.1908	-0.2478	0.0733	-0.1877	**1.0593**
Correlation with seed cotton yield	0.6727**	0.0037	0.3105**	0.6763**	0.6441**	0.3088**	0.2889**	0.2041**	0.2638**	0.1455	-0.2073**	0.0284	-0.1608*	0.9854**

*** = Significant at 5% level, ** = Significant at 1% level, Residual effect = 0.0127, Bold and diagonal values indicate direct effects**

Table 4.7. Contribution of different characters towards genetic divergence in 60 cotton (*Gossypium hirsutum* L.) genotypes

S. No.	Character	Contribution towards divergence (%)	Times ranked first
1	Plant height (cm)	4.41	78
2	Days to 50% flowering	13.62	241
3	Number of monopodia per plant	10.45	185
4	Number of sympodia per plant	0.17	3
5	Number of bolls per plant	6.1	108
6	Boll weight (g)	1.86	33
7	Ginning out-turn (%)	0.34	6
8	Seed index (g)	17.57	311
9	Lint index (g)	1.41	25
10	2.5% span length (mm)	18.14	321
11	Micronaire (10^{-6}g/in)	10.56	187
12	Bundle strength (g/tex)	8.02	142
13	Uniformity ratio	0.68	12
14	Seed cotton yield per plant (g)	5.48	97
15	Lint yield per plant (g)	1.19	21

Table 4.9. Average intra-and inter-cluster D^2 values among 11 clusters in 60 cotton (*Gossypium hirsutum* L.) **genotypes**

Cluster No	**I**	**II**	**III**	**IV**	**V**	**VI**	**VII**	**VIII**	**IX**	**X**	**XI**
I	**24.95 (4.99)**	36.11	44.31	35.50	39.20	32.89	54.01	60.22	55.00	71.39	67.87
II		**31.03 (5.57)**	59.14	47.71	41.25	56.21	47.40	46.12	66.54	67.14	96.02
III			**35.23 (5.94)**	72.00	61.17	51.30	101.74	55.47	69.07	96.15	69.18
IV				**0.00 (0.00)**	14.84	32.80	32.58	100.36	99.37	39.77	95.15
V					**0.00 (0.00)**	53.87	41.62	83.04	110.20	25.77	104.69
VI						**0.00 (0.00)**	64.72	91.44	63.98	99.52	73.68
VII							**0.00 (0.00)**	91.50	90.11	70.71	122.06
VIII								**0.00 (0.00)**	59.03	115.83	87.48
IX									**0.00 (0.00)**	185.35	27.69
X										**0.00 (0.00)**	177.20
XI											**0.00 (0.00)**

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

Table 4.10. The nearest and the farthest cluster from each cluster based on D^2 values

Cluster No.	Nearest cluster with D^2 values	Farthest cluster with D^2 values
I	VI(32.89)	X(71.39)
II	I(36.11)	XI(96.02)
III	I(44.31)	VII(101.74)
IV	V(14.84)	VIII(100.36)
V	IV(14.84)	IX(110.20)
VI	IV(32.80)	X(99.52)
VII	IV(32.58)	XI(122.06)
VIII	II(46.12)	X(115.83)
IX	XI(27.69)	X(185.35)
X	V(25.77)	IX(185.35)
XI	IX(27.69)	X(177.20)

Note: Values in parentheses indicate D^2 values

Table 4.8. Clustering pattern of 60 cotton (*Gossypium hirsutum* L.) **genotypes by Tocher's method**

Cluster No.	No. of genotypes	Name of the genotype
I	34	SCS 1002, CNH 120 M/B, BS-3, GJHV 511, CCH 11-2, ARBH 701, RAH 1066, PRAMUK, GJHV 375, GJHV 02145, L 808, CCH 1831, RB 57, AKALA 15-77 D, CNH 19, CCH 11-1, P 5629, H 1300, SCS 1211, ARBA 271, KH 1101, TSH 04/115, CNH 44, HS 293, L 1058, RHC 0811, CNH 1116, NDLH 1938, NH 644, 241-2-4, L 804, DS 56, GJHV 516, BJA 592
II	9	SCS 1001, HS 292, KH 1301, SCS 1210, ARBH 1301, CPD 1301, L 1801, SCS 1214, HAG 1055
III	9	RSA 2455, H 7, TSH 0499, H 1442, TCH 1741, MCU 5, LH 2256, CPD 1302, L 1011
IV	1	CNH 50
V	1	IH 615
VI	1	L 604
VII	1	TCH 1705
VIII	1	GISV 267
IX	1	HYPS 152
X	1	IH 65
XI	1	L 389

Table 4.11. Mean values of 11 clusters estimated by Tocher's method from 60 genotypes of cotton (*Gossypium hirsutum* L.)

Cl No	Plant height (cm)	Days to 50% flowering	No. of monopodia / plant	No.of sympodia / plant	No.of bolls/ plant	Boll weight (g)	Ginning out-turn (%)	Seed index (g)	Lint index (g)	2.5% span length (mm)	Micronaire (10g/in)	Bundle strength (g/tex)	Uniformity ratio	Seed cotton yield/ plant (g)	lint yield/ plant (g)
I	123.65	65.07	1.85	18.33	48.30	4.28	34.34	9.58	5.02	28.47	4.40	21.68	47.73	124.70	42.78
II	113.26	65.56	1.80	17.15	43.96	4.51	34.46	10.64	5.59	26.90	4.61	21.45	48.30	138.00	47.62
III	135.96	65.70	2.73	19.33	**58.96**	4.25	35.59	10.33	5.71	29.75	3.89	22.44	47.15	**150.53**	**53.60**
IV	95.00	60.00	1.93	15.67	45.33	3.80	33.17	**8.46**	4.20	25.70	4.57	19.09	**46.00**	102.67	34.09
V	103.67	**59.67**	2.80	16.33	45.67	4.17	32.60	10.50	5.07	25.50	4.67	19.03	47.00	114.07	37.15
VI	121.67	61.00	1.33	18.00	47.00	4.20	**31.60**	8.58	**3.96**	28.13	**3.37**	23.09	**46.00**	117.92	37.28
VII	**69.67**	68.00	1.57	**10.33**	**26.00**	4.20	33.67	8.87	4.50	26.50	4.53	21.46	47.67	**65.87**	**22.16**
VIII	**141.33**	**71.67**	2.10	**21.67**	40.67	4.70	36.10	**12.56**	**7.09**	28.23	4.53	21.70	**49.00**	142.60	51.48
IX	120.67	71.00	**0.90**	18.00	34.00	4.70	34.70	10.57	5.62	**33.37**	3.80	**23.35**	47.33	126.97	44.13
X	107.33	63.00	**3.47**	16.33	56.00	**3.73**	**36.13**	8.69	4.91	**21.80**	**5.13**	**17.71**	46.67	124.80	45.09
XI	126.67	70.33	1.87	16.00	39.00	**4.93**	35.63	9.73	5.39	32.27	3.40	19.11	47.00	144.86	51.63

Note: Bold figures are minimum and maximum values

Table 4.12: Eigen values, proportion of the total variance represented by first seven principal components, cumulative per cent variance and component loading of different characters in cotton (*Gossypium hirsutum* L.).

	PC_1	**PC_2**	**PC_3**	**PC_4**	**PC_5**	**PC_6**	**PC_7**
Eigene Value (Root)	2.90	2.41	1.72	1.59	1.34	1.06	0.78
% Var. Exp.	19.33	16.04	11.48	10.62	8.96	7.10	5.18
Cum. Var. Exp.	19.33	35.37	46.85	57.46	66.42	73.52	78.70
Plant Height (cm)	0.38	0.11	0.17	0.18	0.31	0.24	0.37
Days to 50% flowering	0.10	-0.33	0.26	-0.43	-0.07	0.18	0.19
No.of monopodia/ Plant	0.22	0.28	-0.34	-0.31	-0.20	0.22	0.11
No.of sympodia/ Plant	0.05	-0.04	0.12	-0.52	0.31	0.05	-0.43
No.of bolls/ Plant	0.27	0.34	0.05	0.07	0.53	-0.02	0.10
Boll Weight (g)	0.03	-0.15	-0.15	0.50	-0.10	0.41	-0.02
Ginning out-turn (%)	0.31	-0.35	-0.18	0.03	0.05	0.27	-0.12
Seed Index (g)	0.26	-0.34	-0.37	0.05	0.19	-0.03	-0.24
Lint Index (g)	0.26	-0.22	-0.14	0.11	0.24	-0.63	-0.10
2.5% Span length (mm)	0.27	-0.16	0.35	0.27	-0.35	-0.13	-0.22
Micronaire (10^{-6} g/Inch)	-0.47	-0.12	-0.29	0.02	0.11	0.07	-0.17
Bundle Strength (g/tex)	-0.14	-0.34	-0.35	-0.09	0.18	0.04	0.46
Uniformity Ratio	-0.29	-0.23	0.23	0.08	0.15	-0.26	0.39
Seed Cotton Yield/ Plant(g)	0.09	-0.40	0.32	-0.12	-0.03	0.15	0.06
Lint Yield/ Plant (g)	0.30	0.03	-0.28	-0.19	-0.43	-0.33	0.29

PC = Principal component

Table 4.13. **PCA scores of 60 genotypes of cotton** (*Gossypium hirsutum* L.)

Sl.No.	GENOTYPE	PCA I X Vector	PCA II Y Vector	PCA III Z Vector
1	L 1801	-56.578	-8.075	44.636
2	MCU 5	-53.960	-7.178	49.311
3	L 1058	-56.218	-7.865	47.086
4	L 604	-57.674	-5.750	48.855
5	HYPS 152	-56.201	-11.268	51.341
6	RHC 0811	-58.720	-8.782	49.417
7	TCH 1741	-53.739	-4.522	45.236
8	L 804	-56.867	-6.697	47.934
9	L 808	-57.228	-7.943	46.842
10	TSH 0499	-54.617	-6.944	48.674
11	L 389	-54.321	-8.264	51.363
12	LH 2256	-53.342	-6.970	46.293
13	GISV 267	-55.146	-12.453	45.901
14	H 1442	-55.739	-6.947	44.693
15	CCH 11-2	-58.353	-7.047	48.355
16	KH 1101	-58.953	-8.653	46.642
17	NDLH 1938	-57.026	-10.149	46.912
18	SCS 1001	-59.282	-11.610	47.229
19	TCH 1705	-62.157	-9.098	45.537
20	CNH 50	-60.208	-4.949	46.347
21	RAH 1066	-58.206	-5.965	48.754
22	ARBH 701	-57.751	-7.405	48.287
23	SCS 1002	-58.795	-4.963	48.844
24	CCH 11-1	-59.351	-7.879	46.945
25	CNH 44	-57.258	-7.700	45.871
26	TSH 04/115	-58.281	-7.644	45.830
27	CNH 1116	-59.881	-8.934	45.693
28	P 5629	-59.488	-8.522	48.115
29	SCS 1210	-59.401	-9.926	45.251
30	CPD 1301	-60.535	-7.427	46.289

Contd….

Sl.No.	GENOTYPE	PCA I X Vector	PCA II Y Vector	PCA III Z Vector
31	CNH 19	-59.643	-8.407	46.839
32	CPD 1302	-54.204	-8.600	45.855
33	GJHV 516	-57.799	-6.066	49.805
34	HS 292	-60.248	-10.704	46.866
35	KH 1301	-58.716	-10.761	45.362
36	SCS 1211	-57.847	-9.797	47.055
37	SCS 1214	-57.043	-10.557	48.501
38	GJHV 511	-58.166	-6.104	49.102
39	L 1011	-55.263	-10.286	46.713
40	HS 293	-58.857	-7.269	45.882
41	ARBH 1301	-59.766	-7.968	44.354
42	HAG 1055	-59.175	-7.831	47.789
43	241-2-4	-55.399	-8.123	49.249
44	ARBA 271	-59.727	-7.284	47.396
45	CNH 120 M/B	-58.361	-4.258	48.214
46	BS-3	-59.622	-6.406	47.976
47	BJA 592	-56.189	-9.568	48.563
48	RSA 2455	-54.126	-6.751	48.288
49	RB 57	-57.775	-7.115	47.710
50	GJHV 02145	-55.837	-5.786	48.308
51	H 7	-54.474	-7.334	46.780
52	NH 644	-57.839	-8.017	46.258
53	PRAMUK	-57.395	-6.898	48.767
54	IH 615	-59.423	-5.258	44.237
55	IH 65	-60.026	-4.870	42.715
56	CCH 1831	-56.847	-4.908	47.786
57	H 1300	-59.087	-7.895	48.887
58	DS 56	-58.925	-8.593	49.073
59	AKALA 15-77 D	-59.118	-6.324	46.557
60	GJHV 375	-57.340	-6.198	47.427

Chapter IV

RESULTS AND DISCUSSION

A systematic study was conducted to characterize the 60 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 60 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 60 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 69.67 cm (TCH 1705) to 154.00 cm (GJHV 516) with a mean of 122.22 cm. The estimates of PCV and GCV were moderate (13.47 and 11.91) and difference between them is low indicating there is less influence of environment. Similar results were reported by Dhivya *et al.* (2014) and Khan *et al.* (2015).

High heritability (78.1) coupled with high genetic advance as per cent of mean (21.68) was observed for the trait indicating the preponderance of additive gene action making selection effective. Similar results were reported by Lakshmi *et al*. (2012), Haritha *et al*. (2012), Hafiz *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 65.31 days ranging from 57.67 (ARBA 271) to 72.00 days (DS 56). The estimates of PCV and GCV were low (7.02 and 6.46) indicating less variation among the genotypes studied. 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 (84.7) coupled with moderate genetic advance as per cent of mean (12.25) was observed for days to 50% flowering indicating the operation 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 0.80 (HS 292) to 4.47 (TCH 1741) with a mean of 1.99. The estimates of PCV and GCV (36.22 and 33.48) were high indicating high variation among the genotypes studied. Similar results were reported by Rajanna (2010), Kishore *et al.* (2011), Kulkarni *et al.* (2011), Mohan (2011), Hafiz *et al.* (2013) and Khan *et al.* (2015).

High heritability (85.5%) and high genetic advance as per cent of mean (63.76) was observed for this trait indicating the preponderance of additive gene action making selection effective. These results are in agreement with the findings Rao (2008), Mahantesh (2009), Lakshmi *et al*. (2012), Hafiz *et al.* (2013), Patel *et al.* (2013) and Erande *et al.*(2014).

4.1.4 Number of Sympodia Per Plant

The number of sympodia per plant ranged from 10.33 (TCH 1705) to 22.00 (GJHV 516) with a mean of 18.07 (Fig. 4.1.). The estimates of PCV and GCV (15.00 and 10.87) were moderate and there is high difference between them indicating influence of environment. These results are in agreement with the findings of Dhivya *et al.* (2014).

Moderate heritability (52.50) coupled with moderate genetic advance as per cent of mean (16.23) indicating the preponderance of non additive gene action and further improvement of this character would be possible through heterosis breeding rather than simple selection. Similar results were reported by Ravikesavan *et al.* (2008), Rajanna (2010), Lakshmi *et al*. (2012) and Hafiz *et al.* (2013).

4.1.5 Number of Bolls Per Plant

The number of bolls per plant ranged from 26.00 (TCH 1705) to 65.33 (LH 2256) with an average of 48.37 (Fig. 4.2.). The estimates of PCV and GCV (18.52 and 16.76) were moderate and there is high difference between them indicating influence of environment. These results are in agreement with the findings of Dhivya *et al.* (2014).

High heritability (81.8) coupled with high genetic advance as per cent of mean (31.23) was observed for this trait indicating the preponderance of additive gene action making selection effective. Similar results were reported by Bazi (2011), Dinakaran *et al.* (2012), Lakshmi *et al.* (2012), Hafiz *et al.* (2013), Vinodhana *et al.* (2013), Dhivya *et al.* (2014), Erande *et al.* (2014), Ahsan *et al.* (2015) and Khan *et al.* (2015).

4.1.6 Boll Weight (g)

The boll weight ranged from 3.33 g (CCH 1831) to 5.07 g (CPD 1301) with a mean of 4.31g (Fig. 4.3.). The estimates of PCV and GCV (9.62 and 7.95) were low indicating low variation among the genotypes studied. Similar results were reported by Bazi (2011), Vinodhana *et al.* (2013), Dhivya *et al.* (2014) and Erande *et al.* (2014).

High heritability (68.20) and moderate genetic advance as per cent of mean (13.53) were recorded for this trait indicating the presence of both additive and non additive gene action and desired results may not be obtained by simple selection. Similar results were reported by Dinakaran *et al.* (2012), Vinodhana *et al.* (2013) and Erande *et al.* (2014).

4.1.7 Ginning Out-turn (%)

The range of variation among the genotypes for this trait was 31.60 (L 604) to 36.43 (H 1442) with a mean of 34.53. The estimates of PCV and GCV (3.92 and 2.89) were low indicating there is less variability among the genotypes studied. Similar results were reported by Mohan (2011), Dhivya *et al.* (2014), Erande *et al.* (2014), Farooq *et al.* (2014) and Khan *et al.* (2015).

Moderate heritability (54.30) coupled with low genetic advance as per cent of mean (4.39) 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) and Dhivya *et al.* (2014).

4.1.8 Seed Index (g)

Seed index was in the range of 8.18g (HAG 1055) to 12.56g (GISV 267) with a mean of 9.87g. The estimates of PCV and GCV (11.26 and 10.02) were moderate and difference between them is low indicating there is less influence of environment. Similar results were reported by Dhivya *et al.* (2014) and Khan *et al.* (2015).

High heritability (79.2) and moderate genetic advance as per cent of mean (18.37) 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 results were reported by Bazi (2011), Dhivya *et al.* (2014) and Erande *et al.* (2014).

4.1.9 Lint Index (g)

The range of variation observed for this character was from 3.96 (L 604) to 7.09g (GISV 267) with a mean of 5.22g. The estimates of PCV and GCV (13.39 and 12.60) were moderate and difference between them is low indicating there is less influence of environment. Similar results were reported by Khan *et al.* (2015) and Dhivya *et al.* (2014).

High heritability (88.60) coupled with high genetic advance as per cent of mean (24.42) was observed for lint index indicating the preponderance of additive gene action making selection effective. Similar findings were reported by Bazi (2011), Haritha *et al*. (2012), Lakshmi *et al*. (2012), Vinodhana *et al.* (2013), Dhivya *et al.* (2014) and Ahsan *et al.* (2015).

4.1.10 2.5% Span Length (mm)

The mean span length ranged from 21.80 (IH 65) to 33.80 (MCU 5) with a mean of 28.32. The estimates of PCV and GCV (7.63 and 7.16) 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) and Erande *et al.*(2014).

High heritability (88.20) coupled with moderate genetic advance as per cent of mean (13.86) 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 Vinodhana *et al.* (2013), Dhivya *et al.* (2014) and Erande *et al.* (2014).

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

The range of variation for the character was from 3.27 (MCU 5) to 5.13 (IH 65) with a mean of 4.33. The estimates of PCV and GCV (10.78 and 9.28) were moderate and low respectively and difference between them is low indicating there is less influence of environment. Similar results were observed by Rajanna (2010), Sarada *et al.* (2010), Vinodhana *et al.* (2013) and Khan *et al.* (2015).

High heritability (74.2) coupled with moderate genetic advance as per cent of mean (16.47) was recorded for this trait indicating the presence of both additive and non additive gene action and desired results may not be obtained by simple selection. Similar results were observed by Bazi (2011), Vinodhana *et al.* (2013) and Erande *et al.* (2014).

4.1.12 Bundle Strength (g/tex)

The range of variation for bundle strength was from 17.71 (IH 65) to 25.15 (BJA 592) with a mean of 21.61. The estimates of PCV and GCV (6.86 and 6.01) were low indicating there is less variability among the genotypes studied. Similar results were observed by Rao (2008), Srinivasulu (2009), Rajanna (2010), Sarada *et al.* (2010) and Bazi (2011).

High heritability (76.70) coupled with moderate genetic advance as per cent of mean (10.84) was recorded 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 results were observed by An *et al*. (2008), Ravikesavan *et al.* (2008) and Vinodhana *et al.* (2013).

4.1.13 Uniformity Ratio

The range of variation was from 45.00 (AKALA 15-77D and GJHV 375) to 49.33 (SCS 1002, CNH 1116 and ARBA 271) with a mean of 47.64. The estimates of PCV and GCV (3.05 and 1.77) were low indicating there is less variability among the genotypes studied. Similar results were observed by Bazi (2011), Kishore *et al.* (2011), Mohan (2011), Vinodhana *et al.* (2013), Erande *et al.* (2014) and Khan *et al.* (2015).

Moderate heritability (33.60) coupled with low genetic advance as per cent of mean (2.12) was observed for uniformity ratio 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 Bazi (2011) and Dinakaran *et al.* (2012).

4.1.14 Seed Cotton Yield Per Plant (g)

The range of variation was from 65.87 (TCH 1705) to 176.35 (SCS 1214) with a mean of 129.61 (Fig. 4.4.). The estimates of PCV and GCV (18.10 and 15.22) were moderate and there is high difference between them indicating influence of environment. Similar results were observed by Ahsan *et al.* (2015).

High heritability (70.70) coupled with high genetic advance as per cent of mean (26.37) was observed for seed cotton yield per plant making selection effective due to additive gene action. Similar results were observed by

Dinakaran *et al.* (2012), Haritha *et al.* (2012), Vinodhana *et al.* (2013), Dhivya *et al.* (2014), Erande *et al.* (2014), Farooq *et al.* (2014) and Khan *et al.* (2015).

4.1.15 Lint Yield Per Plant (g)

The mean variation ranged from 22.16g (TCH 1705) to 61.81g (SCS 1214) with an average of 44.81g (Fig. 4.5.). The PCV and GCV estimates (19.32 and 16.25) were moderate and there is high difference between them indicating influence of environment.

High heritability (70.80) coupled with high genetic advance as per cent of mean (28.16) was observed for seed cotton yield per plant making selection effective due to additive gene action. Similar results were observed by Rao (2008), Mahantesh (2009), Rajanna (2010) and Dinakaran *et al.* (2012).

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 determines 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 monopodia per plant (0.2285** and 0.2106**), number of sympodia per plant (0.9074** and 0.7546**), number of bolls per plant (0.6053** and 0.4884**), ginning out-turn (0.3015** and 0.1754*), 2.5% span length (0.2319** and 0.1903*), seed cotton yield per plant (0.6727** and 0.5126**) and lint yield per plant (0.6802** and 0.5120**) 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 Lint index (0.1660*) at genotypic level indicating simultaneous improvement of these traits and significant negative association was observed with micronaire (-0.2426**) 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 Kishore *et al*. (2011), Rajanna *et al.*(2011), Erande *et al.*(2014), Farooq *et al.*(2014), Kumar *et al*. (2014) and Ranjan *et al*. (2014).

4.2.2 Days to 50% Flowering

The trait showed significant positive association with ginning out-turn (0.3038** and 0.2088**), lint index (0.2069** and 0.1873*) and 2.5% span length (0.2098** and 0.1980**) at both genotypic and phenotypic levels and significant positive association with bundle strength (0.1762*) at genotypic level indicated that increase in one character will lead to increase in second and vice versa while significant negative association with number of bolls per plant (-0.1944** and -0.1522*) at both phenotypic and genotypic level and micronaire (-0.1859*) at genotypic level indicated increase of these variable cause decrease in another variable and vice versa.

The non-significant positive association with seed cotton yield at both genotypic and phenotypic levels (0.0037 and 0.0179) 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, this trait recorded significant positive association with number of bolls per plant (0.4985** and 0.4559**), ginning out-turn (0.2753** and 0.1955**), seed cotton yield per plant (0.3105** and 0.2772**) and lint yield per plant (0.3442** and 0.3008**) indicating simultaneous improvement of these traits. While, it showed negative and significant association with uniformity ratio (-0.1785*) at genotypic level, boll weight (-0.2575** and -0.2159**) and seed index (-0.1577* and -0.1548*) at genotypic and phenotypic level indicating that simultaneous selection of these traits is not possible.

The selection for high seed cotton yield per plant based on number of monopodia per plant is beneficial as their association is significantly positive at both genotypic and phenotypic levels. Similar results were also reported by Mahantesh (2009), Mohan (2011), Kumar *et al.* (2014) and Ranjan *et al*. (2014).

4.2.4 Number of Sympodia Per Plant

This trait showed significant positive association with number of bolls per plant (0.6613** and 0.4264**), seed cotton yield per plant (0.6763** and 0.3950**), lint yield per plant (0.6711** and 0.3896*) at both genotypic and phenotypic level and ginning out-turn (0.24**), lint index (0.1532*), 2.5% span length (0.1671*) at genotypic level indicating simultaneous improvement of these traits. Whereas, the trait showed negative and significant association with micronaire (-0.1935**) at genotypic level indicating that simultaneous selection of this trait is not possible.

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) and Khan *et al.* (2015).

4.2.5 Number of Bolls Per Plant

Number of bolls per plant showed significant negative association with micronaire (-0.2247**) at genotypic level and boll weight (-0.3757** and -0.3084**), uniformity ratio (-0.3183** and -0.1916**) at both genotypic and phenotypic levels indicating that simultaneous selection of these traits is not possible.

The trait showed significant positive association with seed cotton yield per plant (0.6441** and 0.6328**) and lint yield per plant (0.6259** and 0.6175**) 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 Imran *et al.* (2012), Lakshmi *et al.* (2012), Vinodhana *et al.* (2013), Erande *et al.* (2014), Farooq *et al.* (2014), Kumar *et al.* (2014), and Ranjan *et al.* (2014).

4.2.6 Boll Weight (g)

Boll weight showed significant positive association with seed index (0.3553** and 0.3030**), lint index (0.3101** and 0.2600**), 2.5% span length (0.2160** and 0.1645*), bundle strength (0.2381** and 0.1556*), seed cotton yield per plant (0.3088** and 0.3782**), lint yield per plant (0.3040** and 0.3577**) at genotypic and phenotypic level and with uniformity ratio (0.1927**) at genotypic 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 Kishore *et al.* (2011), Mohan (2011), Ranjan *et al.* (2014), Kumar *et al.* (2014), Erande *et al.* (2014) and Khan *et al.* (2015).

4.2.7 Ginning Out-turn (%)

At genotypic level it showed significant positive association with seed index (0.4552**) and bundle strength (0.2288**) indicating strong association among these characters genetically, but the phenotypic value is lessened by significant interaction of environment. The trait showed significant positive association with lint index (0.7041** and 0.5526**), 2.5% span length (0.2546* and 0.1669*), seed cotton yield per plant (0.2889** and 0.2041**) and lint yield per plant (0.4462** and 0.3964**) at genotypic and phenotypic level indicating simultaneous selection for these traits. Whereas, the trait showed significant negative association with micronaire (-0.1829*) at genotypic level indicating simultaneous selection of this trait is not possible.

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 Naqib *et al*. (2010), Salahuddin *et al.* (2010), Farooq *et al.* (2014) and Erande *et al.* (2014).

4.2.8 Seed Index (g)

At both genotypic and phenotypic levels, the trait showed significant positive association with lint index (0.9516** and 0.9019*), seed cotton yield per plant (0.2041** and 0.1515*) and lint yield per plant (0.2724** and 0.1692*) whereas, at genotypic level, this trait showed significant positive association with uniformity ratio (0.1643*) indicating simultaneous selection for these traits.

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), Kumar *et al*. (2014) and Ranjan *et al*. (2014).

4.2.9 Lint Index (g)

Lint index showed significant positive association with bundle strength (0.1794*) at genotypic level and with 2.5% span length (0.1775* and 0.1552*), seed cotton yield per plant (0.2638** and 0.2184**) and lint yield per plant (0.3723** and 0.3167**) 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) also reported similar results.

4.2.10 2.5% Span Length

The trait showed significant positive association with bundle strength (0.6819** and 0.6606**) and lint yield per plant (0.1802* and 0.1473*) at both genotypic and phenotypic levels whereas, this trait showed significant positive association with seed cotton yield per plant (0.1455*) at only genotypic level indicating simultaneous selection for these traits. Kumar *et al.* (2014) also reported positive significant association of 2.5 % with bundle strength and seed cotton yield per plant.

The trait showed significant negative association with micronaire (-0.6739** and -0.5249**) at both genotypic and phenotypic levels and with uniformity ratio (-0.2213**) at only genotypic level indicating simultaneous selection for these traits was not possible. Rajamani *et al*. (2013), Vinodhana *et al*. (2013), Kumar *et al.* (2014) and Erande *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 uniformity ratio (0.3032** and 0.1512*) while, with bundle strength (-0.447** and -0.3409**) significant negative association was observed at both genotypic and phenotypic level. Seed cotton yield per plant (-0.2073**) and lint yield per plant (-2340**) showed significant negative association with micronaire at genotypic level indicated that simultaneous improvement of these traits is not possible. The significantly negative association of micronaire with seed cotton yield per plant was also reported by Rajanna *et al.* (2011) and Kumar *et al.* (2014).

4.2.12 Bundle Strength (g/tex)

The non significant association of seed cotton yield with bundle strength (0.0284 and 0.0017) 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

At genotypic level, the trait showed significant negative association with seed cotton yield per plant (-0.1608*) and lint yield per plant (-0.1772*) indicated that simultaneous improvement of these traits is not possible. Vijayalaxmi *et al.* (2008) reported negatively significant association of the trait with seed cotton yield per plant.

4.2.14 Lint Yield Per Plant (g)

This trait showed highly significant positive association with seed cotton yield per plant (0.9854** and 0.9790**) both at genotypic and phenotypic levels. Rajanna *et al.* (2011), Lakshmi *et al.* (2012) and Erande *et al.* (2014) 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. 4.6. and 4.7. 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 (0.0071). The indirect effects sympodia per plant (0.0007), number of bolls per plant (0.0043), boll weight (0.0003), seed index(0.0074), 2.5%span length(0.0008) and lint yield per plant(0.5396) were positive. While, monopodia per plant (-0.0004), ginning out turn (-0.0284), lint index (-0.0182), micronaire (-0.0005), bundle strength (-0.0001), were negative.

At genotypic level this trait showed negative direct effects with seed cotton yield per plant (-0.0090). The indirect effects *via.* Days to 50% flowering (0.0001), sympodia per plant (0.0093), number of bolls per plant (0.0126), boll weight (0.0004), seed index (0.0156), 2.5% span length (0.0039) and lint yield (0.7205) were positive. Whereas, monopodia per plant (-0.0031), ginning out turn (-0.0234), lint index (-0.0494), micronaire (-0.0033), bundle strength (-0.0006), and uniformity ratio (-0.0010) was negative.

This trait had positive significant correlation with seed cotton yield per plant (0.6727** and 0.5126**) 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*. (2010), Farooq *et al.* (2013), Vinodhana *et al.* (2013), Rajamani *et al.* (2013), Chitti *et al.* (2014) and Kumar *et al.* (2014).

4.3.2 Days to 50% Flowering

At phenotypic level, the direct contribution of this character on seed cotton yield per plant was positive and low (0.0041). The indirect effects via boll weight (0.0005), seed index (0.0123), 2.5% span length (0.0009) and lint yield(0.0599) were positive. While, number of bolls (-0.0013), ginning out turn (-0.0338), lint index (-0.0238), micronaire (-0.0007) and bundle strength (-0.0002) were negative.

At genotypic level, the direct contribution of this character with seed cotton yield per plant was positive (0.0056). The indirect effects via boll weight (0.0005), seed index (0.0297), 2.5%span length (0.0036), uniformity ratio (0.0001) and lint yield per plant (0.0579) were positive. While, plant height (-0.0001), sympodia per plant (-0.0003), number of bolls per plant (-0.0040), ginning out turn (-0.0236), lint index (-0.0616), micronaire (-0.0025) and bundle strength (-0.0015) were negative.

This trait had positive non significant correlation with seed cotton yield per plant (0.0037 and 0.0179) both at genotypic and phenotypic levels, respectively. The low direct effects indicate that the number of sympodia per plant had little effect on yield as its own but its effect on yield per plant may be through its component traits. Further non significant correlations indicate the independent association of this trait in improving yield per plant**.** The results are in agreement with Kumar *et al*. (2010), Rajanna *et al*. (2011), Patel *et al.* (2013), Rajamani *et al.* (2013) and Ranjan *et al.* (2014).

4.3.3 Number of monopodia per plant

At phenotypic level direct contribution of this character on seed cotton yield per plant was negative (-0.0017). The indirect effects *via* plant height (0.0015), sympodia per plant (0.0001), number of bolls (0.0040), lint index (0.0061), bundle strength (0.0001) and lint yield per plant (0.3170) were positive. While, boll weight (-0.0015), ginning out-turn (-0.0317), seed index (-0.0166), and micronaire (-0.0001) were negative.

At genotypic level, the direct contribution of this character with seed cotton yield per plant was negative (-0.0134). The indirect effect via sympodia per plant (0.0013), number of bolls per plant (0.0103), lint index (0.0107), bundle strength (0.0012) and lint yield (0.3646) were positive. Whereas, plant height (-0.0021), boll weight (-0.0021), ginning out turn (-0.0213), seed index (-0.0358), 2.5%span length (-0.0005), micronaire (-0.0011) and uniformity ratio (-0.0015) were negative.

This trait had positive significant correlation with seed cotton yield per plant (0.3105** and 0.2772**) 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. The results are in agreement with Farooq *et al.* (2013), Rajamani *et al.* (2013), Kumar *et al.* (2014) and Farooq *et al.*(2014).

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 (0.0009). The indirect effects of this trait through plant height (0.0054), number of bolls per plant (0.0038), seed index (0.0088), 2.5%span length (0.0006) and lint yield per plant (0.4106) were positive. While, days to 50% flowering (-0.0002), monopodia per plant (-0.0001), boll weight (-0.0007), ginning out turn (-0.0177), lint index (-0.0159), micronaire (-0.0002) and bundle strength (-0.0001) showed negative effects.

The direct contribution of this character on seed cotton yield per plant was low and positive (0.0103) at genotypic level. The indirect effects *via* number of bolls per plant (0.0137), seed index (0.0175), 2.5%span length (0.0028) and lint yield per plant (0.7109) were positive. While, plant height (-0.0081), days to 50% flowering (-0.0002), monopodia per plant (-0.0017), boll weight (-0.0007), ginning out turn (-0.0186), lint index (-0.0456), micronaire (-0.0026), bundle strength (-0.0003) and uniformity ratio (-0.0010) were negative.

This trait had positive significant correlation with seed cotton yield per plant (0.6763** and 0.3950**) both at genotypic and phenotypic levels respectively. The low direct effects indicate that the number of sympodia per plant 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 results were in conformity with earlier works of Kumar *et al.* (2010), Ekinci *et al.* (2010), Salahuddin *et al.* (2010), Srinivasulu *et al.* (2010), Patel *et al.* (2013), Vinodhana *et al.* (2013), Rajamani *et al.* (2013), Chitti *et al.* (2014) and Farooq *et al.* (2014).

4.3.5 Number of Bolls Per Plant

Direct effect of this trait on seed cotton yield per plant was low and positive (0.0088) at phenotypic level and its indirect effects through plant height (0.0035), sympodia per plant (0.0004), 2.5%span length (0.0001), bundle strength (0.0001) and lint yield per plant (0.6508) were positive. While, days to

50% flowering (-0.0006), monopodia per plant (-0.0008), Boll weight (-0.0021), ginning out turn (-0.0195), seed index (-0.0063), lint index (-0.0009), micronaire (-0.0006) and uniformity ratio (-0.0001) showed negative effects**.**

At genotypic level, the direct effect of this character on seed cotton yield per plant was positive (0.0208). The indirect effects through number of sympodia per plant (0.0068), 2.5%span length (0.0001), bundle strength (0.0009) and lint yield per plant (0.6630) were positive. While negative effects were observed through days to 50% flowering (-0.0011), plant height (-0.0054), monopodia per plant (-0.0067), boll weight (-0.0030), ginning out turn (-0.0106), seed index (-0.0122), lint index (-0.0028), micronaire (-0.0031) and uniformity ratio (-0.0026) shows negative effect.

This trait expressed significant positive (0.6441** and 0.6328**) correlations with seed cotton yield per plant at both genotypic and phenotypic levels. The low direct effects indicate that the number of bolls per plant 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, which was in agreement with the earlier works of Lakshmi *et al.* (2012), Vinodhana *et al.* (2013), Patel *et al.* (2013), Rajamani *et al.* (2013), Chitti *et al.* (2014), Ranjan *et al.* (2014) and Kumar *et al.* (2014).

4.3.6 Boll Weight (g)

With respect to phenotypic level, this trait recorded a positive (0.0068) direct effect on seed cotton yield per plant. The indirect effects of this trait *via* plant height (0.0003), days to 50% flowering (0.0003), monopodia per plant (0.0004), seed index (0.0326), 2.5%span length (0.0007) and lint yield per plant (0.3770) were positive. Sympodia per plant (-0.0001), number of bolls per plant (-0.0027), ginning out turn (-0.0039), lint index (-0.0330) and bundle strength (-0.0002) showed negative effects.

At genotypic level, the direct influence of this character on seed cotton yield per plant was positive (0.0081). The indirect effects *via* days to 50% flowering (0.0003), number of monopodia per plant (0.0035), seed index

(0.0806), 2.5%span length (0.0037), micronaire (0.0005), uniformity ratio (0.0016) and lint yield per plant (0.3220) were positive. plant height (-0.0005), sympodia per plant (-0.0009), number of bolls per plant (-0.0078), ginning out turn (-0.0079), lint index (-0.0923) and bundle strength (-0.0020) showed negative effects**.**

This trait showed significant positive association with seed cotton yield per plant (0.3088** and 0.3782**) both genotypic and phenotypic levels. The low direct effects indicate that the boll weight 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 results were in conformity with earlier works of Mohan (2011), Lakshmi *et al*. (2012), Vinodhana *et al.* (2013), Patel *et al.* (2013), Rajamani *et al.* (2013), Ranjan *et al.* (2014) and Farooq *et al.* (2014).

4.3.7 Seed Index (g)

The direct effect exhibited by seed index on seed cotton yield per plant was positive (0.1074) at phenotypic level. However, the indirect effect of this trait *via* plant height (0.0005), days to 50% flowering (0.0005), number of monopodia per plant (0.0003), number of sympodia per plant (0.0001), boll weight (0.0021), 2.5%span length (0.0004), uniformity ratio (0.0001) and lint yield per plant (0.1783) were positive. Number of bolls per plant (-0.0005), ginning out turn (-0.0231), lint index (-0.1144) and bundle strength (-0.0001) showed negative effects.

The direct effect exhibited by seed index on seed cotton yield per plant was positive (0.2268) at genotypic level. Days to 50% flowering (0.0007), monopodia per plant (0.0021), sympodia per plant (0.0008), boll weight (0.0029), 2.5%span length (0.0018), micronaire (0.0004), uniformity ratio (0.0014) and lint yield per plant (0.2886) showed positive effects. While, plant height (-0.0006), number of bolls per plant (-0.0011), ginning out turn (-0.0353), lint index (-0.2833) and bundle strength (-0.0010) showed negative effects.

This trait possessed significant positive correlation with seed cotton yield per plant at (0.2041** and 0.1515*) at both genotypic and phenotypic levels. Moderate direct effects and pronounced correlations suggest that direct selection for seed cotton yield through this trait will be rewarding. These findings are in agreement with Rajanna *et al*. (2011), Vinodhana *et al.* (2013), Rajamani *et al.* (2013), Ranjan *et al.* (2014) and Kumar *et al.* (2014).

4.3.8 Lint Index (g)

The trait, lint index revealed a negative (-0.1269) direct effect on seed cotton yield per plant at phenotypic level. The indirect effects of this trait through, plant height (0.0010), days to 50% flowering (0.0008), monopodia per plant (0.0001), sympodia per plant (0.0001), number of bolls per plant (0.0.0001), boll weight (0.0018), seed index (0.0969), 2.5%span length (0.0007) and lint yield per plant (0.338) were positive. Ginning out turn (-0.0895), micronaire (-0.0002) and bundle strength (-0.0002) showed negative effects.

At genotypic level, the direct influence of this character on seed cotton yield per plant was negative (-0.2977). The indirect effects through days to 50%flowering (0.0012), monopodia per plant (0.0005), sympodia per plant (0.0016), number of bolls per plant (0.0002), boll weight (0.0025), seed index (0.2158), 2.5%span length (0.0030), uniformity ratio (0.0007) and lint yield per plant (0.3944) were positive. Negative effects were exhibited in plant height (-0.0015), ginning out turn (-0.0546), micronaire (-0.0007) and bundle strength (-0.0015).

This trait exhibited significant positive association with seed cotton yield per plant (0.2638** and 0.2184**) 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 are in agreement with Kaushik and Kapoor (2006), Pratap *et al.* (2007), Venkateswarlu *et al.* (2010a) and Farooq *et al.* (2013).

4.3.9 Ginning Out-turn (%)

The direct effect of ginning out-turn on seed cotton yield per plant was negative (-0.1620) at phenotypic level. However, the indirect effects of this trait *via* plant height (0.0012), days to 50%flowering (0.0009), sympodia per plant (0.0001),number of bolls (0.0011),boll weight (0.0002), seed index (0.0153), 2.5%span length (0.0007) and lint yield per plant (0.2041) showed positive effects. Monopodia per plant (-0.0003), lint index (-0.0701), micronaire (-0.0004) and bundle strength (-0.0001) showed negative effects.

This trait showed a negative (-0.0775) direct effect on seed cotton yield per plant at genotypic level. The indirect effects *via* days to 50% flowering (0.0017), sympodia per plant (0.0025), number of bolls per plant (0.0028), boll weight (0.0008), seed index (0.1032), 2.5%span length (0.0043) and lint yield per plant (0.4727) showed positive effects. Plant height (-0.0027), monopodia per plant (-0.0037), lint index (-0.2096), micronaire (-0.0025), bundle strength (-0.0020) and uniformity ratio (-0.0011) showed negative indirect effects through this character.

The character, ginning out-turn showed significant positive correlation with seed cotton yield per plant (0.2889** and 0.2041**) 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. The results are in conformity with the findings of Farooq *et al.* (2013), Vinodhana *et al.* (2013), Rajamani *et al.* (2013), Chitti *et al.* (2014) and Kumar *et al.* (2014).

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(0.0043). The indirect effects through plant height (0.0014), days to 50% flowering (0.0008), sympodia per plant (0.0001), number of bolls per plant (0.0003), boll weight (0.0011), seed index (0.0098) and lint yield (0.1552) were positive. Whereas, the traits ginning out turn (-0.0270), lint index (-0.0197), micronaire (-0.0026), bundle strength (-0.0009), and uniformity ratio (-0.0001) showed negative indirect effects.

At genotypic level, the direct contribution of this character on seed cotton yield per plant was low and positive (0.0169). The indirect effect of this trait through days to 50% flowering (0.0012), monopodia per plant (0.0004), sympodia per plant (0.0017), number of bolls per plant (0.0001), boll weight (0.0017), seed index (0.0240) and lint yield per plant (0.1908) showed positive effects. Plant height (-0.0021), ginning out turn (-0.0197), lint index (-0.0528), micronaire (-0.0092), bundle strength (-0.0058) and uniformity ratio (-0.0018) showed negative effects.

This trait had non significant positive correlations with seed cotton yield per plant (0.1453 and 0.1227) at both genotypic and phenotypic levels. The non significant positive correlations and low direct 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 are in agreement with earlier works of Kumar *et al*. (2010), Mohan (2011), Rajanna *et al*. (2011), Rajamani *et al.* (2013) and Kumar *et al.* (2014).

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

The direct contribution of this character on seed cotton yield per plant was very low and positive (0.0049) at phenotypic level. The indirect effects of this trait through ginning out turn (0.0146), seed index (0.0008), lint index (0.0037), bundle strength (0.0004) and uniformity ratio (0.0001) showed positive effects. Plant height (-0.0008), days to 50% flowering (-0.0006), number of bolls (-0.0012), 2.5% span length (-0.0023) and lint yield per plant (-0.1400) were negative.

The direct influence of this character was low and positive (0.0136) on seed cotton yield per plant at genotypic level. The indirect effects through plant height (0.0022), monopodia per plant (0.0011), boll weight (0.0003), ginning out turn (0.0142), seed index (0.0069), lint index (0.0151), bundle strength (0.0038) and uniformity ratio (0.0025) were showed positive effects. While, days to 50% flowering (-0.0010), sympodia per plant (-0.0020), number of bolls per plant (-0.0047), 2.5% span length (-0.0114) and lint yield per plant (-0.2478) were negative.

However, this trait showed significant negative correlation and non significant negative correlation with seed cotton yield per plant (-0.2073** and -0.1183) at genotypic and phenotypic levels respectively. Low direct effect and significant negative correlation at genotypic level showed that selection of this trait not useful for improving seed cotton yield per plant. The results are in agreement with the earlier effects of Kumar *et al.* (2010), Mohan (2011), Rajanna *et al*. (2011) and Rajamani *et al.* (2013).

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 negative (-0.0013). This trait showed positive effects with plant height (0.0005), days to 50% flowering (0.0006),monopodia per plant (0.0002), sympodia per plant (0.0001), boll weight (0.0011), seed index (0.0083), 2.5% span length (0.0028) and lint yield per plant (0.0230) while, number of bolls per plant (-0.0006), ginning out turn (-0.0163), lint index (-0.0148), micronaire (-0.0017) and bundle strength (-0.0013) showed negative effects.

The direct contribution of this character on seed cotton yield per plant was low negative (-0.0085) at genotypic level. The indirect effect of this trait *via* days to 50% flowering (0.0010), monopodia per plant (0.0019), sympodia per plant (0.0004), boll weight (0.0019), seed index (0.0271), 2.5% span length (0.0115) and lint yield per plant (0.0733) showed positive effects. Plant height (-0.0006), number of bolls per plant (-0.0021), ginning out turn (-0.0177), lint index (-0.0534), micronaire (-0.0061) and uniformity ratio (-0.0002) showed negative effects.

This trait had positive non significant correlation with seed cotton yield per plant (0.0284 and 0.0017) at both genotypic and phenotypic levels. Non significant association and low negative direct effects indicate that greater emphasis in selection should be placed on above positive indirect effects for improvement in seed cotton yield per plant. The results are in agreement with the earlier effects of Farooq *et al.* (2013), Vinodhana *et al.* (2013), Rajamani *et al.* (2013) and Kumar *et al.* (2014).

4.3.13 Uniformity Ratio

At phenotypic level, the direct effect of this trait on seed cotton yield per plant was very low and positive (0.0006). The indirect effects of this trait *via* monopodia per plant (0.0001), boll weight (0.0005), ginning out turn (0.0100), seed index (0.0123), micronaire (0.0007) and bundle strength (0.0001) were positive. Plant height (-0.0002), days to 50%flowering (-0.0001), sympodia per plant (-0.0001), number of bolls per plant (-0.0017), lint index (-0.0089), 2.5% span length (-0.0006) and lint yield per plant (-0.1143) were negative.

Direct effect of uniformity ratio on seed cotton yield per plant low and positive (0.0083) at genotypic level. Plant height (0.0011), days to 50% flowering (0.0001), monopodia per plant (0.0024), boll weight (0.0016), ginning out turn (0.0103), seed index (0.0373), micronaire (0.0041) and bundle strength (0.0002) were positive. Sympodia per plant (-0.0012), number of bolls per plant (-0.0066), lint index (-0.0267), 2.5% span length (-0.0037) and lint yield (-0.1877) was negative.

This trait had negative significant correlation with seed cotton yield per plant (-0.1608*) and negative non-significant correlation (-0.1014) 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 Srinivasulu *et al*. (2010), Mohan (2011), Rajanna *et al*. (2011), Rajamani *et al.* (2013) 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 (1.0538). The indirect effects *via* plant height (0.0036), days to 50% flowering (0.0002), number of sympodia per plant (0.0004), number of bolls per plant (0.0054), boll weight (0.0024), seed index (0.0182) and 2.5% span length (0.0006) were positive. While, monopodia per plant (-0.0005), ginning out turn (-0.0642), lint index (-0.0402), micronaire (-0.0006) and uniformity ratio (-0.0001) were negative.

At genotypic level, the direct contribution of this trait on seed cotton yield per plant was high and positive (1.0593). The indirect effects *via* days to 50% flowering (0.0003), sympodia per plant (0.0069), number of bolls per plant (0.0130), boll weight (0.0025), seed index (0.0618) and 2.5% span length (0.0030) were positive. While, plant height (-0.0061), monopodia per plant (-0.0046), ginning out turn (-0.0346), lint index (-0.1108), micronaire (-0.0032), bundle strength (-0.0006) and uniformity ratio (-0.0015) were negative.

This trait showed significant positive association with seed cotton yield per plant (0.9854** and 0.9790**) at both genotypic and phenotypic levels. High direct effects and pronounced correlations suggest that direct selection for seed cotton yield through this trait will be rewarding. These results were in conformity with earlier works of Tomar and Singh (1996), Pratap *et al.* (2007), Vijayalaxmi *et al.* (2008) and Rajanna *et al*. (2011).

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 Mahalanobi's 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 60 genotypes of cotton studied during Kharif 2014-15 were subjected to multivariate analysis like Mahalanobi's 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 Mahalanobi's D^2 Analysis

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

Significant differences among the genotypes for individual characters were first determined and later the statistical significant differences between the genotypes based on the pooled effects of all the characters were carried out using the *Wilk's criterion* '^' . The *Wilk's* criterion thus obtained was used in calculations of 'V' statistic. The statistic was highly significant indicating that genotypes differ significantly when all the characters were considered simultaneously. The value of 'V' statistic was 3139.9 in the present investigation.

4.4.1.2 Mahalanobi's 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. 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 2.5% span length (18.14) followed by seed index (17.57), days to 50% flowering (13.62), micronaire (10.56), number of monopodia per plant (10.45), bundle strength (8.02), number of bolls per plant (6.1), seed cotton yield per plant (5.48), plant height (4.41), boll weight (1.86), lint index (1.41), lint yield per plant (1.19), uniformity ratio (0.68), ginning out-turn (0.34) and number of sympodia per plant (0.17).

4.4.1.3 Grouping of genotypes into various clusters

The 60 genotypes were grouped into 11 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 60 genotypes into 11 clusters was at random with maximum number of genotypes in cluster I (34 genotypes) from different locations. Cluster II and cluster III are the second largest with nine genotypes each. Clusters IV, V, VI, VII, VIII, IX, X and XI were solitary clusters with nil intra-cluster D^2 values. The mutual relationship between clusters is represented diagrammatically (Fig. 4.9.) by taking average intra- and inter- clusters Euclidean^2 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), Rajamani and Rao (2009), Satish *et al.* (2009), Lakshmi *et al*. (2009), Asha *et al*. (2013), Haritha and Ahamed (2013), Kavithamani *et al.* (2013), Bhailume *et al*. (2014) and Tulasi *et al*. (2014) 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. 4.8.) 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 11 clusters are indicated in Table 4.10.

The maximum intra cluster distance was observed for cluster III (35.23) followed by cluster II (31.03) and cluster I (24.95), while, it was zero for clusters IV, V, VI, VII, VIII, IX, X and XI. The high intra-cluster distance in cluster III indicates the presence of wide genetic diversity among the genotypes present within this cluster.

Cluster I, with 34 genotypes, was the largest of all clusters. It was closest to cluster VI (32.89) followed by Cluster IV (35.50) and it was farthest from cluster X (71.39) followed by cluster XI (67.87).

Nine genotypes were grouped into cluster II. It was nearest to cluster I (36.11) followed by cluster V (41.25) and it was farthest from cluster XI (96.02) followed by cluster X (67.14).

Cluster III was with nine genotypes. It was nearest to cluster I (44.31) followed by cluster VI (51.30) and it was farthest from cluster VII (101.74) followed by cluster X (96.15).

Cluster IV was monogenotypic (CNH 50). It was nearest to cluster V (14.84) followed by cluster VII (32.58) while, it was farthest from cluster VIII (100.36) followed by cluster IX (99.37).

Cluster V was monogenotypic (IH 615). It was nearest to the cluster IV (14.84) followed by cluster X (25.77) and it was farthest from cluster IX (110.20) followed by cluster XI (104.69).

Cluster VI was monogenotypic (L 604). It was closest to the cluster IV (32.80) followed by cluster I (32.89) and was farthest from cluster X (99.52) followed by cluster VIII (91.44).

Cluster VII was monogenotypic (TCH 1705). It was closest to the cluster IV (32.58) followed by cluster V (41.62) and was farthest from cluster XI (122.06) followed by cluster III (101.74).

Cluster VIII was monogenotypic (GISV 267). It was closest to the cluster II (46.12) followed by cluster III (55.47) and was farthest from cluster X (115.83) followed by cluster IV (100.36).

Cluster IX was monogenotypic (HYPS 152). It was closest to the cluster XI (27.69) followed by cluster I (55.00) and was farthest from cluster X (185.35) followed by cluster V (110.20).

Cluster X was monogenotypic (IH 65). It was closest to the cluster V (25.77) followed by cluster IV (39.77) and was farthest from cluster IX (185.35) followed by cluster XI (177.20).

Cluster XI was monogenotypic (L 389). It was closest to the cluster IX (27.69) followed by cluster I (67.87) and was farthest from cluster X (177.20) followed by cluster VII (122.06).

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 14.84 (between cluster IV and V) to 185.35 between cluster IX and X.

The inter-cluster distance was maximum between cluster IX and X (185.35), followed by cluster X and XI (177.20), cluster VII and XI (122.06), cluster VIII and X (115.83), cluster V and IX (110.20), cluster V and XI (104.69), cluster III and VII (101.74) and cluster IV and VIII (100.36). This suggested that there is wide genetic diversity between these clusters. Based on these studies crosses can be made between genotypes of these clusters to obtain desirable transgressive segregants.

Choice of the particular cluster and selection of particular genotype from selected cluster are the two important points to be considered before initiating the crossing programme. 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 69.67 for cluster VII to 141.33 for cluster VIII; Days to 50% flowering had a range of 59.67 for cluster V to 71.67 for cluster VIII; number of monopodia per plant ranged from 0.90 for cluster IX to 3.47 for cluster X; number of sympodia per plant ranged from 10.33 for cluster VII to 21.67 for cluster VIII; number of bolls per plant varied from 26.00 for cluster VII to 58.96 for cluster III; boll weight ranged from 3.73 for cluster X to 4.93 for cluster XI; ginning out-turn ranged from 31.60 for cluster VI to 36.13 for cluster X; seed index varied from 8.46 for cluster IV to 12.56 for cluster VIII; lint index ranged from 3.96 for cluster VI to 7.09 for cluster VIII; 2.5% span length varied from 21.80 for cluster X to 33.37 for cluster IX; micronaire ranged from 3.37 for cluster VI to 5.13 for cluster X; bundle strength varied from 17.71 for cluster X to 23.35 for cluster IX; uniformity ratio ranged from 46.00 for clusters IV and VI to 49.00 for cluster VIII; seed cotton yield per plant ranged from 65.87 for cluster VII to 150.53 for cluster III and lint yield per plant ranged from 22.16 for cluster VII to 53.60 for cluster III.

Higher mean values for boll weight were seen in cluster XI, VIII and IX and higher means for number of boll per plant were observed in clusters III and X 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 Raju (2005), Padmavathi (2008), Rao *et al*. (2009), Gopinath *et al.* (2009), Rajamani and Rao (2009), Satish *et al*. (2009), Lakshmi *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) and Tulasi *et al.* (2014).

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 60 genotypes without changing their relative positions. These 15 new variables are the principal components (PC_1, PC_2 …….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 seven significant principal components having eigen value more than one. The PCA scores for individual genotypes were used for clustering the genotypes as suggested by Anderberg (1993). Results of PCA and cluster analysis are discussed here under.

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 seven principal components with eigen values more than one contributed 78.70 per cent towards the total variability. It was therefore inferred that the essential features of data set had been represented in the first seven principal components. The first principal component contributed maximum towards variability (19.33). The characters *viz*., plant height (0.38), days to 50% flowering (0.10), number of monopodia per plant (0.22), number of bolls per plant (0.27), ginning out turn (0.31), seed index (0.26), lint index (0.26), 2.5% span length (0.27), micronaire (-0.469), bundle strength (-0.142), uniformity ratio (-0.286) and lint yield per plant (0.29) explained the maximum variance in the first principal component (PC_1) and signifying their importance in divergence.

The second principal component (PC_2) described 16.04 per cent of total variance and the characters *viz.*, plant height (0.11), days to 50% flowering (-0.329), number of monopodia per plant (0.28), number of bolls per plant

(0.34), boll weight (-0.14), ginning out turn (-0.34), seed index (-0.34), lint index (-0.22), 2.5% span length (-0.160), bundle strength (-0.34), uniformity ratio (-0.23), micronaire (-0.12) and seed cotton yield (-0.40) showed the maximum variance in this principal component.

The third principal component (PC_3) was characterized by 11.48 per cent contribution towards the total variability. The characters *viz.*, plant height (0.17), days to 50% flowering (0.26), monopodia per plant (-0.34), boll weight (-0.15), ginning out turn (-0.18), seed index (-0.36), lint index (-0.13), micronaire (-0.28), bundle strength (-0.34), lint yield (-0.27), number of sympodia per plant (0.12), 2.5% span length (0.35), uniformity ratio (0.23) and seed cotton yield per plant (0.32) showed the maximum variance in this principal component.

The fourth principal component (PC_4) was conspicuously characterized by high loading of plant height (0.18), days to 50% flowering (-0.43),monopodia per plant (-0.31), sympodia per plant (-0.52), boll weight (0.50), ginning out-turn (0.03), seed index (0.05), lint index (0.11), 2.5% span length (0.27), micronaire (0.02), uniformity ratio (0.08) and lint yield per plant (-0.19). Contribution of this principal component towards the total variability was 10.62 per cent.

The fifth principal component (PC_5) described 8.96 per cent of total variance. The characters *viz.,* plant height (0.31), number of monopodia per plant (-0.19), 2.5% span length (-0.35), number of sympodia per plant (0.31), number of bolls per plant (0.53), ginning out-turn (0.05), seed index (0.19), lint index (0.24), micronaire (0.11), bundle strength (0.18), uniformity ratio (0.15) and lint yield (-0.43) showed the maximum variance in this principal component.

The sixth principal component (PC_6) was characterized by 7.10 per cent contribution towards the total variability. The characters *viz.*, plant height (0.24), days to 50% flowering (0.18), number of monopodia per plant (0.22), number of sympodia per plant (0.05), boll weight (0.41), lint index (-0.62), uniformity ratio (-0.25), ginning out-turn (0.27), micronaire (0.07), bundle strength (0.04) and seed cotton yield per plant (0.15) showed the maximum variance in this principal component.

The seventh principal component (PC_7) was conspicuously characterized by high loading of plant height (0.37), days to 50% flowering (0.19), number of monopodia per plant (0.11), number of sympodia per plant (-0.42), seed index (-0.24), number of bolls per plant (0.10), bundle strength (0.46), micronaire (-0.17), uniformity ratio (0.39), seed cotton yield per plant (0.06) and lint yield per plant (0.29) showed the maximum variance in this principal component. Contribution of this principal component towards the total variability was 5.18 per cent.

The PCA scores for 60 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.*, plant height, ginning out turn, lint yield per plant, number of bolls per plant, 2.5% span length, seed index, lint index, number of monopodia per plant, days to 50% flowering, seed cotton yield per plant, number of sympodia per plant and boll weight 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 60 genotypes were plotted in graph to get two dimensional and three dimensional scatter diagrams (Fig. 4.10. and Fig. 4.11.) 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 Raju (2005), Rajamani and Rao (2009), Srinivasulu (2009), Lakshmi *et al*. (2009), Venkateswarulu *et al.* (2010b), Asha *et al*. (2013), Haritha and Ahamed (2013) and Tulasi *et al.* (2014).

4.4.3 Comparative Study of Both D^2 Analysis and Principal Component Analysis

Both methods of grouping revealed a single concept of non correspondence of genetic divergence and geographic diversity.

Mahalanobi's D^2 statistic and Jackson's principal component analysis both are the tools for analyzing multivariate data. PCA confirms the group constellations obtained by D^2 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, 2.5% span length, seed index, days to 50% flowering, micronaire and number of monopodia per plant contributed maximum towards the divergence. While in PCA the characters viz., plant height, ginning out turn, lint yield per plant, number of bolls per plant, 2.5% span length, seed index, lint index, number of monopodia per plant, days to 50% flowering, seed cotton yield per plant, number of sympodia per plant and boll weight were significantly loaded in PC_1 and contributed more towards variability. It can be concluded that the characters which contributed more towards divergence in D^2 analysis were loaded in PC_1.

FUTURE LINE OF WORK

The genotypes HYPS 152, GISV 267, MCU 5, L 389 and TCH 1741 showed maximum inter-cluster distance in Mahalanobi's D^2 analysis, principal component 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.

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Chapter V

SUMMARY AND CONCLUSIONS

The present investigation was carried out during *kharif* 2014-15 at Regional Agricultural Research Station, Lam farm, Guntur, Andhra Pradesh with 60 genotypes of cotton (*Gossypium hirsutum* L.).

The mean, genetic variability, heritability, genetic advance as per cent of mean, genetic divergence, character association and the magnitude of direct and indirect effects of yield component traits on seed cotton yield were studied for 15 characters *viz.*, plant height, 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, number of monopodia per plant, number of bolls per plant, lint index, seed cotton yield per plant and lint yield 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, boll weight, seed index, 2.5% span length, micronaire and bundle strength revealing the role of additive and non additive gene action. The other traits viz., number of sympodia per plant, ginning out turn 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 monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, ginning out turn, seed index, lint index 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 monopodia per plant, number of sympodia per plant, number of bolls per plant, boll weight, ginning out turn, seed index, lint index 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 60 genotypes studied. The 60 genotypes were grouped into 11 clusters using tocher's method in D^2 analysis.

By Mahalanobi's D^2 statistic, it could be inferred that 2.5% span length, seed index, days to 50% flowering, micronaire, number of monopodia per plant and bundle strength 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 IX (HYPS 152) and cluster X (IH 65), between genotypes of cluster IX (HYPS 152) and cluster XI (L 389), between the genotypes of cluster VII (TCH 1705) and cluster XI (L 389), between the genotypes of cluster VIII (GISV 267) and cluster X (IH 65) after confirming their general combining ability.

Principal component analysis identified seven principal components (PCs), which contributed 78.696 per cent of cumulative variance. The significant factors loaded in PC1 towards maximum genetic divergence were plant height, ginning out turn, lint yield per plant, number of bolls per plant, 2.5% span length, seed index, lint index, number of monopodia per plant, days to 50% flowering, seed cotton yield per plant, number of sympodia per plant and boll weight. 2D and 3D graphs showed wide divergence between GISV 267, MCU 5, HYPS 152, TCH 1741, CNH 120 M/B, LH 2256 and IH 65 signifying their usefulness in cotton breeding to develop high heterotic hybrids.

The genotypes HYPS 152, GISV 267, MCU 5, L 389 and TCH 1741 showed maximum inter-cluster distance in Mahalanobi's D^2 analysis, principal component 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 2.1. Review of literature on genetic variability in cotton (*Gossypium hirsutum* L.).

Sl. No.	Character	Wider genetic variability	Narrow genetic variability
1.	Plant height (cm)	Neelam *et al.* (2002) Laxman and Ganesh (2003) Patnaik *et al.*(2004) Neelima *et al.* (2005) Tuteja *et al.* (2006a) Sarada *et al.* (2010) Hafiz *et al.*(2013) Khan *et al.* (2015) Dhivya *et al.* (2014)	Deshpande and Baig (2003) Kaushik and Kapoor (2006) Pratap (2006) Kale *et al.* (2007) Rao (2008) Neelima *et al.* (2008) Rajanna (2010) Kulkarni *et al.* (2011) Farooq *et al.*(2014) Erande *et al.*(2014) Ahsan *et al.* (2015)
2.	Days to 50% flowering	Ahuja and Tuteja (2000) Laxman and Ganesh (2003) Neelima *et al.* (2005)	Neelam *et al.* (2002) Altaher and Singh (2003a) Narisireddy and Ratnakumari (2004) Raju (2005) Kaushik and Kapoor (2006) Pratap (2006) Neelima *et al.* (2008) Rajanna (2010) Sarada *et al.* (2010) Kulkarni *et al.* (2011) Venkatesh (2012) Erande *et al.*(2014) Dhivya *et al.* (2014)
3.	No. of monopodiaplant^{-1}	Kaushik*et al.* (2003) Sivaprasad (2003) Raju (2005) Kaushik and Kapoor (2006) Tuteja *et al.* (2006a) Verma *et al.* (2006) Rao (2008) Neelima *et al.* (2008) Rajanna (2010) Kishore *et al.* (2011) Mohan (2011) Kulkarni *et al.* (2011) Hafiz *et al.* (2013) Khan *et al.* (2015)	Ahuja and Tuteja (2000) Gururajan (2000) Girase and Mehetre (2002) Erande *et al.*(2014)

Table 2.1. (cont…)

Sl. No.	Character	Wider genetic variability	Narrow genetic variability
4.	No. of sympodiaplant^{-1}	Gururajan (2000) Neelam *et al.* (2002) Deshpande and Baig (2003) Tuteja *et al.* (2003) Kaushik and Kapoor (2006) Tuteja *et al.* (2006a) Neelima *et al.* (2008) Kulkarni *et al*. (2011) Hafiz *et al.* (2013) Erande *et al.*(2014) Dhivya *et al.* (2014) Khan *et al.* (2015)	Girase and Mehetre (2002) Laxman and Ganesh (2003) Vinodhana *et al.* (2013) Farooq *et al.*(2014)
5.	No. of bolls plant^{-1}	Sivaprasad(2003) Gururajan and Sundar (2004) Narisireddy andRatnakumari (2004) Neelima *et al.* (2005) Kaushik and Kapoor (2006) Pratap (2006) Tuteja *et al.* (2006a) Neelima *et al.* (2008) Kishore *et al.* (2011) Mohan (2011) Bazi (2011) Vinodhana *et al.* (2013) Erande *et al.*(2014) Dhivya *et al.* (2014) Ahsan *et al.* (2015) Khan *et al.* (2015)	Girase and Mehetre (2002) Pratap (2006) Hafiz *et al.* (2013)
6.	Boll weight (g)	Kaushik *et al.* (2003) Laxman and Ganesh (2003) Muthuswamy *et al.* (2003) Gururajan and Sundar (2004) Sivaprasad *et al.* (2004) Tuteja *et al.* (2006a) Mohan (2011) Kulkarni *et al*. (2011)	Reddy (2001) Altaher and Singh (2003a) Neelima *et al.* (2008) Rajanna (2010) Bazi (2011) Vinodhana *et al.* (2013) Erande *et al.*(2014) Dhivya *et al.* (2014)

Table 2.1. (cont…)

Sl. No.	Character	Wider genetic variability	Narrow genetic variability
7.	Ginning out- turn (%)	Muthuswamy *et al.* (2003) Laxman and Ganesh (2003) Tuteja *et al.* (2003) Patnaik *et al.* (2004) Neelima *et al.* (2005) Tuteja *et al.* (2006a) Naqib *et al.* (2010)	Rao and Reddy (2001) Neelima (2002) Muraleedhar (2005) Kaushik and Kapoor (2006) Rao (2008) Neelima *et al.* (2008)Mahantesh (2009) Rajanna (2010) Sarada *et al.* (2010) Mohan (2011) Vinodhana *et al.* (2013), Dhivya *et al.* (2014) Farooq *et al.*(2014) Erande *et al.*(2014) Khan *et al.* (2015)
8.	Seed index (g)	Muthuswamy *et al.* (2003) Gururajan and Sundar (2004) Patnaik *et al.*(2004) Kumar (2004) Sivaprasad (2003) Kaushik and Kapoor (2006) Kishore *et al.* (2011) Dhivya *et al.* (2014) Khan *et al.* (2015)	Rao and Reddy (2001) Neelam *et al.* (2002) Altaher and Singh (2003a) Laxman and Ganesh (2003) Neelima *et al.* (2008) Mahantesh (2009) Srinivasulu (2009) Rajanna (2010) Vinodhana *et al.* (2013) Erande *et al.*(2014) Ahsan *et al.* (2015)
9.	Lint index (g)	Laxman and Ganesh (2003) Muthuswamy *et al.* (2003) Sivaprasad (2003) Gururajan and Sundar (2004) Patnaik *et al.* (2004) Neelima *et al.* (2005) Kaushik and Kapoor (2006) Kishore *et al.* (2011) Kulkarni *et al.* (2011) Dhivya *et al.* (2014) Khan *et al.* (2015) Ahsan *et al.* (2015)	Rao and Reddy (2001) Altaher and Singh (2003a) Neelima *et al.* (2008) Naqib *et al.* (2010) Rajanna (2010) Vinodhana *et al.* (2013)

Table 2.1. (cont…)

Sl. No.	Character	Wider genetic variability	Narrow genetic variability
10.	2.5% span length (mm)	Muthuswamy *et al.* (2003) Naphade *et al.* (2004) Patnaik *et al.* (2004) Gururajan and Sundar (2004) Kale *et al.* (2007)	Altaher and Singh (2003a) Neelima *et al.* (2005) Kaushik and Kapoor (2006) Pratap (2006) Tuteja *et al.* (2006a) Verma *et al.* (2006) Rao (2008) Neelima *et al.* (2008) Srinivasulu (2009) Rajanna (2010) Sarada *et al.* (2010) Kishore *et al.* (2011) Mohan (2011) Vinodhana *et al.* (2013) Erande *et al.*(2014) Dhivya *et al.* (2014)
11.	Micronaire (10^{-6} g/inch)	Rao and Reddy (2001) Neelam *et al.* (2002) Muthuswamy *et al.* (2003) Naphade *et al.* (2004) Patnaik *et al.* (2004) Neelima *et al.* (2005) Kulkarni *et al*. (2011)	Reddy (2001) Neelima (2002) Altaher and Singh (2003a) Kaushik and Kapoor (2006) Neelima *et al.* (2008) Srinivasulu (2009) Rajanna (2010) Sarada *et al.* (2010) Vinodhana *et al.* (2013) Khan *et al.* (2015)
12.	Bundle strength (g/tex)	Muthuswamy *et al.* (2003) Gururajan and Sundar (2004) Naphade *et al.* (2004) Patnaik *et al.* (2004) Neelima *et al.* (2005) Kulkarni *et al*. (2011)	Rao and Reddy (2001) Girase and Mehetre (2002) Neelam *et al.* (2002) Altaher and Singh (2003a) Rao (2008) Srinivasulu (2009) Rajanna (2010) Sarada *et al.* (2010) Bazi (2011)

Table 2.1. (cont…)

Sl. No.	Character	Wider genetic variability	Narrow genetic variability
13.	Uniformity ratio	Patnaik *et al.* (2004) Neelima *et al.* (2005)	Muraleedhar (2005) Pratap (2006) Rao (2008) Neelima *et al*. (2008) Srinivasulu (2009) Rajanna (2010) Sarada *et al.* (2010) Kishore *et al.* (2011) Mohan (2011) Bazi (2011) Vinodhana *et al.* (2013) Erande *et al.*(2014) Khan *et al.* (2015)
14.	Seed cotton yield plant^{-1}(g)	Kaushik and Kapoor (2006) Pratap (2006) Verma *et al.* (2006) Naqib *et al*. (2010) Sarada *et al.* (2010) Kishore *et al.* (2011) Mohan (2011) Kulkarni *et al*. (2011) Vinodhana *et al.* (2013) Dhivya *et al.* (2014) Farooq *et al.*(2014) Erande *et al.*(2014) Khan *et al.* (2015) Ahsan *et al.* (2015)	Mahantesh (2009) Rajanna (2010) Bazi (2011)
15.	Lint yield plant^{-1}(g)	Deshpande and Baig (2003) Patnaik *et al.* (2004) Pratap (2006) Patil (2010) Rajanna (2010) Erande *et al.*(2014)	------

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

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

Table 2.2. (cont…)

S. No.	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
3.	Number of monopodia plant^{-1}	Raju (2005) Kaushik and Kapoor (2006) Pratap (2006) Rao (2008) Mahantesh (2009) Lakshmi *et al*. (2012) Hafiz *et al.* (2013) Patel *et al.* (2013) Erande *et al.*(2014)	Reddy (2001) Farooq *et al.*(2014) Khan *et al.* (2015)	Neelima (2002) Sivaprasad (2003)	Rao and Reddy (2001) Kale *et al.* (2007) Rajamani and Rao (2009) Rajanna (2010)
4.	Number of sympodia plant^{-1}	Girase and Mehetre (2002) Neelam *et al.* (2002) Kaushik *et al.* (2003) Kaushik and Kapoor (2006) Verma *et al.* (2006) Sakthi *et al*. (2007) An *et al*. (2008) Ravikesavan *et al.* (2008) Rajanna (2010) Haritha *et al.* (2012) Lakshmi *et al.* (2012) Hafiz *et al.* (2013) Dhivya *et al.* (2014) Erande *et al.*(2014) Khan *et al.* (2015)	Gururajan (2000) Reddy (2001) Vinodhana *et al.* (2013) Farooq *et al.*(2014)	Mahantesh (2009)	Rao and Reddy (2001) Sivaprasad *et al.* (2004) Rajamani and Rao (2009) Bazi (2011) Patel *et al.* (2013)

Table 2.2. (cont…)

S. No.	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
5.	Number of bolls plant^{-1}	Kaushik *et al*. (2003) Sivaprasad (2003) Kaushik and Kapoor (2006) Pratap (2006) Kale *et al*. (2007) Sakthi *et al*. (2007) An *et al*. (2008) Mahantesh (2009) Rajanna (2010) Bazi (2011) Lakshmi *et al*. (2012) Dinakaran *et al*. (2012) Hafiz *et al*. (2013) Vinodhana *et al*. (2013) Dhivya *et al*. (2014) Erande *et al*.(2014) Khan *et al*. (2015) Ahsan *et al*. (2015)	Gururajan and Sundar (2004) Patel *et al*. (2013) Farooq *et al*.(2014)	---	Rajamani and Rao (2009)
6.	Boll weight (g)	Sakthi *et al*. (2007) An *et al*. (2008) Ravikesavan *et al*. (2008) Rajanna (2010) Bazi (2011) Lakshmi *et al*. (2012) Haritha *et al*. (2012)	Gururajan (2000) Gururajan and Sundar (2004) Kale *et al*. (2007) Mahantesh (2009) Farooq *et al*.(2014)	Sivaprasad (2003) Dhivya *et al*. (2014)	Rajamani and Rao (2009)

Table 2.2. (cont…)

S. No	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
6.	Boll weight (g)	Dinakaran *et al.* (2012) Vinodhana *et al.* (2013) Erande *et al.*(2014) Khan *et al.* (2015) Ahsan *et al.* (2015)			
7.	Ginning out-turn (%)	Gururajan and Sundar (2004) Ravikesavan *et al.* (2008) Dinakaran *et al.* (2012) Haritha *et al*. (2012) Ahsan *et al.* (2015)	An *et al.* (2008) Mahantesh (2009) Rajanna (2010) Bazi (2011) Vinodhana *et al.* (2013) Patel *et al.* (2013) Dhivya *et al.* (2014) Erande *et al.* (2014) Farooq *et al.*(2014) Khan *et al.* (2015)	---	Sivaprasad (2003)
8.	Seed index (g)	Raju (2005) Kaushik and Kapoor (2006) An *et al*. (2008) Ravikesavan *et al.* (2008) Mahantesh (2009) Naqib *et al.* (2010) Bazi (2011) Dhivya *et al.* (2014) Erande *et al.*(2014) Ahsan *et al.* (2015)	Gururajan (2000) Neelam *et al.* (2002) Sivaprasad (2003) Sakthi *et al.* (2007) Rajanna (2010) Haritha *et al.* (2012) Vinodhana *et al.* (2013) Khan *et al.* (2015)	---	Reddy (2001) Gururajan and Sundar (2004)

Table 2.2. (cont…)

S. No.	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
9.	Lint index (g)	Raju (2005) Kaushik and Kapoor (2006) Sambamurthy *et al.* (2006) An *et al*. (2008) Ravikesavan *et al.* (2008) Mahantesh (2009) Naqib *et al.* (2010) Bazi (2011) Lakshmi *et al*. (2012) Haritha *et al*. (2012) Vinodhana *et al.* (2013) Dhivya *et al.* (2014) Ahsan *et al.* (2015)	Sakthi *et al.* (2007) Rajanna (2010) Khan *et al.* (2015)	Erande *et al.* (2014)	---
10.	2.5% span length (mm)	Rao and Reddy (2001) Reddy (2001) Gururajan and Sundar (2004) Bazi (2011) Dinakaran *et al.* (2012) Hafiz *et al.* (2013) Vinodhana *et al.* (2013) Dhivya *et al.* (2014) Erande *et al.*(2014)	Sakthi *et al.* (2007) An *et al.* (2008) Ravikesavan *et al.* (2008) Mahantesh (2009) Rajamani and Rao (2009) Rajanna (2010)	---	Haritha *et al.* (2012)

Table 2.2. (cont…)

S. No.	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
11.	Micronaire value (10^{-6}g/inch)	Rao and Reddy (2001) An *et al*. (2008) Ravikesavan *et al*. (2008) Bazi (2011) Vinodhana *et al*. (2013) Erande *et al*.(2014)	Reddy (2001) Sakthi *et al*. (2007) Mahantesh (2009) Dinakaran *et al*. (2012) Haritha *et al*. (2012) Khan *et al*. (2015)	---	Sivaprasad (2003) Rajamani and Rao (2009) Rajanna (2010)
12.	Bundle strength (g/tex)	Reddy (2001) Sambamurthy *et al*. (2006) An *et al*. (2008) Ravikesavan *et al*. (2008) Vinodhana *et al*. (2013)	Rao and Reddy (2001) Sakthi *et al*. (2007) Rajanna (2010)	---	Rao (2008) Mahantesh (2009) Rajamani and Rao (2009) Bazi (2011)
13.	Uniformity ratio	---	Sakthi *et al*. (2007) Mahantesh (2009) Bazi (2011) Dinakaran *et al*. (2012) Haritha *et al*. (2012) Erande *et al*.(2014) Khan *et al*. (2015)	Neelima (2002) Raju (2005)	Muraleedhar (2005) Rajamani and Rao (2009) Rajanna (2010)

Table 2.2. (cont…)

S. No.	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
14.	Seed cotton yield plant^{-1} (g)	An *et al*. (2008) Mahantesh (2009) Rajanna (2010) Bazi (2011) Dinakaran *et al.* (2012) Haritha *et al*. (2012) Vinodhana *et al.* (2013) Dhivya *et al.* (2014) Erande *et al.*(2014) Farooq *et al.*(2014) Khan *et al.* (2015) Ahsan *et al.* (2015)	Gururajan and Sundar (2004) Kale *et al.* (2007)	---	Rajamani and Rao (2009)
15.	Lint yield plant^{-1} (g)	Pratap (2006) Rao (2008) Mahantesh (2009) Rajanna (2010) Dinakaran *et al.* (2012) Erande *et al.*(2014)	---	---	---

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

S. No	Character	Association	S/NS	Reference
1.	Plant height (cm)	Positive	S	Kaushik and Kapoor (2006) Rao (2008) Kishore *et al*. (2011) Rajanna *et al.*(2011) Ranjan *et al*. (2014) Kumar *et al*. (2014) Farooq *et al.*(2014) Erande *et al.*(2014)
			NS	Murthy (1997) Khan *et al.* (2015)
		Negative	S	Reddy (2001) Pratap *et al.* (2007)
			NS	Kaushik *et al.* (2003) Raju (2005) Annapurve *et al.* (2007) Kale *et al.* (2007) Vijayalaxmi *et al.* (2008) Farooq *et al*. (2013) Vinodhana *et al.* (2013)
2.	Days to 50% flowering	Positive	S	Tuteja *et al.* (2006a) Lakshmi *et al.* (2012) Ranjan *et al.* (2014)
			NS	Kaushik and Kapoor (2006) Kale *et al.* (2007) Erande *et al.*(2014)
		Negative	S	Neelima *et al.* (2005)
			NS	Annapurve *et al.* (2007) Rao (2008) Vijayalaxmi *et al.* (2008) Rajanna *et al.*(2011) Kumar *et al.* (2014)
3.	Number of monopodia plant^{-1}	Positive	S	Mahantesh (2009) Mohan (2011) Ranjan *et al.* (2014) Kumar *et al.* (2014)
			NS	Annapurve *et al.* (2007) Kale *et al.* (2007) Vijayalaxmi *et al.* (2008) Kishore *et al.* (2011) Rajanna *et al.*(2011) Erande *et al.*(2014) Khan *et al.* (2015)

Table 2.3 (cont…)

S. No	Character	Association	S/NS	Reference
3.	Number of monopodia plant^{-1}	Negative	S	Batool *et al.* (2010)
			NS	Rao (2008) Venkateswarlu *et al.* (2010a),Farooq *et al.* (2013) Farooq *et al.*(2014)
4.	Number of sympodia plant^{-1}	Positive	S	Vijayalaxmi *et al.* (2008) Patnaik and Sial (2010) Ekinci *et al.* (2010) Batool *et al.*(2010) Mohan (2011) Rajanna *et al.*(2011) Erande *et al.*(2014) Khan *et al.* (2015)
			NS	Neelam *et al.* (2002) Raju (2005) Pradeep and Sumalini (2005) Kishore *et al.* (2011) Farooq *et al.*(2014)
		Negative	NS	Rao (2008) Farooq *et al.* (2013) Vinodhana *et al.* (2013)
5.	Number of bolls plant^{-1}	Positive	S	Makhdoom *et al.* (2010) Patnaik and Sial (2010) Kishore *et al.* (2011) Mohan (2011) Lakshmi *et al.* (2012) Imran *et al.* (2012) Vinodhana *et al.* (2013) Ranjan *et al.* (2014) Kumar *et al.* (2014) Farooq *et al.*(2014) Erande *et al.*(2014)
			NS	Pradeep and Sumalini (2005) Annapurve *et al.* (2007)
		Negative	NS	Farooq *et al.* (2013)
6.	Boll weight (g)	Positive	S	Batool *et al.*(2010) Kishore *et al.* (2011) Mohan (2011) Ranjan *et al.* (2014) Kumar *et al.* (2014) Erande *et al.*(2014) Khan *et al.* (2015)
			NS	Kaushik *et al.* (2003) Vijayalaxmi *et al.* (2008) Vinodhana *et al.* (2013) Farooq *et al.*(2014)

Table 2.3 (cont…)

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

Table 2.3 (cont…)

S. No	Character	Association	S/NS	Reference
9.	Lint index (g)	Positive	S	Sivaprasad (2003) Sambamurthy *et al.* (2006) Naqib *et al.* (2010) Salahuddin *et al.* (2010) Kumar *et al.* (2014)
			NS	Rao (2008) Mohan (2011) Rajanna *et al.*(2011) Erande *et al.*(2014) Ranjan *et al.* (2014) Khan *et al.* (2015)
		Negative	S	Venkateswarlu *et al.* (2010a) Imran *et al.* (2012)
			NS	Mandloi *et al.* (2003) Kaushik and Kapoor (2006) Kishore *et al.* (2011) Vinodhana *et al.* (2013)
10.	2.5% span length (mm)	Positive	S	Erande *et al.*(2014) Kumar *et al.* (2014)
			NS	Neelima (2002) Mandloi *et al.* (2003) Kumar *et al.* (2010) Vinodhana *et al.* (2013)
		Negative	S	Gururajan and Sundar (2004) Venkateswarlu *et al.* (2010a) Kishore *et al.* (2011) Mohan (2011)
			NS	Kale *et al.* (2007) Rao (2008) Vijayalaxmi *et al.* (2008) Rajanna *et al.*(2011) Farooq *et al.* (2013)
11.	Micronaire (10^{-6} g/inch)	Positive	S	Raju (2005) Neelima *et al.* (2005) Sambamurthy *et al.* (2006) Kumar and Ravikesavan (2008), Venkateswarlu *et al.* (2010a), Khan *et al.* (2015)
		Negative	S	Rajanna *et al.* (2011) Erande *et al.*(2014) Kumar *et al.* (2014)
			NS	Kumar *et al.* (2010) Mohan (2011) Farooq *et al.* (2013) Vinodhana *et al.* (2013)

Table 2.3 (cont…)

S. No	Character	Association	S/NS	Reference
12.	Bundle strength (g/tex)	Positive	S	Muhammad *et al.* (2003) Kumar *et al.* (2010) Bazi (2010) Kumar *et al.* (2014)
			NS	Neelam *et al.* (2002) Neelima (2002) Mandloi *et al.* (2003) Kumar *et al.* (2010) Bazi (2011) Mohan (2011)
		Negative	S	Vinodhana *et al.* (2013) Farooq *et al.* (2013)
13.	Uniformity ratio	Positive	S	Sivaprasad (2003) Neelima *et al.* (2005) Khan *et al.* (2015)
			NS	Neelima (2002) Raju (2005)
		Negative	S	Vijayalaxmi *et al.* (2008) Erande *et al.*(2014)
			NS	Tuteja *et al.* (2005) Kishore *et al.* (2011) Mohan (2011) Rajanna *et al.*(2011) Kumar *et al.* (2014)
14.	Lint yield plant^{-1}(g)	Positive	S	Mandloi *et al.* (2003) Deshpande and Baig (2003) Pratap *et al.*(2007) Vijayalaxmi *et al.* (2008) Rajanna *et al.*(2011) Lakshmi *et al.* (2012) Erande *et al.*(2014)

Note: S: Significant NS: Non-significant

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

S. No	Character	Association	S/NS	Reference
I.Plant height (cm) with				
1.	Days to 50% flowering	Positive	S	Erande *et al.*(2014)
			NS	Sangeetha (1998)
		Negative	S	Vijayalaxmi *et al.* (2008) Rajanna *et al.* (2011)
			NS	Sakthi *et al.* (2007) Rao (2008)
2.	Number of monopodia plant^{-1}	Positive	S	Kaushik and Kapoor (2006) Hafiz *et al.* (2013) Rajamani *et al.* (2013) Chitti *et al.* (2014)
			NS	Rao (2008) Kumar *et al.* (2014) Khan *et al.* (2015)
		Negative	S	Ranjan *et al.* (2014)
			NS	Pradeep and Sumalini (2005) Kale *et al.* (2007) Vijayalaxmi *et al.* (2008) Farooq *et al.*(2014) Erande *et al.*(2014)
3.	Number of sympodia plant^{-1}	Positive	S	Sakthi *et al.* (2007) Vijayalaxmi *et al.* (2008) Rajanna *et al.* (2011) Vinodhana *et al.* (2013) Hafiz *et al.*(2013) Farooq *et al.*(2014) Erande *et al.*(2014) Chitti *et al.* (2014)
			NS	Kale *et al.* (2007) Rao (2008) Khan *et al.* (2015)
4.	Number of bolls plant^{-1}	Positive	S	Kaushik and Kapoor (2006) Rajanna *et al.* (2011) Hafiz *et al.* (2013) Vinodhana *et al.* (2013)

Table 2.4 (cont…)

S. No	Character	Association	S/NS	Reference
4.	Number of bolls plant^{-1}	Positive	S	Chitti *et al.* (2014) Ranjan *et al.* (2014) Kumar *et al.* (2014) Farooq *et al.*(2014) Erande *et al.*(2014)
			NS	Sangeetha (1998) Annapurve *et al.* (2007) Khan *et al.* (2015)
		Negative	NS	Sakthi *et al.* (2007)
5.	Boll weight (g)	Positive	S	Rajamani *et al.* (2013) Ranjan *et al.* (2014) Kumar *et al.* (2014) Farooq *et al.*(2014)
			NS	Pradeep and Sumalini (2005)
				Annapurve *et al.* (2007) Vijayalaxmi *et al.* (2008) Vinodhana *et al.* (2013) Erande *et al.*(2014) Khan *et al.* (2015)
		Negative	S	Chitti *et al.* (2014)
			NS	Sakthi *et al.* (2007) Rajanna *et al.* (2011)
6.	Ginning out-turn (%)	Positive	S	Farooq *et al.*(2014)
			NS	Kale *et al.* (2007) Vijayalaxmi *et al.* (2008) Rajanna *et al.* (2011) Erande *et al.*(2014) Khan *et al.* (2015)
		Negative	S	Tyagi (1994)
			NS	Annapurve *et al.* (2007) Vinodhana *et al.* (2013) Rajamani *et al.* (2013) Chitti *et al.* (2014) Ranjan *et al.* (2014)

Table 2.4 (cont…)

S. No	Character	Association	S/NS	Reference
7.	Seed index (g)	Positive	S	Rajanna *et al.* (2011) Vinodhana *et al.* (2013) Erande *et al.*(2014)
			NS	Kale *et al.* (2007) Sakthi *et al.* (2007) Vijayalaxmi *et al.* (2008) Ranjan *et al.* (2014) Khan *et al.* (2015)
		Negative	S	Pratap *et al.* (2007) Kumar *et al.* (2014)
			NS	Rajamani *et al.* (2013) Chitti *et al.* (2014)
8.	Lint index (g)	Positive	S	Rajanna *et al.* (2011) Ranjan *et al.* (2014) Kumar *et al.* (2014)
			NS	Vijayalaxmi *et al.* (2008) Khan *et al.* (2015)
		Negative	NS	Vinodhana *et al.* (2013) Rajamani *et al.* (2013) Erande *et al.*(2014) Chitti *et al.* (2014)
9.	2.5% span length (mm)	Positive	S	Muthu *et al.* (2004) Kumar *et al.* (2014)
			NS	Vijayalaxmi *et al.* (2008) Rajanna *et al.* (2011) Hafiz *et al.* (2013) Vinodhana *et al.* (2013) Erande *et al.*(2014)
		Negative	S	Rajamani *et al.* (2013)
			NS	Kaushik and Kapoor (2006)
10.	Micronaire value (10^{-6}g/inch)	Positive	NS	Vijayalaxmi *et al.* (2008) Vinodhana *et al.* (2013) Erande *et al.*(2014) Khan *et al.* (2015)

Table 2.4 (cont…)

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

Table 2.4 (cont…)

S. No	Character	Association	S/NS	References
II. Days to 50% flowering with				
1.	Number of monopodia plant^{-1}	Positive	NS	Ladole and Meshram (2000) Reddy (2001)
		Negative	S	Rajanna *et al.* (2011) Rajamani *et al.* (2013)
			NS	Neelam *et al.* (2002) Annapurve *et al.* (2007) Kale *et al.* (2007)
2.	Number of sympodia plant^{-1}	Positive	S	Ladole and Meshram (2000) Muraleedhar (2005)
			NS	Basha (1997) Erande *et al.*(2014)
		Negative	S	Altaher and Singh (2003b) Raju (2005) Vijayalaxmi *et al.* (2008)
			NS	Kaushik and Kapoor (2006) Annapurve *et al.* (2007) Kale *et al.* (2007) Sakthi *et al.* (2007) Rajanna *et al.* (2011) Rajamani *et al.* (2013)
3.	Number of bolls plant^{-1}	Positive	S	Muraleedhar (2005) Vijayalaxmi *et al.* (2008) Erande *et al.*(2014) Ranjan *et al.* (2014)
			NS	Kaushik and Kapoor (2006) Kale *et al.* (2007) Rajanna *et al.* (2011) Kumar *et al.* (2014)
		Negative	S	Reddy (2001)
			NS	Raju (2005) Annapurve *et al.* (2007) Sakthi *et al.* (2007) Rajamani *et al.* (2013)

Table 2.4 (cont…)

S. No	Character	Association	S/NS	Reference
4.	Boll weight (g)	Positive	S	Altaher and Singh (2003b) Sivaprasad (2003) Ranjan *et al.* (2014)
			NS	Erande *et al.*(2014)
		Negative	S	Pratap *et al.* (2007) Vijayalaxmi *et al.* (2008) Rajanna *et al.* (2011) Rajamani *et al.* (2013) Kumar *et al.* (2014)
			NS	Neelima (2002) Annapurve *et al.* (2007) Sakthi *et al.* (2007)
5.	Ginning out turn (%)	Positive	S	Neelam *et al.* (2002) Raju (2005)
			NS	Kaushik and Kapoor (2006) Vijayalaxmi *et al.* (2008) Erande *et al.*(2014)
		Negative	S	Pratap *et al.* (2007)
			NS	Rajamani *et al.* (2013) Kumar *et al.* (2014)
6.	Seed index (g)	Positive	S	Raju (2005) Erande *et al.*(2014) Ranjan *et al.* (2014)
			NS	Kale *et al.* (2007) Rajamani *et al.* (2013) Kumar *et al.* (2014)
		Negative	S	Muraleedhar (2005) Vijayalaxmi*et al.* (2008) Rajanna *et al.* (2011)
			NS	Neelam *et al.* (2002) Kaushik and Kapoor (2006)
7.	Lint index (g)	Positive	S	Raju (2005) Ranjan *et al.* (2014) Kumar *et al.* (2014)
			NS	Basha (1997) Neelam *et al.* (2002)

Table 2.4 (cont…)

S. No	Character	Association	S/NS	Reference
7.	Lint index (g)	Negative	S	Pratap *et al.* (2007) Vijayalaxmi *et al.* (2008) Rajanna *et al.* (2011)
			NS	Rajamani *et al.* (2013) Erande *et al.* (2014)
8.	2.5% span length (mm)	Positive	S	Muraleedhar (2005)
			NS	Neelima (2002) Raju (2005) Vijayalaxmi *et al.* (2008) Rajamani *et al.* (2013)
		Negative	NS	Kaushik and Kapoor (2006) Sakthi *et al.* (2007) Rajanna *et al.* (2011) Kumar *et al.* (2014) Erande *et al.*(2014)
9.	Micronaire value (10^{-6}g/inch)	Positive	S	Pratap *et al.* (2007) Rajanna *et al.* (2011)
			NS	Sangeetha (1998) Sakthi *et al.* (2007) Erande *et al.*(2014)
		Negative	S	Altaher and Singh (2003b) Muraleedhar (2005) Vijayalaxmi *et al.* (2008)
			NS	Neelam *et al.* (2002) Rajamani *et al.* (2013) Kumar *et al.* (2014)
10.	Bundle strength (g/tex)	Positive	S	Sivaprasad (2003) Vijayalaxmi *et al.* (2008)
			NS	Neelam *et al.* (2002)
		Negative	S	Altaher and Singh (2003b) Raju (2005)
			NS	Sakthi *et al.* (2007) Rajanna *et al.* (2011) Rajamani *et al.* (2013)

Table 2.4 (cont…)

S. No	Character	Association	S/NS	Reference
11.	Uniformity ratio	Positive	S	Neelima (2002) Neelima *et al.* (2005)
			NS	Rajanna *et al.* (2011) Rajamani *et al.* (2013) Erande *et al.*(2014)
		Negative	NS	Raju (2005) Sakthi *et al.* (2007) Vijayalaxmi *et al.* (2008) Kumar *et al.* (2014)
12.	Lint yield plant^{-1}(g)	Positive	S	Patel *et al.* (2013)
			NS	Erande *et al.*(2014)
		Negative	S	Pratap *et al.* (2007) Rao (2008)
			NS	Vijayalaxmi *et al.* (2008) Rajanna *et al.* (2011)
III. No. of monopodia plant^{-1}with				
1.	Number of sympodia plant^{-1}	Positive	S	Rajanna *et al.* (2011) Mohan (2011) Erande *et al.*(2014) Chitti *et al.* (2014)
			NS	Hafiz *et al.* (2013) Rajamani *et al.* (2013) Khan *et al.* (2015)
		Negative	S	Verma *et al.* (2006) Vijayalaxmi *et al.* (2008) Farooq *et al.*(2014)
			NS	Neelam *et al.* (2002) Pradeep and Sumalini (2005)
2	Number of bolls plant^{-1}	Positive	S	Verma *et al.* (2006) Vijayalaxmi *et al.* (2008) Kishore *et al.* (2011) Mohan (2011) Hafiz *et al.* (2013) Rajamani *et al.* (2013) Erande *et al.*(2014) Kumar *et al.* (2014)

Table 2.4 (cont…)

S. No	Character	Association	S/NS	Reference
2	Number of bolls plant^{-1}	Positive	NS	Annapurve *et al.* (2007) Kale *et al.* (2007) Rajanna *et al.* (2011) Patel *et al.* (2013) Chitti *et al.* (2014) Khan *et al.* (2015)
		Negative	S	Farooq *et al.*(2014)
			NS	Reddy (2001)
3.	Boll weight (g)	Positive	S	Basha (1997)
			NS	Reddy (2001) Neelima (2002) Rajamani *et al.* (2013) Chitti *et al.* (2014) Ranjan *et al.* (2014)
		Negative	S	Pratap *et al.* (2007) Kumar *et al.* (2014)
			NS	Annapurve *et al.* (2007) Rao (2008) Vijayalaxmi *et al.* (2008) Rajanna *et al.* (2011) Farooq *et al.*(2014) Khan *et al.* (2015)
4.	Ginning out-turn (%)	Positive	S	Pratap *et al.* (2007) Annapurve *et al.* (2007) Vijayalaxmi *et al.* (2008) Rajanna *et al.* (2011) Erande *et al.*(2014) Ranjan *et al.* (2014) Kumar *et al.* (2014)
			NS	Neelima (2002) Kale *et al.* (2007) Rao (2008) Farooq *et al.*(2014) Chitti *et al.* (2014)

Table 2.4 (cont…)

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

Table 2.4 (cont…)

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

Table 2.4 (cont…)

S. No	Character	Association	S/NS	Reference
IV. Number of sympodiaplant^{-1} with				
1.	Number of bolls plant^{-1}	Positive	S	Rajanna *et al.* (2011) Salahuddin *et al.* (2010) Mohan (2011) Hafiz *et al.* (2013) Patel *et al.* (2013) Rajamani *et al*. (2013) Farooq *et al.*(2014) Erande *et al.*(2014)
			NS	Pradeep and Sumalini (2005) Annapurve *et al.* (2007) Kale *et al. (*2007) Vinodhana *et al.* (2013) Chitti *et al.* (2014) Khan *et al.* (2015)
		Negative	NS	Raju (2005) Vijayalaxmi *et al.* (2008)
2.	Boll weight (g)	Positive	S	Sakthi *et al*. (2007) Salahuddin *et al.* (2010) Mohan (2011)
			NS	Rao (2008) Vijayalaxmi *et al.* (2008) Rajamani *et al*. (2013) Farooq *et al.*(2014) Erande *et al.*(2014) Khan *et al.* (2015)
		Negative	S	Pratap *et al.* (2007) Rajanna *et al.* (2011) Vinodhana *et al.* (2013)
			NS	Pradeep and Sumalini (2005) Annapurve *et al.* (2007) Kale *et al.* (2007) Chitti *et al.* (2014)
3.	Ginning out-turn (%)	Positive	S	Annapurve *et al.* (2007) Kale *et al.* (2007) Mohan (2011) Farooq *et al.* (2014) Erande *et al.* (2014)

Table 2.4 (cont…)

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

Table 2.4 (cont…)

S. No	Character	Association	S/NS	Reference
5.	Lint index (g)	Negative	S	Muraleedhar (2005) Venkateswarlu *et al*. (2010a) Chitti *et al.* (2014)
			NS	Rao *et al.* (2001) Erande *et al.*(2014)
6.	2.5% Span length (mm)	Positive	S	Neelam *et al.* (2002) Sakthi *et al.* (2007) Mohan (2011) Vinodhana *et al.* (2013)
			NS	Verma *et al.* (2006)
		Negative	S	Raju (2005) Kale *et al.* (2007) Rao (2008) Vijayalaxmi *et al.* (2008) Erande *et al.*(2014)
			NS	Muraleedhar (2005) Rajanna *et al.* (2011) Rajamani *et al.* (2013)
7.	Micronaire value (10^{-6}g/inch)	Positive	S	Raju (2005) Vijayalaxmi *et al.* (2008) Mohan (2011)
			NS	Neelam *et al.* (2002) Sakthi *et al.* (2007) Khan *et al.* (2015)
		Negative	S	Rajanna *et al.* (2011)
			NS	Vinodhana *et al.* (2013) Rajamani *et al.* (2013) Erande *et al.*(2014)
8.	Bundle strength (g/tex)	Positive	S	Altaher and Singh (2003b) Muthu *et al.* (2004) Mohan (2011) Rajanna *et al.* (2011)
			NS	Sakthi *et al.* (2007) Rao (2008) Vinodhana *et al.* (2013)

Table 2.4 (cont…)

S. No	Character	Association	S/NS	Reference
8.	Bundle strength (g/tex)	Negative	NS	Raju (2005) Vijayalaxmi *et al.* (2008) Rajamani *et al.* (2013)
9.	Uniformity ratio	Positive	S	Vijayalaxmi *et al.* (2008) Mohan (2011)
			NS	Rajanna *et al.* (2011) Rajamani *et al.* (2013) Erande *et al.*(2014) Khan *et al.* (2015)
		Negative	S	Rao (2008) Venkateswarlu *et al.* (2010a)
10.	Lint yield plant^{-1} (g)	Positive	S	Pratap *et al.* (2007) Rao (2008) Rajanna *et al.* (2011) Patel *et al.* (2013) Erande *et al.*(2014)
			NS	Vijayalaxmi *et al.* (2008)
V. Number of bolls plant^{-1} with				
1.	Boll weight (g)	Positive	S	Neelima (2002) Altaher and Singh (2003b) Neelima *et al.*(2005) Sakthi *et al.* (2007) Salahuddin *et al.* (2010) Ranjan *et al.* (2014) Farooq *et al.*(2014) Erande *et al.*(2014)
			NS	Rao (2008) Rajamani *et al.* (2013) Khan *et al.* (2015)
		Negative	S	Rajanna *et al.* (2011) Kumar *et al.* (2014)
			NS	Kale *et al.* (2007) Vinodhana *et al.* (2013)
2.	Ginning out-turn (%)	Positive	S	Muthu *et al.* (2004) Pratap *et al.* (2007) Salahuddin *et al.* (2010)

Table 2.4 (cont…)

S. No	Character	Association	S/NS	Reference
2.	Ginning out-turn (%)	Positive	NS	Kale *et al.* (2007) Vijayalaxmi *et al.* (2008) Rajamani *et al.* (2013) Chitti *et al.* (2014) Ranjan *et al.* (2014) Farooq *et al.*(2014) Erande *et al.*(2014) Khan *et al.* (2015)
		Negative	S	Venkateswarlu *et al.* (2010a) Mohan (2011) Vinodhana *et al.* (2013) Kumar *et al.* (2014)
			NS	Sangeetha (1998) Rajanna *et al.* (2011)
3.	Seed index (g)	Positive	S	Neelima *et al.* (2005) Mahantesh (2009) Vinodhana *et al.* (2013) Erande *et al.*(2014) Chitti *et al.* (2014)
			NS	Reddy (2001) Ranjan *et al.* (2014) Khan *et al.* (2015)
		Negative	S	Vijayalaxmi *et al.* (2008) Mohan (2011) Kumar *et al.* (2014)
			NS	Rao (2008) Rajanna *et al.* (2011) Rajamani *et al.* (2013)
4.	Lint index (g)	Positive	S	Muthu *et al.* (2004) Neelima *et al.* (2005) Chitti *et al.* (2014)
			NS	Sakthi *et al.* (2007) Mahantesh (2009) Rajamani *et al.* (2013) Erande *et al.*(2014) Ranjan *et al.* (2014) Khan *et al.* (2015)

Table 2.4 (cont…)

S. No	Character	Association	S/NS	Reference
4.	Lint index (g)	Negative	S	Vijayalaxmi *et al.* (2008) Venkateswarlu *et al.* (2010a) Mohan (2011) Kumar *et al.* (2014)
			NS	Rao (2008) Rajanna *et al.* (2011) Vinodhana *et al.* (2013)
5.	2.5% Span length (mm)	Positive	S	Mohan (2011) Vinodhana *et al.* (2013) Hafiz *et al.* (2013)
			NS	Sakthi *et al.* (2007) Rao (2008) Rajamani *et al.* (2013) Erande *et al.*(2014) Kumar *et al.* (2014)
		Negative	S	Tyagi (1994) Muraleedhar (2005)
			NS	Vijayalaxmi *et al.* (2008) Rajanna *et al.* (2011)
6.	Micronaire value (10^{-6}g/inch)	Positive	S	Muthu *et al.* (2004) Raju (2005) Sakthi *et al.* (2007) Rao (2008) Venkateswarlu *et al.* (2010a)
			NS	Rao *et al.* (2001) Neelam *et al.* (2002) Khan *et al.* (2015)
		Negative	S	Pratap *et al.* (2007) Vijayalaxmi *et al.* (2008) Mohan (2011) Vinodhana *et al.* (2013) Kumar *et al.* (2014)
			NS	Rajanna *et al.* (2011) Rajamani *et al.* (2013) Erande *et al.*(2014)

Table 2.4 (cont…)

S. No	Character	Association	S/NS	Reference
7.	Bundle strength (g/tex)	Positive	S	Altaher and Singh (2003b) Muthu *et al.* (2004) Kumar *et al.* (2014)
			NS	Sakthi *et al.* (2007) Vijayalaxmi *et al.* (2008) Rajanna *et al.* (2011) Vinodhana *et al.* (2013)
		Negative	S	Sangeetha (1998)
			NS	Raju (2005) Rao (2008)
8.	Uniformity ratio	Positive	S	Muthu *et al.* (2004)
			NS	Rajanna *et al.* (2011) Rajamani *et al.* (2013)
		Negative	S	Vijayalaxmi *et al.* (2008) Mohan (2011)
			NS	Neelima (2002) Sakthi *et al.* (2007) Erande *et al.*(2014) Kumar *et al.* (2014) Khan *et al.* (2015)
9.	Seed cotton yield plant^{-1} (g)	Positive	S	Chitti *et al.* (2014) Farooq *et al.*(2014) Erande *et al.*(2014) Khan *et al.* (2015)
10.	Lint yield plant^{-1} (g)	Positive	S	Pratap *et al.* (2007) Rao (2008) Vijayalaxmi *et al.* (2008) Rajanna *et al.* (2011)
			NS	Erande *et al.*(2014)

Table 2.4 (cont…)

S. No	Character	Association	S/NS	Reference
VI. Boll weight (g) with				
1.	Ginning out-turn (%)	Positive	S	Muthuswamy and Vivekanandan (2004) Raju (2005) Mohan (2011) Chitti *et al.* (2014) Kumar *et al.*(2014)
			NS	Rajanna *et al.* (2011) Rajamani *et al.* (2013) Farooq *et al.*(2014) Erande *et al.*(2014) Khan *et al.* (2015)
		Negative	NS	Sakthi *et al.* (2007) Vijayalaxmi *et al.* (2008) Ranjan *et al.* (2014)
2.	Seed index (g)	Positive	S	Neelima *et al.* (2005) Venkateswarlu *et al.* (2010a) Rajanna *et al.* (2011) Mohan (2011) Vinodhana *et al.* (2013) Rajamani *et al.* (2013) Ranjan *et al.* (2014) Kumar *et al.* (2014)
			NS	Erande *et al.*(2014) Khan *et al.* (2015)
		Negative	S	Rao (2008)
			NS	Chitti *et al.* (2014)
3.	Lint index (g)	Positive	S	Vijayalaxmi *et al.* (2008) Venkateswarlu *et al.* (2010a) Rajanna *et al.* (2011) Mohan (2011) Vinodhana *et al.* (2013) Rajamani *et al.* (2013) Kuma *et al.* (2014)
			NS	Ranjan *et al.* (2014) Erande *et al.*(2014) Khan *et al.* (2015)

Table 2.4 (cont…)

S. No	Character	Association	S/NS	Reference
4.	2.5% Span length (mm)	Positive	S	Sivaprasad (2003) Verma *et al.* (2006) Vijayalaxmi *et al.* (2008)
			NS	Rajanna *et al.* (2011) Vinodhana *et al.* (2013) Rajamani *et al.* (2013) Erande *et al.*(2014) Kumar *et al.* (2014)
		Negative	S	Mohan (2011)
			NS	Neelima (2002)
5.	Micronaire value (10^{-6} g/inch)	Positive	S	Tyagi (1994) Vinodhana *et al.* (2013) Kumar *et al.* (2014)
			NS	Sakthi *et al.* (2007) Rao (2008) Khan *et al.* (2015)
		Negative	S	Rao *et al.* (2001) Neelima (2002) Erande *et al.*(2014)
			NS	Vijayalaxmi *et al.* (2008) Rajamani *et al.* (2013)
6.	Bundle strength (g/tex)	Positive	S	Muraleedhar (2005) Rao (2008) Mahantesh (2009) Rajamani *et al.* (2013)
			NS	Sakthi *et al.* (2007) Vijayalaxmi *et al.* (2008)
		Negative	S	Rao *et al.* (2001) Mohan (2011) Vinodhana *et al.* (2013)
			NS	Rajanna *et al.* (2011) Kumar *et al.* (2014)
7	Uniformity ratio	Positive	NS	Rajanna *et al.* (2011) Khan *et al.* (2015)
		Negative	S	Neelima (2002) Muraleedhar (2005) Rajamani *et al.* (2013)
			NS	Sakthi *et al.* (2007) Rao (2008) Vijayalaxmi *et al.* (2008) Erande *et al.*(2014)

S. No	Character	Association	S/NS	Reference
8.	Seed cotton yield plant^{-1} (g)	Positive	S	Chitti *et al.* (2014) Erande *et al.*(2014) Khan *et al.* (2015)
			NS	Farooq *et al.*(2014)
9.	Lint yield plant^{-1} (g)	Positive	S	Dedaniya and Pethani (1994) Rao (2008) Rajanna *et al.* (2011) Erande *et al.*(2014)
			NS	Patel *et al.* (2013)
IX. Ginning out-turn (%) with				
1.	Seed index (g)	Positive	S	Neelima (2002) Altaher and Singh (2003b)
			NS	Rao *et al.* (2001) Kale *et al.* (2007) Rajamani *et al.* (2013) Erande *et al.*(2014)
		Negative	S	Rajanna *et al.* (2011) Mohan (2011) Kumar *et al.* (2014)
			NS	Chitti *et al.* (2014) Khan *et al.* (2015)
2.	Lint index (g)	Positive	S	Muthu *et al.* (2004) Raju (2005) Pratap *et al.* (2007) Sakthi *et al.* (2007) Vijayalaxmi *et al.* (2008) Mohan (2011) Rajanna *et al.* (2011) Chitti *et al.* (2014) Kumar *et al.* (2014)
			NS	Rao *et al.* (2001) Neelam *et al.* (2002) Rajamani *et al.* (2013) Erande *et al.*(2014) Khan *et al.* (2015)

Table 2.4 (cont…)

Table 2.4 (cont…)

S. No	Character	Association	S/NS	Reference
3.	2.5% span length (mm)	Positive	S	Sivaprasad(2003) Kale *et al.* (2007)
			NS	Reddy (2001) Neelima (2002) Rajamani *et al*. (2013)
		Negative	S	Muthu *et al.* (2004) Sakthi *et al*. (2007) Mahantesh (2009) Mohan (2011) Kumar *et al.* (2014)
			NS	Neelam *et al.* (2002) Kale *et al.* (2007) Vijayalaxmi *et al.* (2008) Rajanna *et al.* (2011) Erande *et al.*(2014)
4.	Micronaire value (10^{-6}g/inch)	Positive	S	Rao *et al.* (2001) Muthu *et al.* (2004) Mohan (2011)
			NS	Rao (2008) Rajanna *et al.* (2011) Vinodhana *et al.* (2013) Rajamani *et al*. (2013) Erande *et al.*(2014) Kumar *et al.* (2014) Khan *et al.* (2015)
		Negative	S	Vijayalaxmi *et al.* (2008)
			NS	Mandloi *et al.* (2003) Raju (2005)
5.	Bundle strength (g/tex)	Positive	S	Mandloi *et al.* (2003) Sambamurthy *et al.* (2006) Rao (2008)
			NS	Neelima (2002) Vijayalaxmi *et al.* (2008)
		Negative	S	Neelam *et al.* (2002) Mahantesh (2009) Mohan (2011) Vinodhana *et al.* (2013) Kumar *et al.* (2014)

S. No	Character	Association	S/NS	Reference
5.	Bundle strength (g/tex)	Negative	NS	Sakthi *et al*. (2007) Rajanna *et al*. (2011) Rajamani *et al*. (2013)
6.	Uniformity ratio	Positive	S	Sakthi *et al*. (2007) Mohan (2011) Kumar *et al.* (2014)
			NS	Rajanna *et al*. (2011) Rajamani *et al*. (2013) Erande *et al.*(2014) Khan *et al.* (2015)
		Negative	S	Altaher and Singh (2003b)
			NS	Vijayalaxmi *et al.* (2008) Eswar (2008)
7.	Lint yield plant^{-1} (g)	Positive	S	Pratap *et al*. (2007) Vijayalaxmi *et al.* (2008) Rao (2008) Rajanna *et al*. (2011) Patel *et al.* (2013)
			NS	Dedaniya and Pethani (1994) Mandloi *et al.* (2003) Erande *et al.*(2014)
VII. Seed index (g) with				
1.	Lint index (g)	Positive	S	Mahantesh (2009) Venkateswarlu *et al*. (2010a) Rajanna *et al*. (2011) Mohan (2011) Vinodhana *et al.* (2013) Rajamani *et al*. (2013) Chitti *et al.* (2014) Ranjan *et al.* (2014) Kumar *et al.* (2014)
			NS	Neelam *et al.* (200[illegible] Erande *et al.*(2014) Khan *et al.* (2015)

Table 2.4 (cont…)

Table 2.4 (cont…)

S. No	Character	Association	S/NS	Reference
2.	2.5% span length (mm)	Positive	S	Vijayalaxmi *et al.* (2008) Mohan (2011) Rajanna *et al.* (2011) Vinodhana *et al.* (2013) Rajamani *et al.* (2013) Kumar *et al.* (2014)
			NS	Neelam *et al.* (2002)
		Negative	S	Kale *et al.* (2007)
			NS	Neelima (2002) Mandloi *et al.* (2003) Erande *et al.*(2014)
3.	Micronaire value (10^{-6} g/inch)	Positive	S	Rao (2008) Vijayalaxmi *et al.* (2008) Rajamani *et al.* (2013)
			NS	Neelam *et al.* (2002) Neelima (2002) Erande *et al.*(2014) Khan *et al.* (2015)
		Negative	S	Rajanna *et al.* (2011) Mohan (2011) Kumar *et al.* (2014)
			NS	Vinodhana *et al.* (2013)
4.	Bundle strength (g/tex)	Positive	S	Muthu *et al.* (2004) Mohan (2011) Vinodhana *et al.* (2013) Kumar *et al.* (2014)
			NS	Neelam *et al.* (2002) Neelima (2002) Altaher and Singh (2003b)
		Negative	S	Rao *et al.* (2001) Rajanna *et al.* (2011)
			NS	Rao (2008) Vijayalaxmi *et al.* (2008) Rajamani *et al.* (2013)
5.	Uniformity ratio	Positive	NS	Erande *et al.*(2014) Khan *et al.* (2015)

Table 2.4 (cont…)

S. No	Character	Association	S/NS	Reference
5.	Uniformity ratio	Negative	S	Neelima (2002) Muraleedhar (2005) Rajanna *et al.* (2011) Kumar *et al.* (2014)
			NS	Rao (2008) Vijayalaxmi *et al.* (2008) Rajamani *et al*. (2013)
6.	Seed cotton yield plant^{-1} (g)	Positive	NS	Erande *et al.*(2014) Khan *et al.* (2015)
		Negative	NS	Chitti *et al.* (2014)
7.	Lint yield plant^{-1} (g)	Positive	NS	Rao (2008) Erande *et al.*(2014)
		Negative	NS	Mandloi *et al.* (2003) Vijayalaxmi *et al.* (2008) Rajanna *et al.* (2011)
VIII. Lint index (g) with				
1.	2.5% span length (mm)	Positive	S	Muthu *et al.* (2004) Sambamurthy *et al.* (2006) Sakthi *et al*. (2007) Vijayalaxmi *et al.* (2008) Rajamani *et al*. (2013) Kumar *et al.* (2014)
			NS	Rajanna *et al.* (2011) Erande *et al.*(2014)
		Negative	S	Mohan (2011)
			NS	Neelima (2002) Mandloi *et al.* (2003) Vinodhana *et al.* (2013)
2.	Micronaire value (10^{-6} g/inch)	Positive	S	Neelam *et al.* (2002) Rao (2008) Rajamani *et al*. (2013)

Table 2.4 (cont…)

Sl. No	Character	Association	S/NS	Reference
2.	Micronaire value (10^{-6} g/inch)	Positive	NS	Sakthi *et al*. (2007) Rajanna *et al*. (2011) Vinodhana *et al*. (2013) Erande *et al*.(2014) Khan *et al*. (2015)
		Negative	S	Mandloi *et al*. (2003) Mahantesh (2009) Kumar *et al*. (2014)
			NS	Rao *et al*. (2001)
3.	Bundle strength (g/tex)	Positive	S	Muthu *et al*. (2004) Sambamurthy *et al*. *(*2006)
			NS	Neelima (2002) Sakthi *et al*. (2007) Vijayalaxmi *et al*. (2008)
		Negative	S	Vinodhana *et al*. (2013)
			NS	Reddy (2001) Neelam *et al*. (2002) Mandloi *et al*. (2003) Raju (2005) Rajanna *et al*. (2011) Rajamani *et al*. (2013) Kumar *et al*. (2014)
4.	Uniformity ratio	Positive	S	Mohan (2011)
			NS	Raju (2005) Vijayalaxmi *et al*. (2008) Erande *et al*.(2014) Khan *et al*. (2015)
		Negative	S	Muthu *et al*. (2004) Sakthi *et al*. (2007) Rajanna *et al*. (2011)
			NS	Sangeetha (1998) Neelima (2002) Rao (2008) Rajamani *et al*. (2013) Kumar *et al*. (2014)

Table 2.4 (cont…)

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

Table 2.4 (cont…)

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

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

Table 2.4 (cont…)

<table>
<tr><th>S. No</th><th>Character</th><th>Association</th><th>S/NS</th><th>Reference</th></tr>
<tr><td colspan="5">XII. Bundle strength (g/tex) with</td></tr>
<tr><td rowspan="3">2.</td><td rowspan="3">Lint yield plant^{-1} (g)</td><td>Positive</td><td>S</td><td>Dedaniya and Pethani (1994)</td></tr>
<tr><td rowspan="2">Negative</td><td>S</td><td>Mandloi et al. (2003)</td></tr>
<tr><td>NS</td><td>Rao (2008)
Rajanna et al. (2011)</td></tr>
<tr><td colspan="5">XIII. Uniformity ratio with</td></tr>
<tr><td rowspan="2">1.</td><td rowspan="2">Lint yield plant^{-1} (g)</td><td>Positive</td><td>S</td><td>Rajanna et al. (2011)</td></tr>
<tr><td>Negative</td><td>NS</td><td>Dedaniya and Pethani (1994)
Vijayalaxmi et al. (2008)
Erande et al.(2014)</td></tr>
</table>

Note: S: Significant NS: Non-significant

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

S. No	Character	Positive Direct effect	Negative Direct effect
1.	Plant height (cm)	Reddy (2001) Neelima (2002) Altaher and Singh (2003a) Sivaprasad (2003) Muthu *et al.* (2004) Kaushik and Kapoor (2006) Sakthi *et al.* (2007) Rajanna *et al.* (2011) Ranjan *et al.* (2014) Farooq *et al.*(2014) Erande *et al.*(2014)	Raju (2005) Verma *et al.* (2006) Annapurve *et al.* (2007) Kale *et al.* (2007) Vijayalaxmi *et al.* (2008) Kumar *et al.* (2010) Farooq *et al.* (2013) Vinodhana *et al.* (2013) Rajamani *et al.* (2013) Chitti *et al.* (2014) Kumar *et al.* (2014)
2.	Days to 50% flowering	Sangeetha (1998) Tuteja *et al.* (2006b) Kumar *et al.* (2010) Rajanna *et al.* (2011) Patel *et al.* (2013) Rajamani *et al.* (2013) Ranjan *et al.* (2014)	Gururajan (2000) Muthu *et al.* (2004) Kaushik and Kapoor (2006) Annapurve *et al.* (2007) Kale *et al.* (2007) Sakthi *et al.* (2007) Vijayalaxmi *et al.* (2008) Kumar *et al.* (2014) Erande *et al.*(2014)
3.	Number of monopodia plant^{-1}	Vijayalaxmi *et al.* (2008) Salahuddin *et al.* (2010) Ekinci *et al.* (2010) Srinivasulu *et al.* (2010) Mohan (2011) Rajanna *et al.* (2011) Patel *et al.* (2013) Chitti *et al.* (2014) Ranjan *et al.* (2014)	Sivaprasad (2003) Raju (2005) Kaushik and Kapoor (2006) Tuteja *et al.* (2006b) Verma *et al.* (2006) Annapurve *et al.* (2007) Kale *et al.* (2007) Farooq *et al.* (2013) Rajamani *et al.* (2013) Kumar *et al.* (2014) Farooq *et al.*(2014) Erande *et al.*(2014)
4.	Number of sympodia plant^{-1}	Vijayalaxmi *et al.* (2008) Kumar *et al.* (2010) Ekinci *et al.* (2010) Salahuddin *et al.* (2010) Srinivasulu *et al.* (2010) Patel *et al.* (2013) Vinodhana *et al.* (2013), Rajamani *et al.* (2013) Chitti *et al.* (2014) Farooq *et al.*(2014) Erande *et al.*(2014)	Gururajan (2000) Reddy (2001) Sivaprasad (2003) Muthu *et al.* (2004) Raju (2005) Tuteja *et al.* (2006b) Venkateswarlu *et al.* (2010a) Farooq *et al.* (2013)

Table 2.5 (cont…)

S. No	Character	Positive Direct effect	Negative Direct effect
5.	Number of bolls plant^{-1}	Vijayalaxmi *et al.* (2008) Kumar *et al.* (2010) Ekinci *et al.* (2010) Salahuddin *et al.* (2010) Srinivasulu *et al.* (2010) Mohan (2011) Lakshmi *et al.* (2012) Vinodhana *et al.* (2013) Patel *et al.* (2013) Rajamani *et al.* (2013) Chitti *et al.* (2014) Ranjan *et al.* (2014) Erande *et al.*(2014) Kumar *et al.* (2014)	Kaushik *et al.* (2003) Tuteja *et al.* (2006b) Farooq *et al.* (2013) Farooq *et al.*(2014)
6.	Boll weight (g)	Vijayalaxmi *et al.* (2008) Kumar *et al.* (2010) Ekinci *et al.* (2010) Salahuddin *et al.* (2010) Srinivasulu *et al.* (2010) Lakshmi *et al.* (2012) Mohan (2011) Vinodhana *et al.* (2013) Patel *et al.* (2013) Rajamani *et al.* (2013) Ranjan *et al.* (2014) Farooq *et al.*(2014) Erande *et al.*(2014)	Ladole and Meshram (2000) Verma *et al.* (2006) Farooq *et al.* (2013) Chitti *et al.* (2014) Kumar *et al.* (2014)
7.	Seed index (g)	Vijayalaxmi *et al.* (2008) Kumar *et al.* (2010) Mohan (2011) Rajanna *et al.* (2011) Vinodhana *et al.* (2013) Rajamani *et al.* (2013) Ranjan *et al.* (2014) Kumar *et al.* (2014)	Ladole and Meshram (2000) Neelima (2002) Altaher and Singh (2003a) Gururajan and Sundar (2004) Raju (2005) Kale *et al.* (2007) Farooq *et al.* (2013)
8.	Lint index (g)	Vijayalaxmi *et al.* (2008) Kumar *et al.* (2010) Vinodhana *et al.* (2013), Rajamani *et al.* (2013) Chitti *et al.* (2014) Ranjan *et al.* (2014) Erande *et al.*(2014) Kumar *et al.* (2014)	Sivaprasad (2003) Muthu *et al.* (2004) Kaushik and Kapoor (2006) Pratap *et al.* (2007) Venkateswarlu *et al.* (2010a) Farooq *et al.* (2013)

Table 2.5 (cont…)

S. No	Character	Positive Direct effect	Negative Direct effect
9.	Ginning out-turn (%)	Gururajan (2000) Reddy (2001) Muthu *et al.*(2004) Kaushik and Kapoor (2006) Tuteja *et al.* (2006b) Verma *et al.* (2006) Kale *et al.* (2007) Pratap *et al.* (2007) Mohan (2011) Patel *et al.* (2013) Ranjan *et al.* (2014) Farooq *et al.*(2014) Erande *et al.*(2014)	Vijayalaxmi *et al.* (2008) Kumar *et al.* (2010) Salahuddin *et al.* (2010) Venkateswarlu *et al.* (2010a) Farooq *et al.*(2013) Vinodhana *et al.*(2013) Rajamani *et al.* (2013) Chitti *et al.* (2014) Kumar *et al.* (2014)
10.	2.5% span length (mm)	Raju (2005) Kaushik and Kapoor (2006) Tuteja *et al.* (2006b) Kale *et al.* (2007) Kumar *et al.* (2010) Mohan (2011) Rajanna *et al.* (2011) Rajamani *et al.* (2013) Erande *et al.*(2014) Kumar *et al.* (2014)	Reddy (2001) Neelima (2002) Muhammad *et al.* (2003) Sakthi *et al.* (2007) Venkateswarlu *et al.* (2010a) Farooq *et al.* (2013) Vinodhana *et al.* (2013)
11.	Micronaire value (10^{-6} g/inch)	Neelima *et al.* (2005) Sambamurthy *et al.* (2006) Pratap *et al.* (2007) Sakthi *et al.* (2007) Vijayalaxmi *et al.* (2008) Kumar *et al.* (2010) Mohan (2011) Rajanna *et al.* (2011) Rajamani *et al.* (2013) Erande *et al.*(2014)	Gururajan and Sundar (2004) Raju (2005) Verma *et al.* (2006) Venkateswarlu *et al.* (2010a) Vinodhana *et al.* (2013) Kumar *et al.* (2014)
12.	Bundle strength (g/tex)	Neelima (2002) Sivaprasad (2003) Sambamurthy *et al.* (2006) Sakthi *et al.* (2007) Rajanna *et al.* (2011)	Raju (2005) Vijayalaxmi *et al.* (2008) Kumar *et al.* (2010) Venkateswarlu *et al.* (2010a) Farooq *et al.* (2013) Vinodhana *et al.* (2013) Rajamani *et al.* (2013) Kumar *et al.* (2014)

Table 2.5 (cont…)

Sl. No	Character	Positive Direct effect	Negative Direct effect
13.	Uniformity ratio	Sivaprasad (2003) Raju (2005) Sambamurthy *et al.*(2006) Vijayalaxmi *et al.* (2008) Srinivasulu *et al*. (2010) Mohan (2011) Rajanna *et al*. (2011) Rajamani *et al.* (2013) Erande *et al.*(2014) Kumar *et al.* (2014)	Neelima (2002) Muthu *et al.* (2004) Pratap *et al.* (2007) Sakthi *et al*. (2007) Padmavathi (2008) Anandan (2009) Venkateswarulu *et al.* (2010a)
14.	Lint yieldplant^{-1}(g)	Dedaniya and Pethani (1994) Tomar and Singh (1996) Pratap *et al.*(2007) Vijayalaxmi *et al.* (2008) Rajanna *et al*. (2011)	----------

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 is 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 behaviour 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 × 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 relationship between two variables. The study of correlation 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 fibre quality parameters and other yield components on seed cotton yield are reviewed and presented in Table2.5.

2.5. GENETIC DIVERGENCE

2.5.1 Mahalanobi's 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.

Mahalanobi'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 fibre length, fibre 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 plant^{-1}, number of sympodia plant^{-1}, 2.5% span length 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 plant^{-1}, seed index, number of sympodia plant^{-1}, plant height, 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.

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 Mahalanobi's 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.

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.

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 Mahalanobi's 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 Mahalanobi's 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 hierarchial 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 intracluster 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 Mahalanobi's 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 intracluster 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 Mahalanobi's 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 21characters and assessed diversity using Mahalanobi's 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 intracluster 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.

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 Mahalanobi's D^2 analysis. Cluster I and II were the largest with 13 genotypes each. Based on hierarchial 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.

2.5.2 Principal Component 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 analyses 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. PC_1 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. PC_1 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 PC_1 alone shown 38.73 per cent of variability towards the total variability.