

**GENETIC ANALYSIS OF YIELD AND
FIBRE QUALITY TRAITS IN
INTER-SPECIFIC HYBRIDS OF
COTTON (*Gossypium hirsutum* L. ×
Gossypium barbadense L.)**

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M.Sc. (Ag.)

**DOCTOR OF PHILOSOPHY
(GENETICS AND PLANT BREEDING)**



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HYBRIDS OF COTTON (*Gossypium hirsutum* L. ×
Gossypium barbadense L.)**

BY
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M.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**

**DOCTOR OF PHILOSOPHY
(GENETICS AND PLANT BREEDING)**

CHAIRPERSON: Dr. V. CHENGA REDDY



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

2016

DECLARATION

I, **BALAKRISHNA B** hereby declare that the thesis entitled “**GENETIC ANALYSIS OF YIELD AND FIBRE QUALITY TRAITS IN INTER-SPECIFIC HYBRIDS OF COTTON (*Gossypium hirsutum* L. × *Gossypium barbadense* L.)**” submitted to Acharya N.G. Ranga Agricultural University for the Degree of **Doctor of Philosophy** in Agriculture 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 : Bapatla

Date :

(BALAKRISHNA B)
I.D. No. BAD-12-04

CERTIFICATE

Mr. **BALAKRISHNA B** has satisfactorily prosecuted the course of research and that thesis entitled “**GENETIC ANALYSIS OF YIELD AND FIBRE QUALITY TRAITS IN INTER-SPECIFIC HYBRIDS OF COTTON (*Gossypium hirsutum* L. × *Gossypium barbadense* 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:

(V. CHENGA REDDY)

Chairperson
Principal Scientist (Cotton)
RARS, Lam Farm, Guntur.

CERTIFICATE

This is to certify that the thesis entitled “**GENETIC ANALYSIS OF YIELD AND FIBRE QUALITY TRAITS IN INTER-SPECIFIC HYBRIDS OF COTTON (*Gossypium hirsutum* L. × *Gossypium barbadense* L.)**” submitted in partial fulfilment of the requirements for the degree of **Doctor of Philosophy in Agriculture** of the Acharya N.G. Ranga Agricultural University, Hyderabad is a record of the bonafide original research work carried out by Mr. **BALAKRISHNA B** 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 and help received during the course of investigation have been duly acknowledged by the author of the thesis.

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LIST OF SYMBOLS AND ABBREVIATIONS

μ	:	Mid homozygote value
$\mu_a (B+G)$	:	Unbiased estimator based on combining ability model
μ_B'	:	Relative number of loci where both P_1 and P_2 have favourable alleles and P_w does not.
$\mu_{C'} + \mu_{F'}$	:	Total relative number of loci for which P_1 and P_w have the same alleles.
$\mu_{C'}$	:	Relative number of loci where both P_1 and P_w have favourable alleles and P_2 does not.
$\mu_{D'} + \mu_{E'}$	:	Total relative number of loci which P_2 and P_w have the same alleles.
$\mu_{D'}$	:	Relative number of loci where both P_2 and P_w have unfavourable alleles and P_1 with favourable alleles.
$\mu_{E'}$	:	Relative number of loci where P_2 and P_w have favourable alleles and P_1 does not.
$\mu_{F'}$	:	Relative number of loci where P_1 and P_w have unfavourable alleles and P_2 with favourable alleles.
$\mu_{G'}$	:	Relative number of loci where P_1 and P_2 have unfavourable alleles and P_w with favourable alleles.
a	:	Value of dominance
AICCIP	:	All India Co-ordinated Cotton Improvement Project
ANOVA	:	Analysis of Variance
AM	:	Ante Meridiem
AMMI	:	Additive Main effects and Multiplicative Interaction
ARS	:	Agricultural Research Station
BP	:	Better Parent
CD	:	Critical Difference
cm	:	Centimetre
CV	:	Coefficient of Variation
d.f	:	Degrees of Freedom
<i>et al.</i> ,	:	And others
<i>etc.</i>	:	And so on
F_1	:	First filial generation
Fig.	:	Figure
g	:	Gram
g/inch	:	Grams per inch
g/tex	:	Grams per tex
GAM	:	Genetic Advance as per cent of Mean

GCV	:	Genotypic Coefficient of Variation
<i>gca</i>	:	General Combining Ability
ha	:	Hectare
h^2 (b)	:	Heritability in broad sense
<i>i.e.</i> ,	:	That is
kg/ha	:	Kilogram per hectare
K	:	Potassium
kg	:	Kilogram
$L \times T$	:	Line $\times$ Tester
m	:	Metre
MSL	:	Mean Sea Level
MSS	:	Mean Sum of Squares
N	:	Nitrogen
NS	:	Non-Significant
No.	:	Number
P	:	Phosphorous
PCV	:	Phenotypic Co-efficient of Variation
<i>per se</i>	:	As such with mean
PM	:	Post Meridiem
PNG _g	:	Probability of net gain of favourable alleles
PTC	:	Predicted threewaycross
P _w	:	Donor inbred line
q _j , q _k	:	Frequency of recessive alleles in donor inbred at class j and k loci
RARS	:	Regional Agricultural Research Station
RCBD	:	Randomized Complete Block Design
S	:	Significant
<i>sca</i>	:	Specific Combining Ability
SE	:	Standard Error
SEm	:	Standard Error of mean
UBND	:	Minimum upper bound statistic
<i>viz.</i> ,	:	Namely
vs	:	Against
$\bar{X}$	:	Grand mean
σ^2	:	Variance
%	:	Per cent
2D	:	Two dimensional
3D	:	Three dimensional

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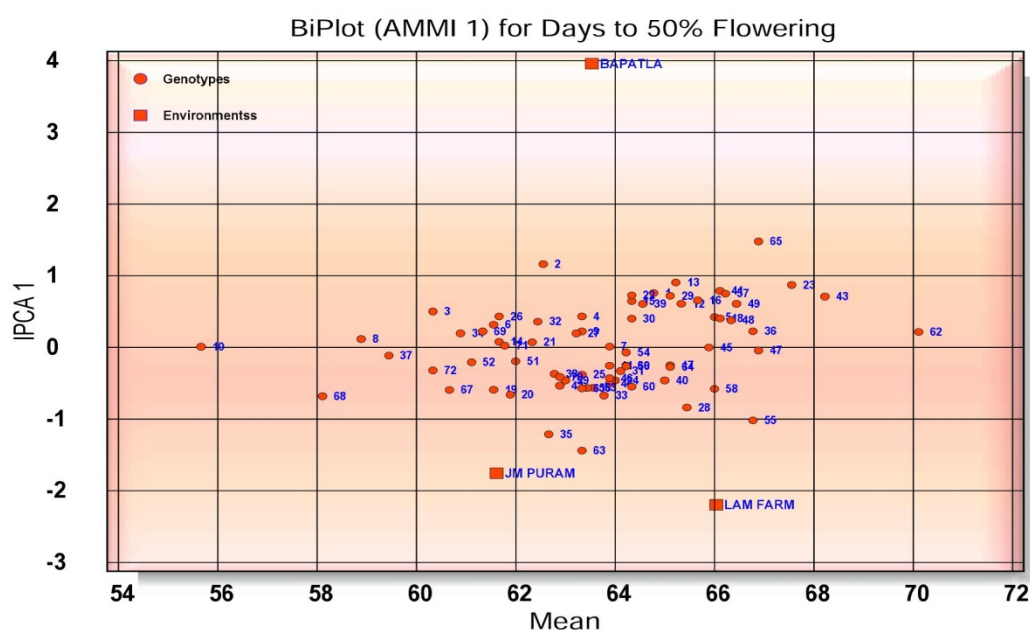


Fig. 4.11. AMMI biplot for mean days to 50% flowering and IPCA I of inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.)

1. NDLH 1938 × GSB 40	25. WGCV 48 × GSB 40	49. SCS 793 × GSB 40
2. NDLH 1938 × DB 16	26. WGCV 48 × DB 16	50. SCS 793 × DB 16
3. NDLH 1938 × DB 11	27. WGCV 48 × DB 11	51. SCS 793 × DB 11
4. NDLH 1938 × GSB 41	28. WGCV 48 × GSB 4	52. SCS 793 × GSB 41
5. NDLH 1938 × TCB 37	29. WGCV 48 × TCB 37	53. SCS 793 × TCB 37
6. NDLH 1938 × SUVIN	30. WGCV 48 × SUVIN	54. SCS 793 × SUVIN
7. H 1442 × GSB 40	31. MR 786 × GSB 40	55. MCU 5 × GSB 40
8. H 1442 × DB 16	32. MR 786 × DB 16	56. MCU 5 × DB 16
9. H 1442 × DB 11	33. MR 786 × DB 11	57. MCU 5 × DB 11
10. H 1442 × GSB 41	34. MR 786 × GSB 41	58. MCU 5 × GSB 41
11. H 1442 × TCB 37	35. MR 786 × TCB 37	59. MCU 5 × TCB 37
12. H 1442 × SUVIN	36. MR 786 × SUVIN	60. MCU 5 × SUVIN
13. ADB 542 × GSB 40	37. TSH 0250 × GSB 40	61. L 1058 × GSB 40
14. ADB 542 × DB 16	38. TSH 0250 × DB 16	62. L 1058 × DB 16
15. ADB 542 × DB 11	39. TSH 0250 × DB 11	63. L 1058 × DB 11
16. ADB 542 × GSB 41	40. TSH 0250 × GSB 41	64. L 1058 × GSB 41
17. ADB 542 × TCB 37	41. TSH 0250 × TCB 37	65. L 1058 × TCB 37
18. ADB 542 × SUVIN	42. TSH 0250 × SUVIN	66. L 1058 × SUVIN
19. ADB 532 × GSB 40	43. BS 37 × GSB 40	67. L 762 × GSB 40
20. ADB 532 × DB 16	44. BS 37 × DB 16	68. L 762 × DB 16
21. ADB 532 × DB 11	45. BS 37 × DB 11	69. L 762 × DB 11
22. ADB 532 × GSB 41	46. BS 37 × GSB 41	70. L 762 × GSB 41
23. ADB 532 × TCB 37	47. BS 37 × TCB 37	71. L 762 × TCB 37
24. ADB 532 × SUVIN	48. BS 37 × SUVIN	72. L 762 × SUVIN

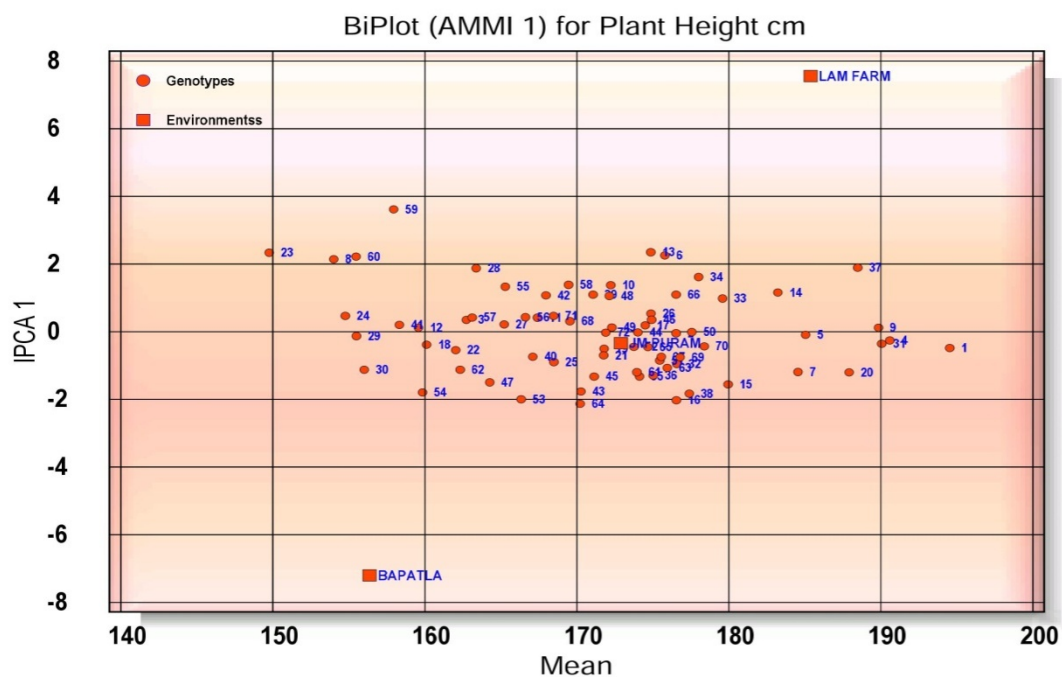


Fig. 4.12. AMMI biplot for mean plant height and IPCA I of inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.)

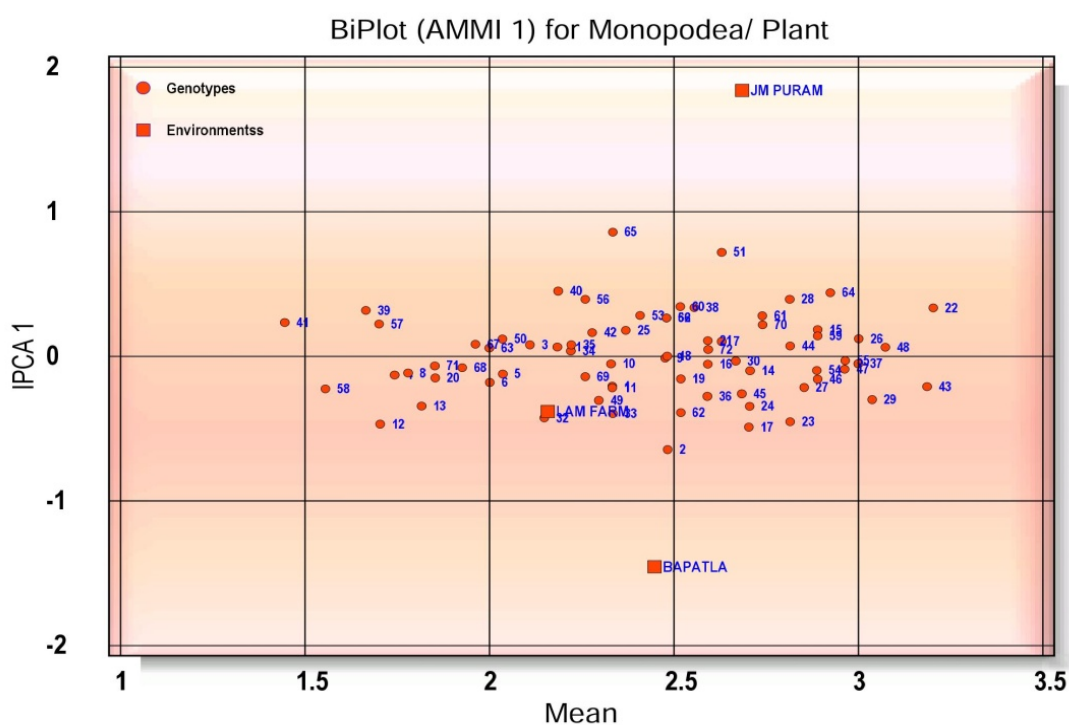


Fig. 4.13. AMMI biplot for mean number of monopodia plant⁻¹ and IPCA I of inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.)

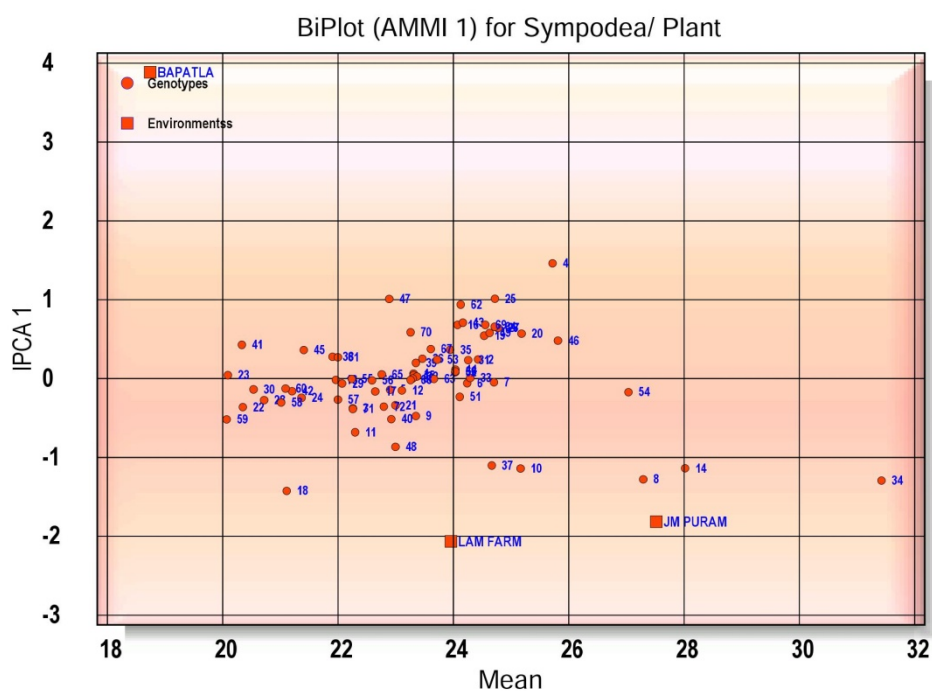


Fig. 4.14. AMMI biplot for mean number of sympodia plant⁻¹ and IPCA I of inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.)

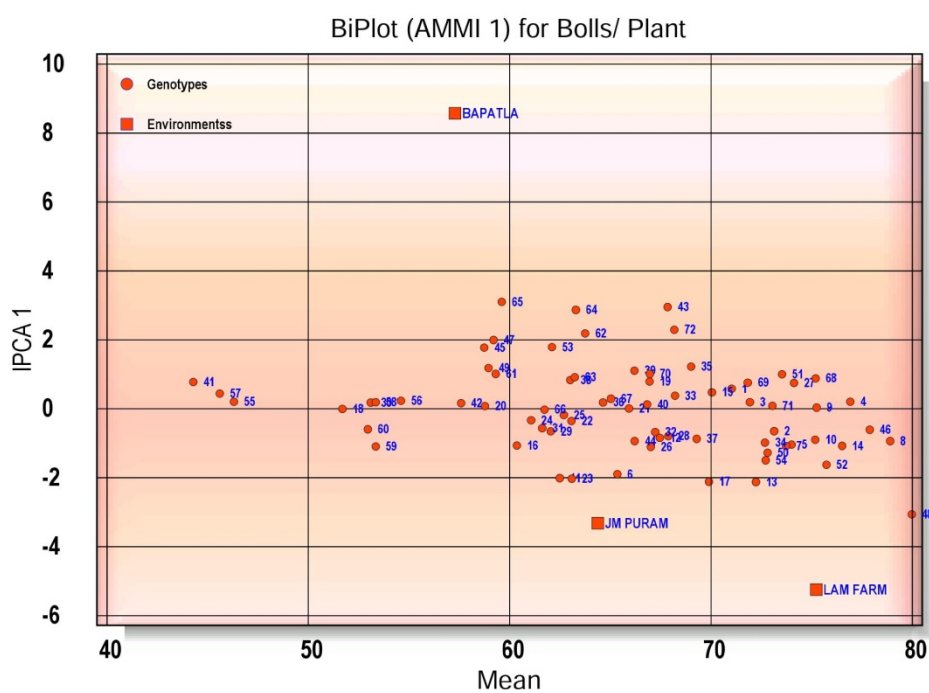


Fig. 4.15. AMMI biplot for mean number of bolls plant⁻¹ and IPCA I of inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.)

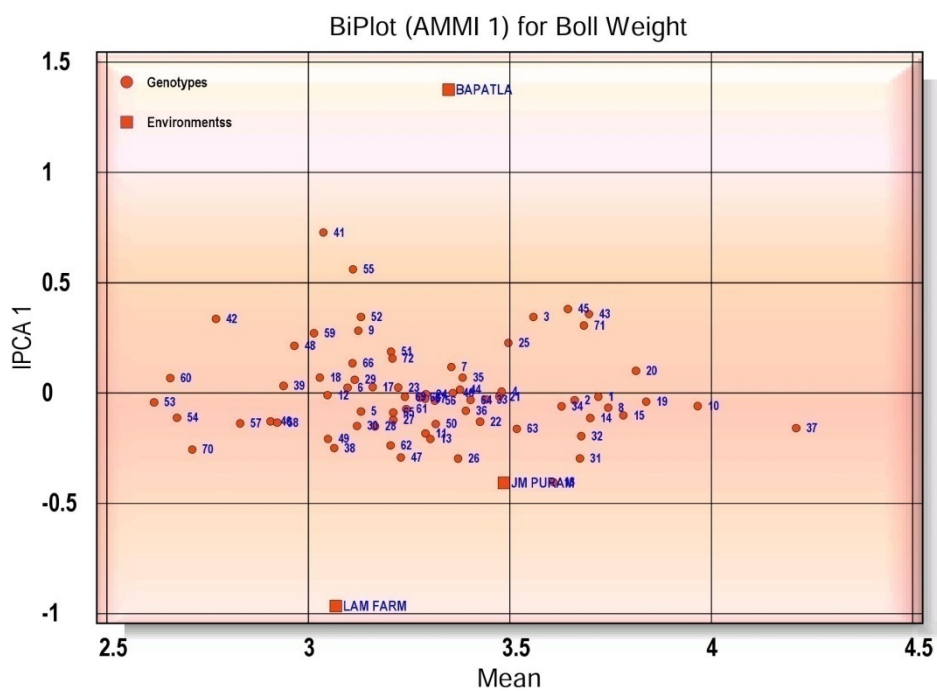


Fig. 4.16. AMMI biplot for mean boll weight and IPCA I of inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.)

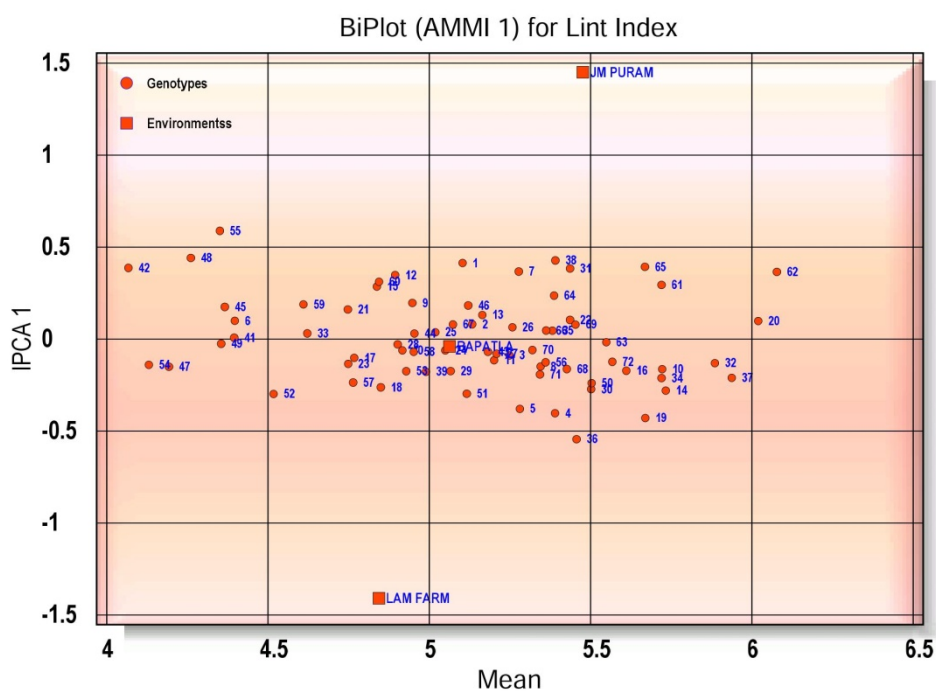


Fig. 4.17. AMMI biplot for mean lint index and IPCA I of inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.)

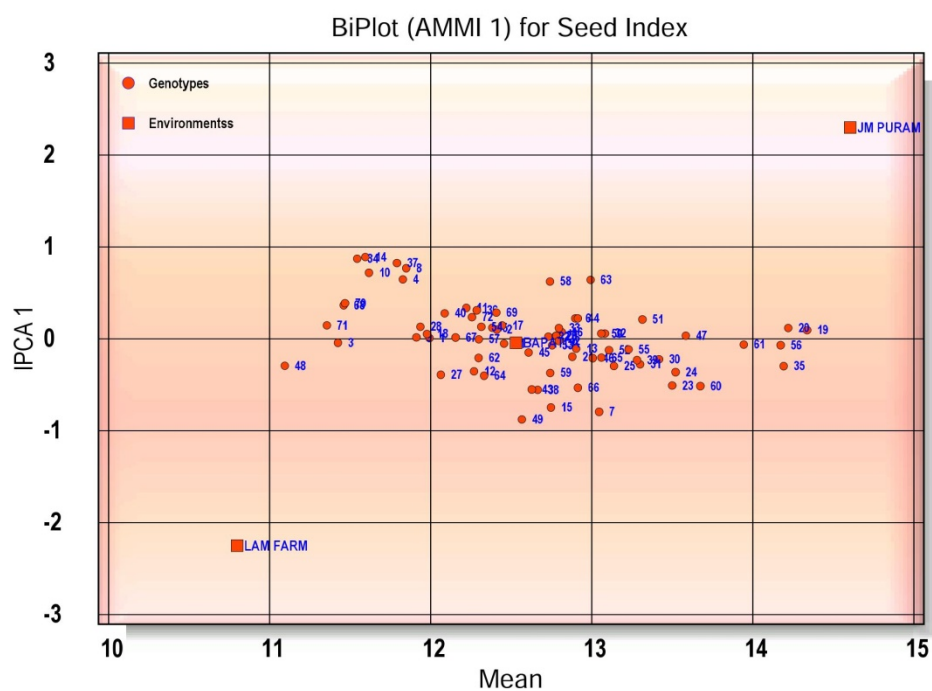


Fig. 4.18. AMMI biplot for mean seed index and IPCA I of inter-specific hybrids of cotton (*G. hirsutum* L. $\times$ *G. barbadense* L.)

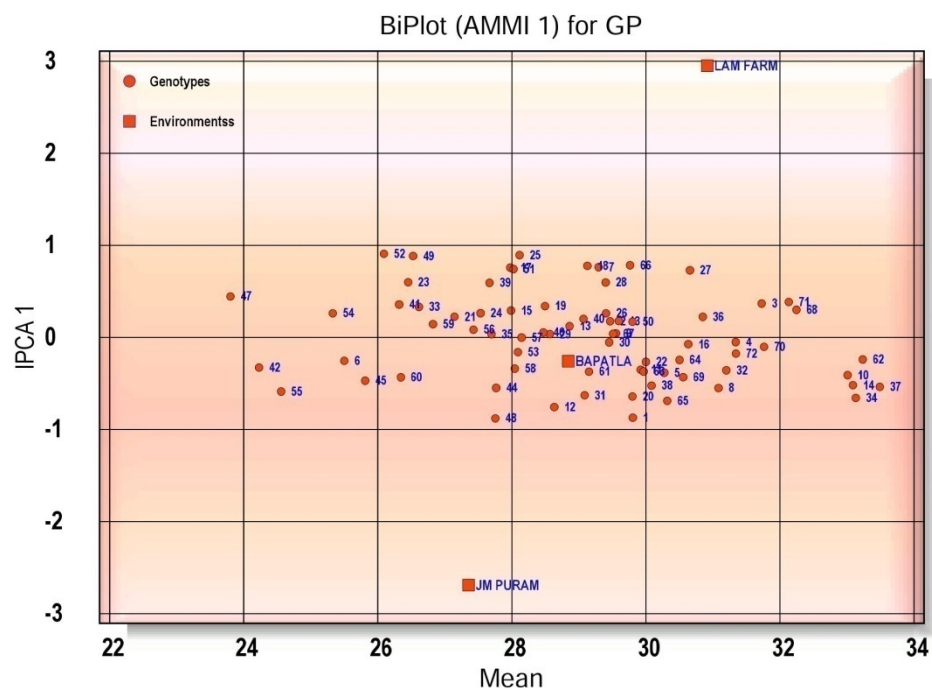


Fig. 4.19. AMMI biplot for mean ginning out-turn and IPCA I of inter-specific hybrids of cotton (*G. hirsutum* L. $\times$ *G. barbadense* L.)

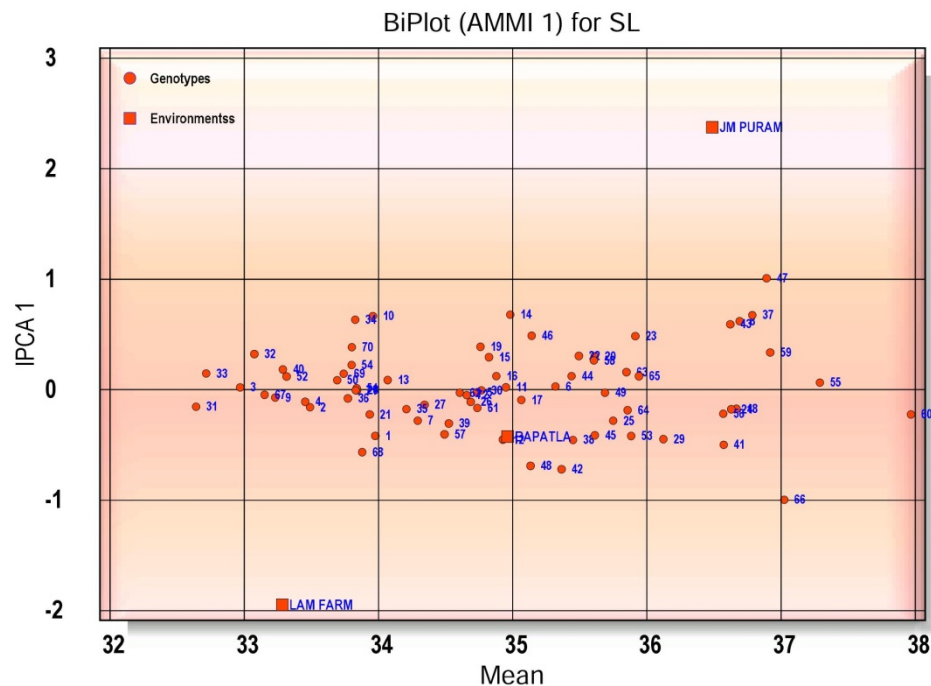


Fig. 4.20. AMMI biplot for mean 2.5% span length and IPCA I of inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.)

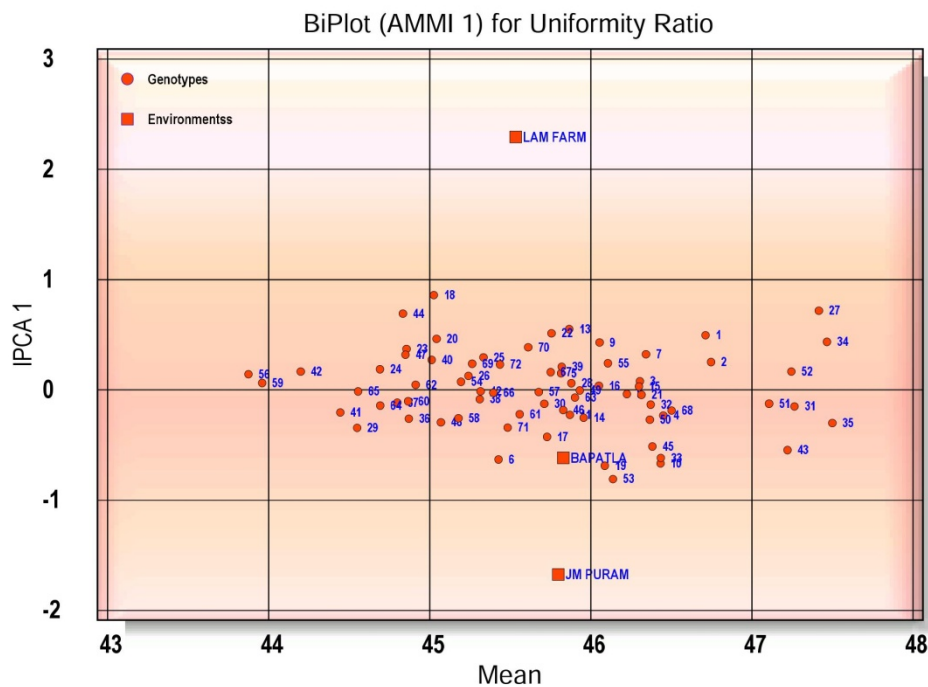


Fig. 4.21. AMMI biplot for mean uniformity ratio and IPCA I of inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.)

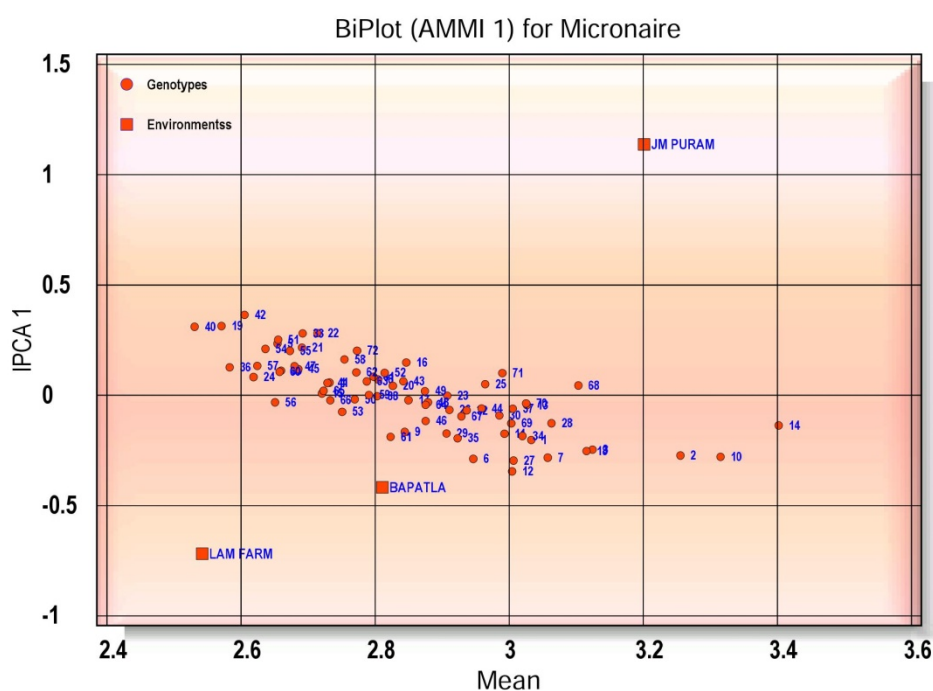


Fig. 4.22. AMMI biplot for mean micronaire value and IPCA I of inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.)

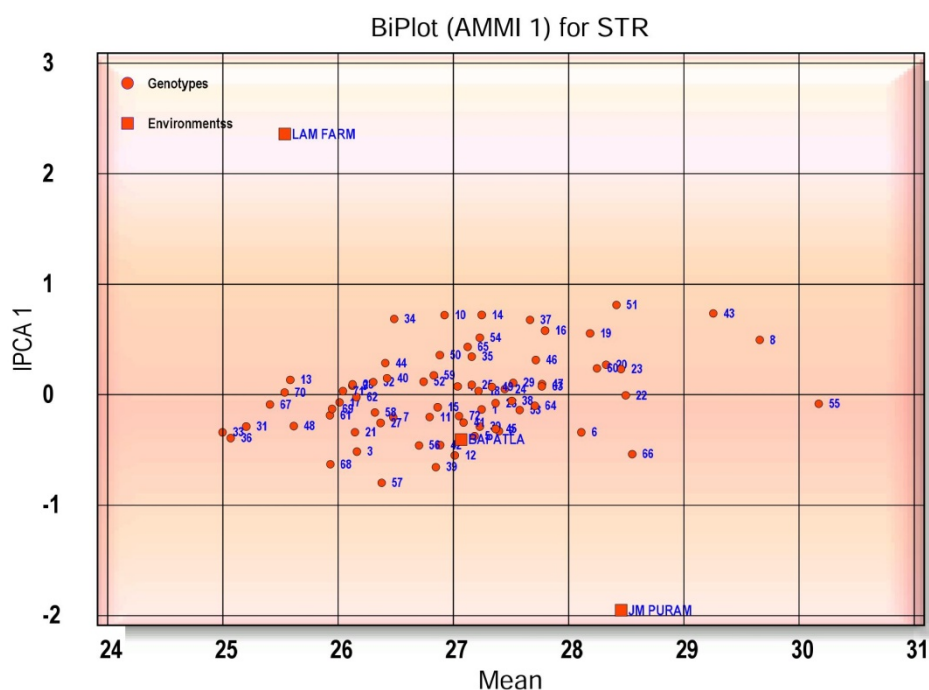


Fig. 4.23. AMMI biplot for mean bundle strength and IPCA I of inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.)

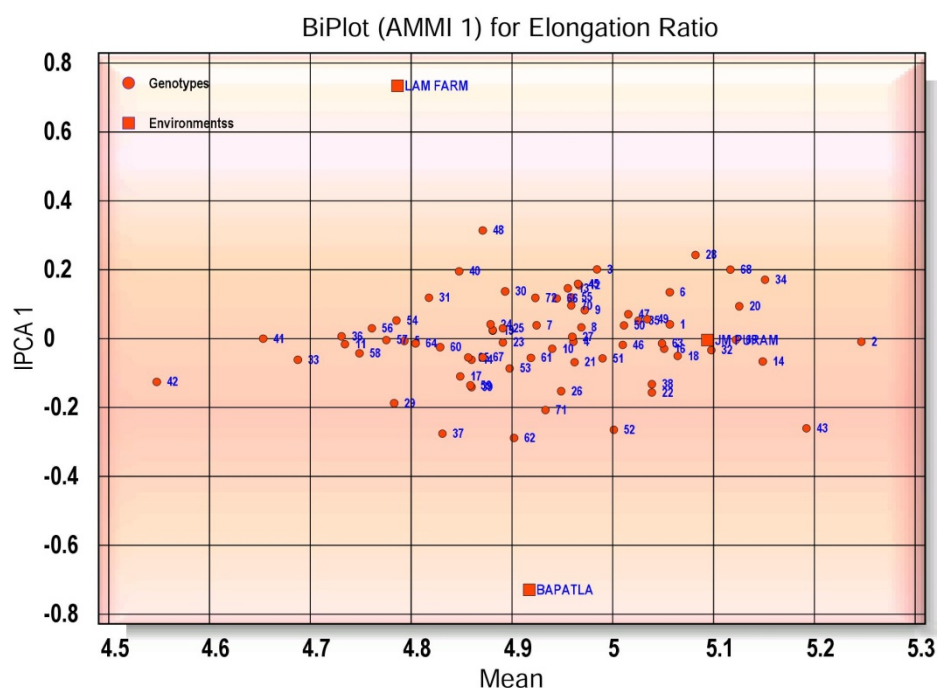


Fig. 4.24. AMMI biplot for mean fibre elongation and IPCA I of inter-specific hybrids of cotton (*G. hirsutum* L. $\times$ *G. barbadense* L.)

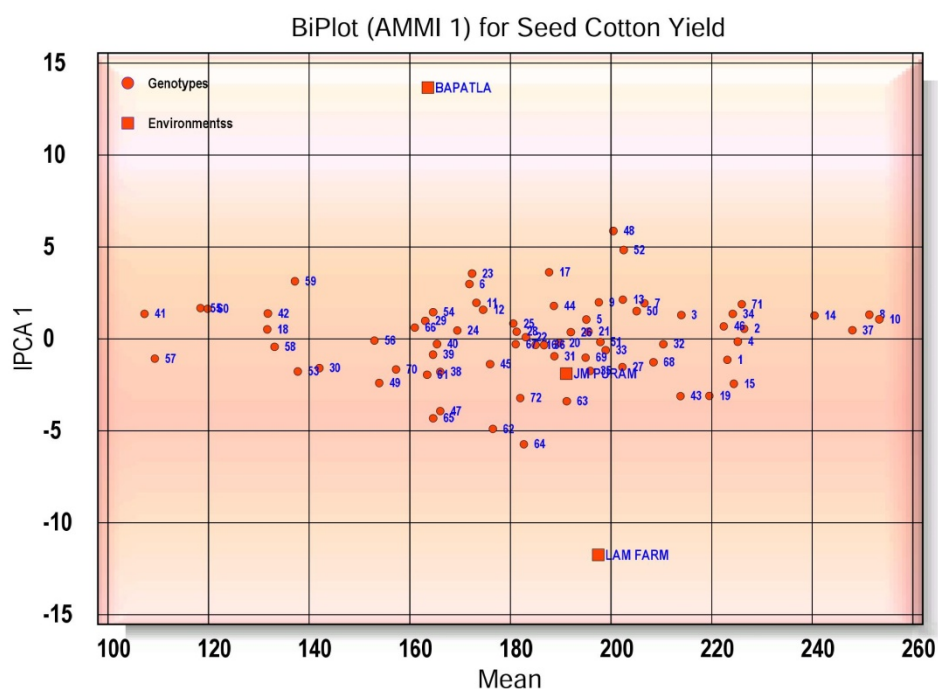


Fig. 4.25. AMMI biplot for mean seed cotton yield plant⁻¹ and IPCA I of inter-specific hybrids of cotton (*G. hirsutum* L. $\times$ *G. barbadense* L.)

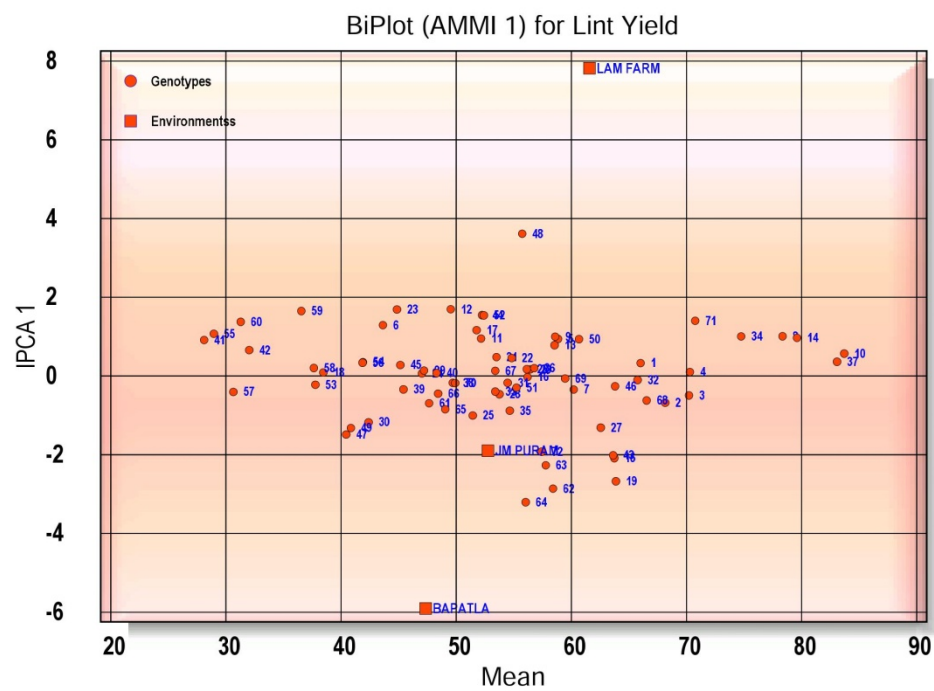


Fig. 4.26. AMMI biplot for mean lint yield plant⁻¹ and IPCA I of inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.)

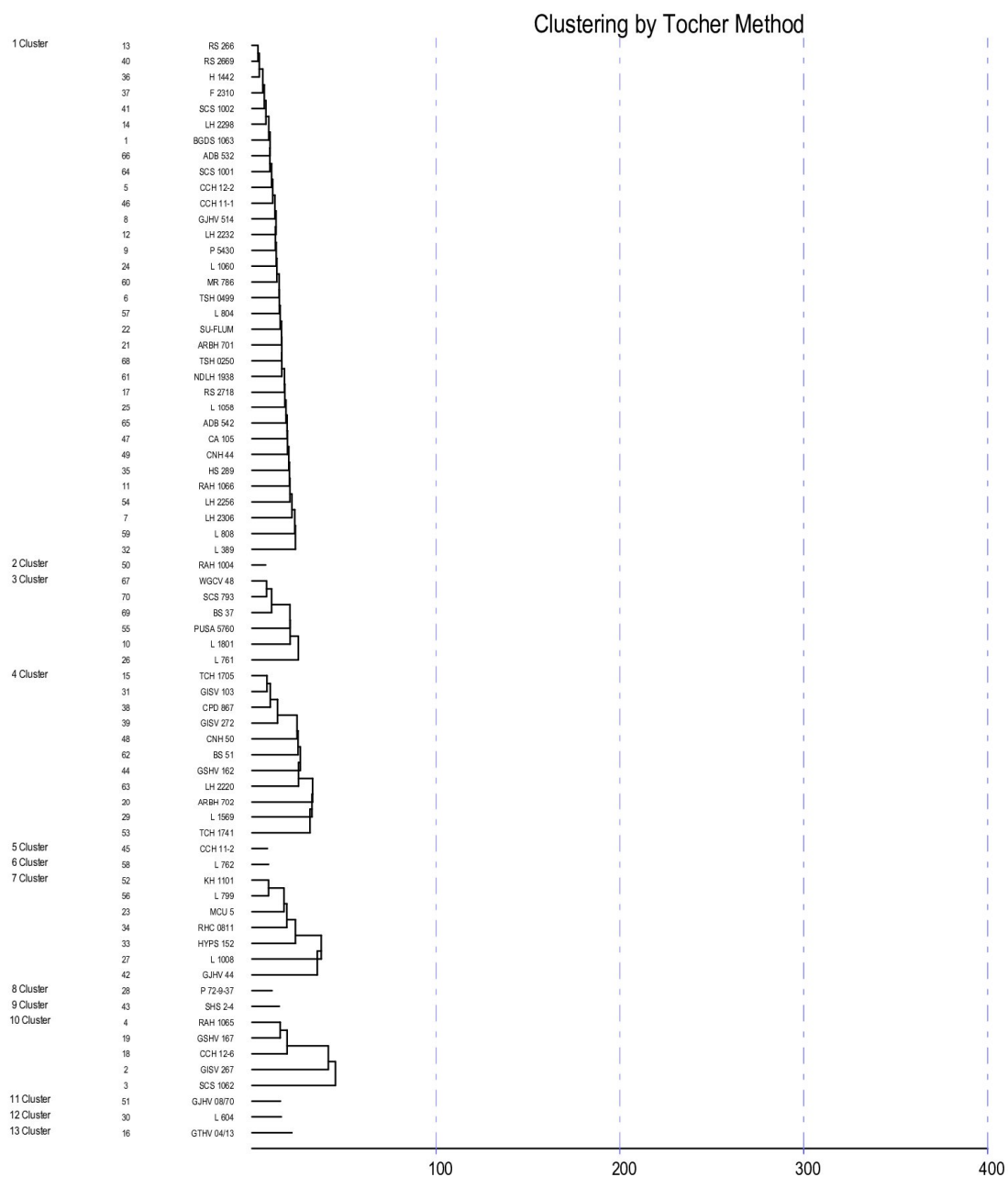
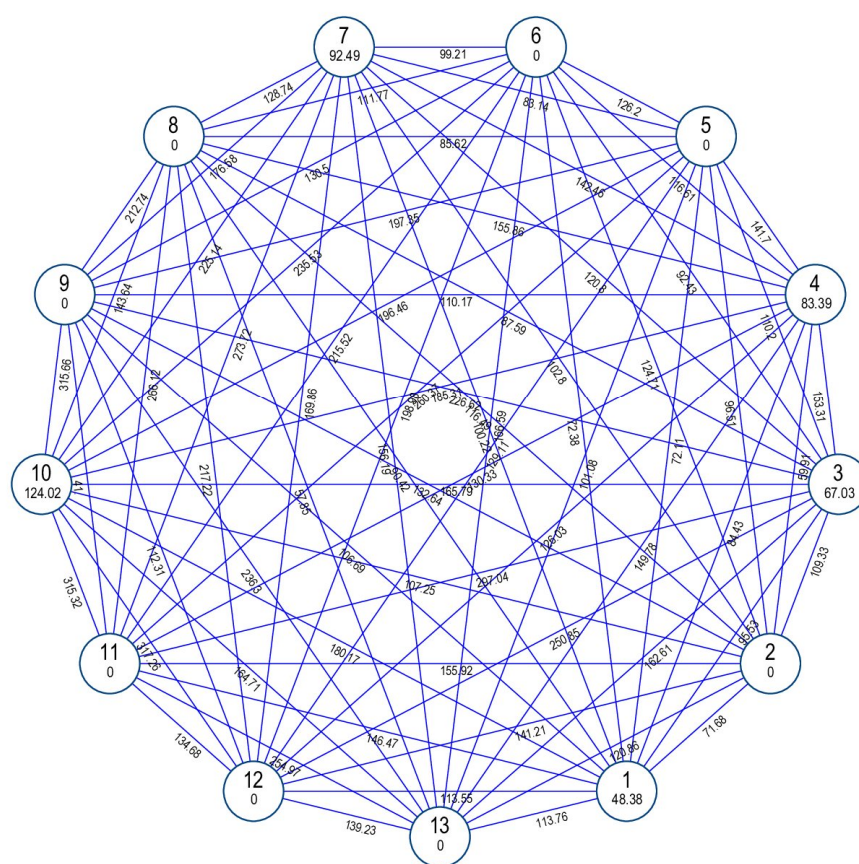


Fig. 4.1. Dendrogram showing relationship of 70 American cotton (*Gossypium hirsutum* L.) genotypes in thirteen clusters based on Mahalanobis' D^2 values (Genotype numbers as per Table. 3.1)

Tocher Method



Mahalanobis Euclidean Distance (Not to the Scale)

Fig. 4.2. Intra-and inter-cluster distance of 70 American cotton (*Gossypium hirsutum* L.) genotypes in thirteen clusters based on Mahalanobis Euclidean distance

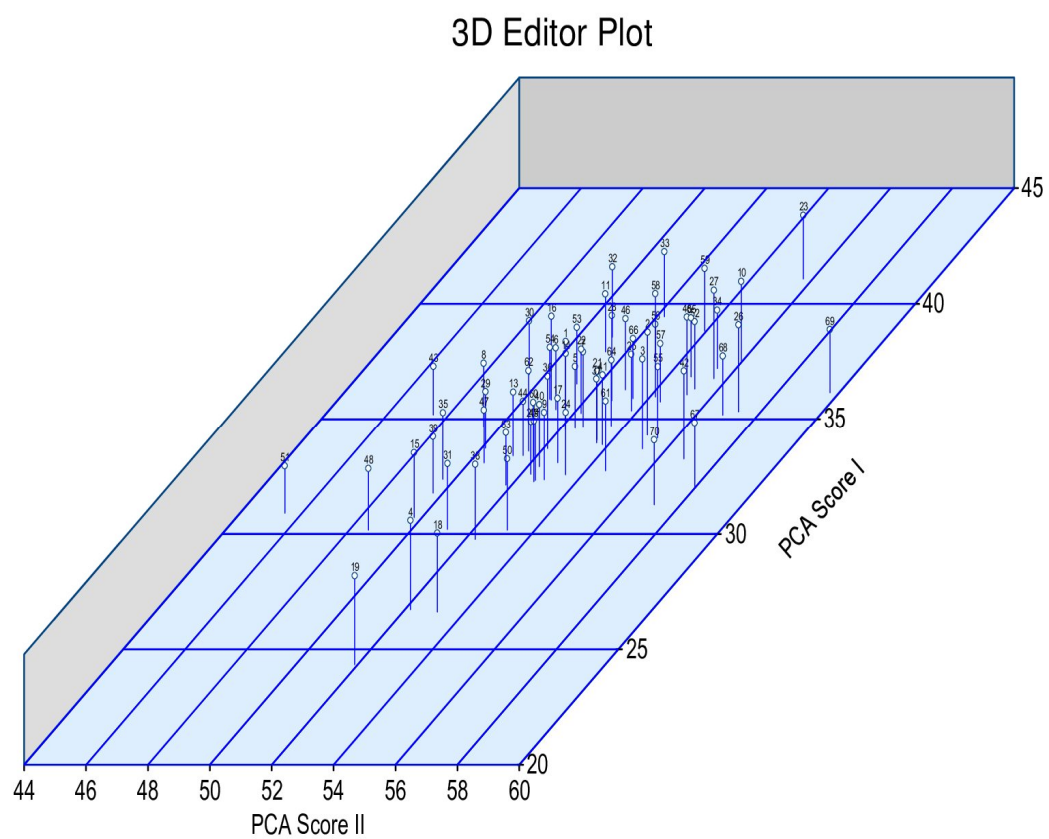


Fig. 4.6. Three dimensional graph showing relative position of 70 American cotton (*Gossypium hirsutum* L.) genotypes based on PCA scores. (Genotype numbers as per Table 3.1)

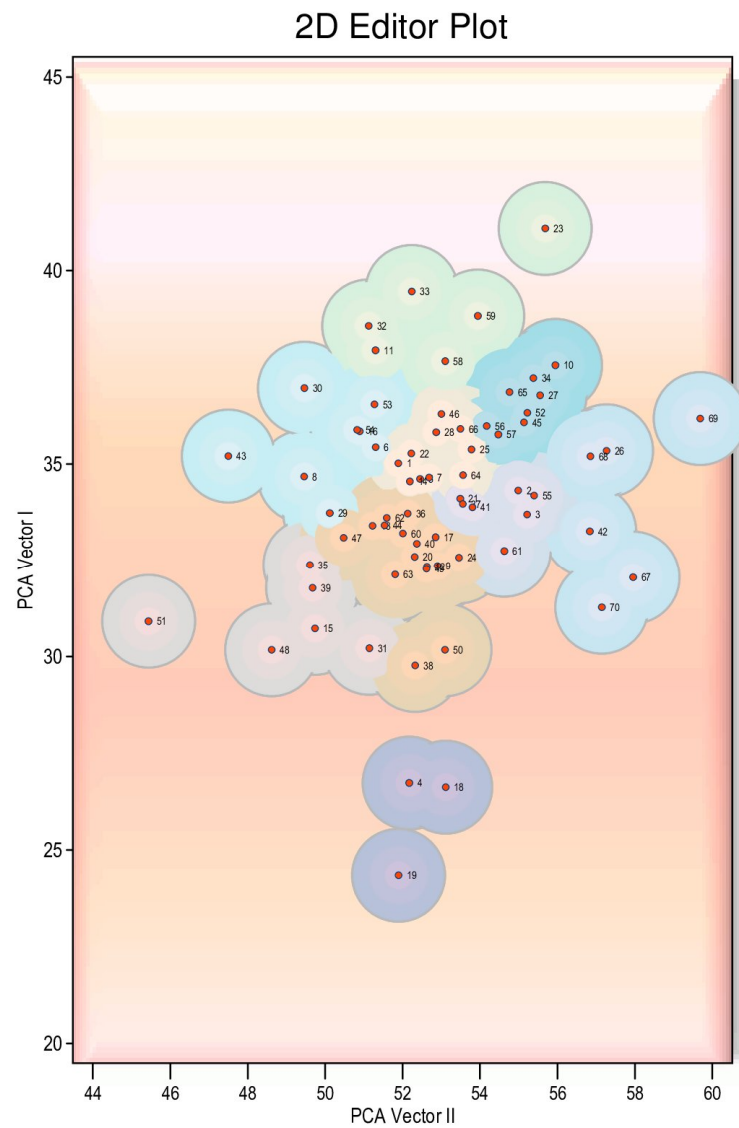


Fig. 4.5. Two dimensional graph showing relative position of 70 American cotton (*Gossypium hirsutum* L.) genotypes based on PCA scores (Genotype numbers as per Table 3.1)

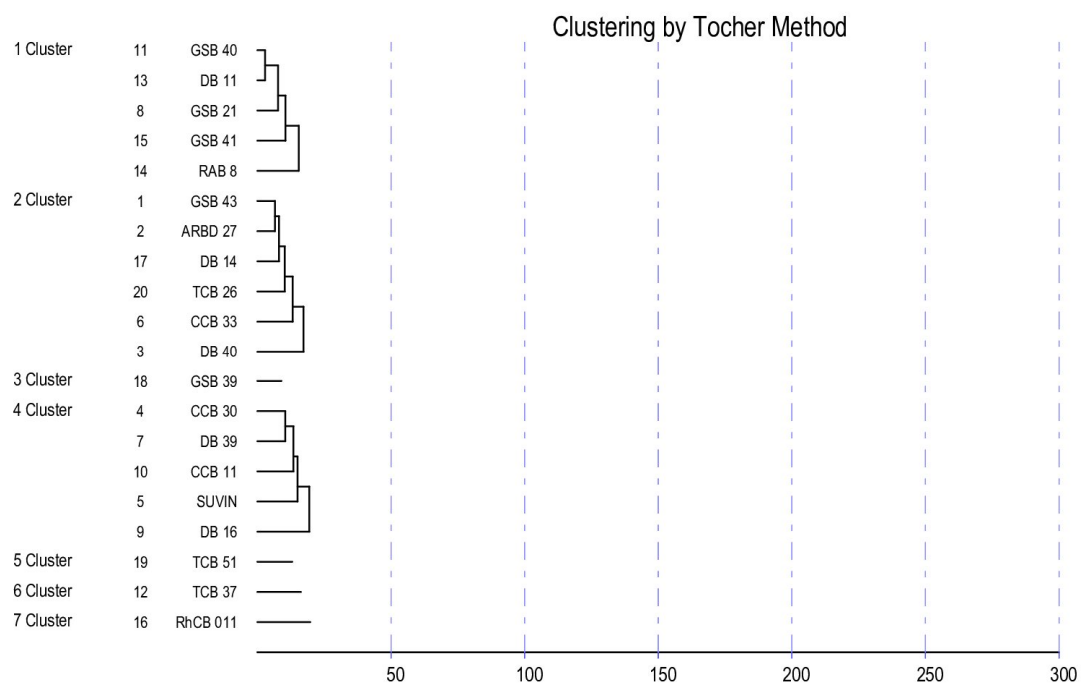
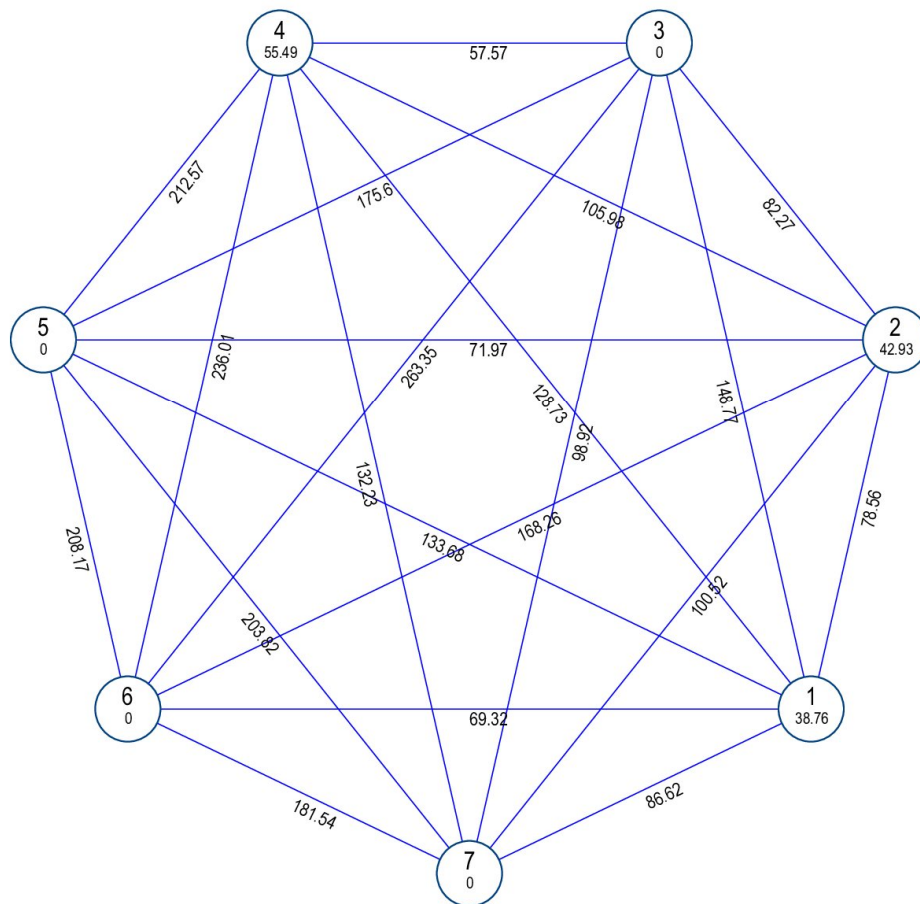


Fig. 4.3. Dendrogram showing relationship of 20 Egyptian cotton (*Gossypium barbadense* L.) genotypes in seven clusters based on Mahalanobis' D^2 values (Genotype numbers as per Table 3.2)

Tocher Method



Mahalanobis Euclidean Distance (Not to the Scale)

Fig. 4.4. Intra-and inter-cluster distance of 20 Egyptian cotton (*Gossypium barbadense* L.) genotypes in seven clusters based on Mahalanobis Euclidean distance

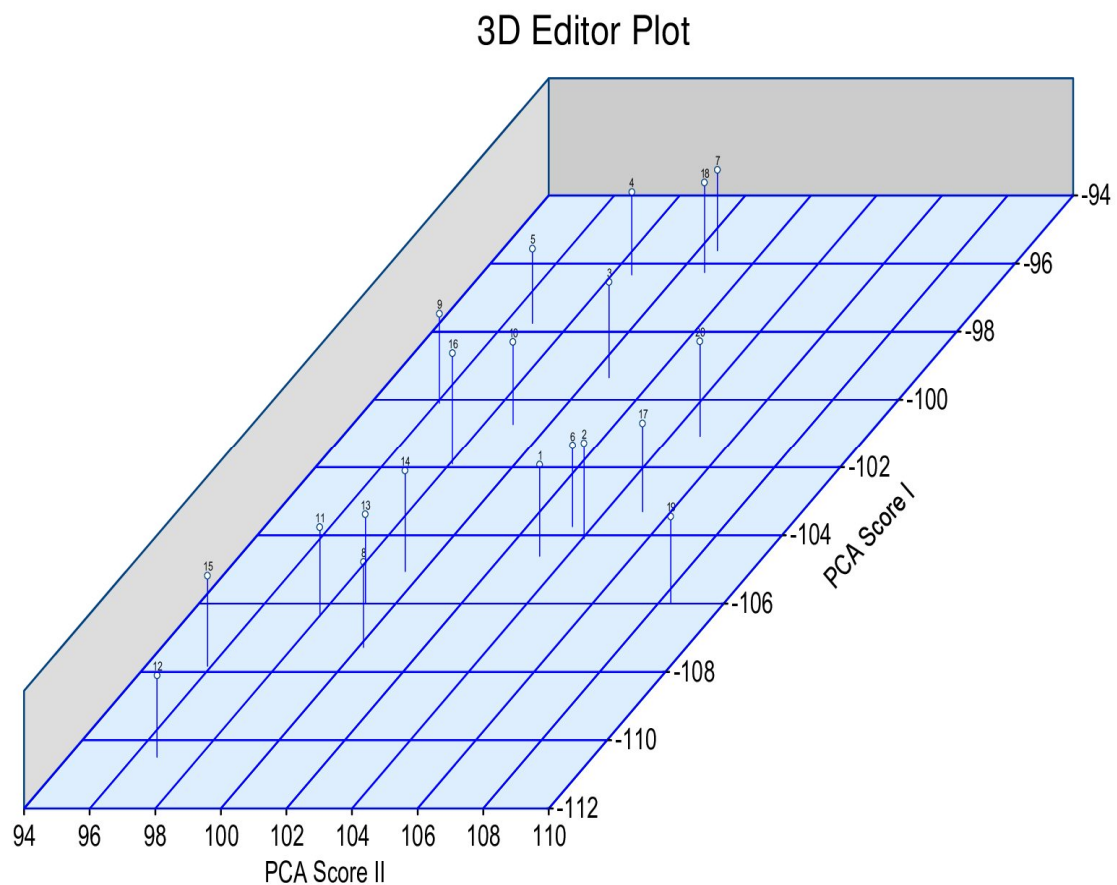


Fig. 4.8. Three dimensional graph showing relative position of 20 Egyptian cotton (*Gossypium barbadense* L.) genotypes based on PCA scores (Genotype numbers as per Table 3.2)

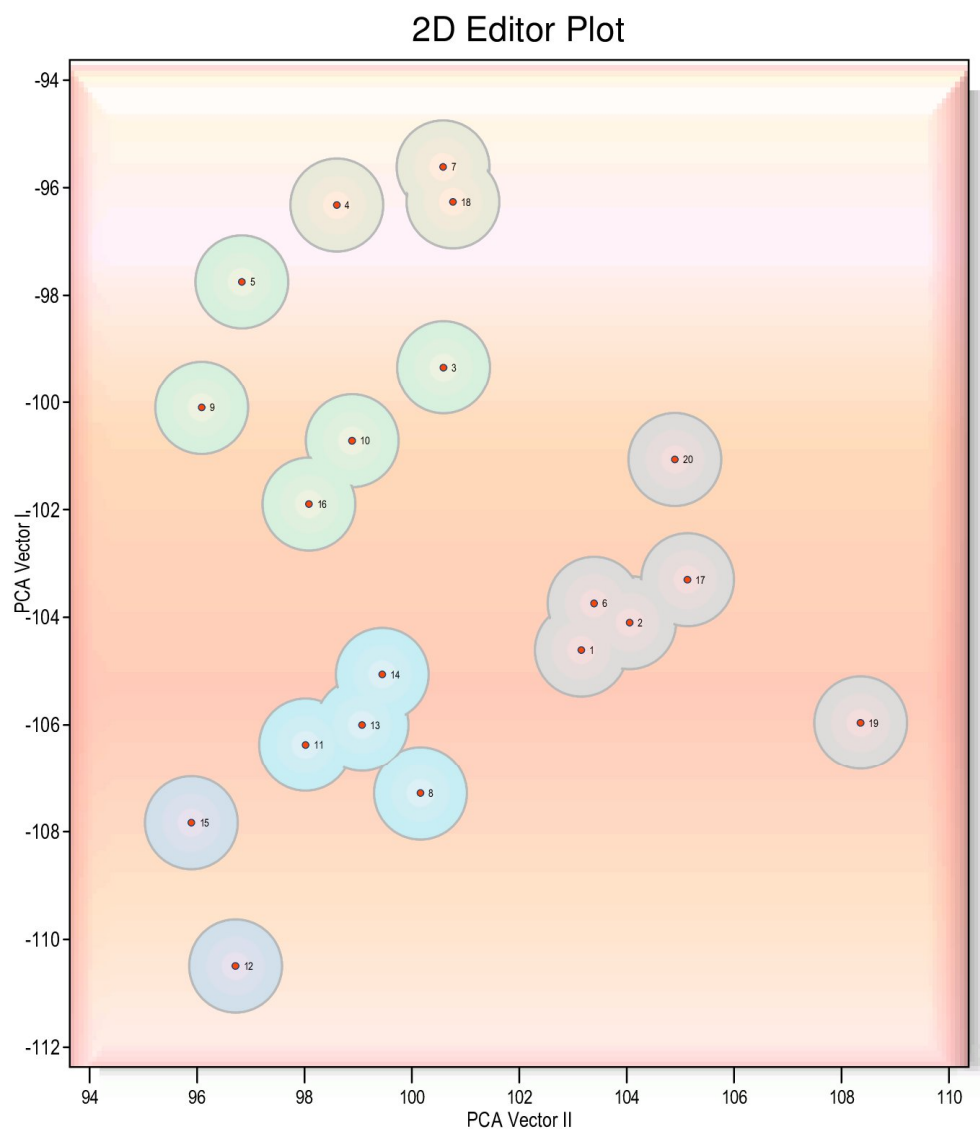


Fig. 4.7. Two dimensional graph showing relative position of 20 Egyptian cotton (*Gossypium barbadense* L.) genotypes based on PCA scores (Genotype numbers as per Table 3.2)

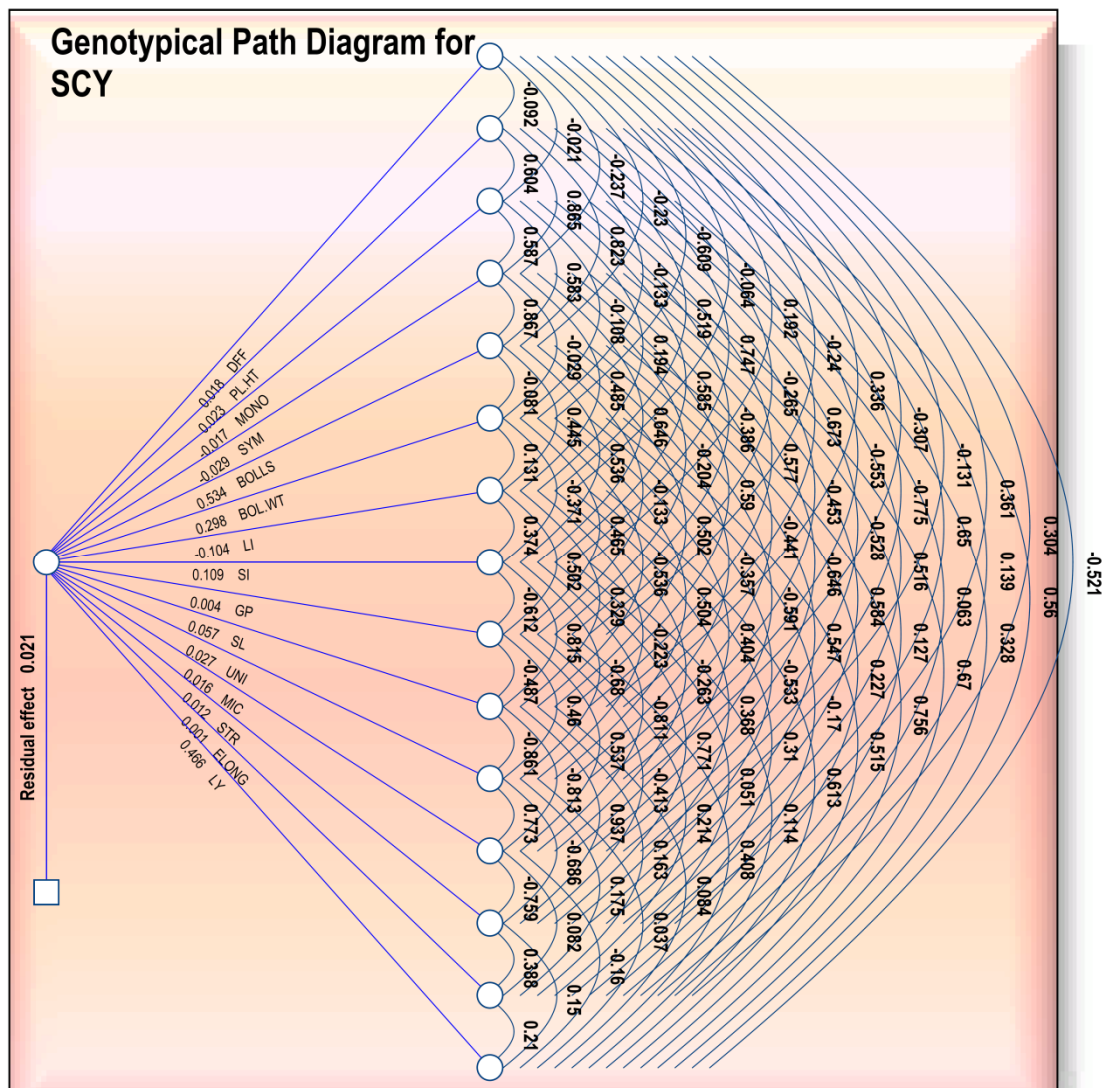


Fig. 4.10. Genotypic path diagram showing cause- effect relationship of yield components with seed cotton yield plant⁻¹ in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.)

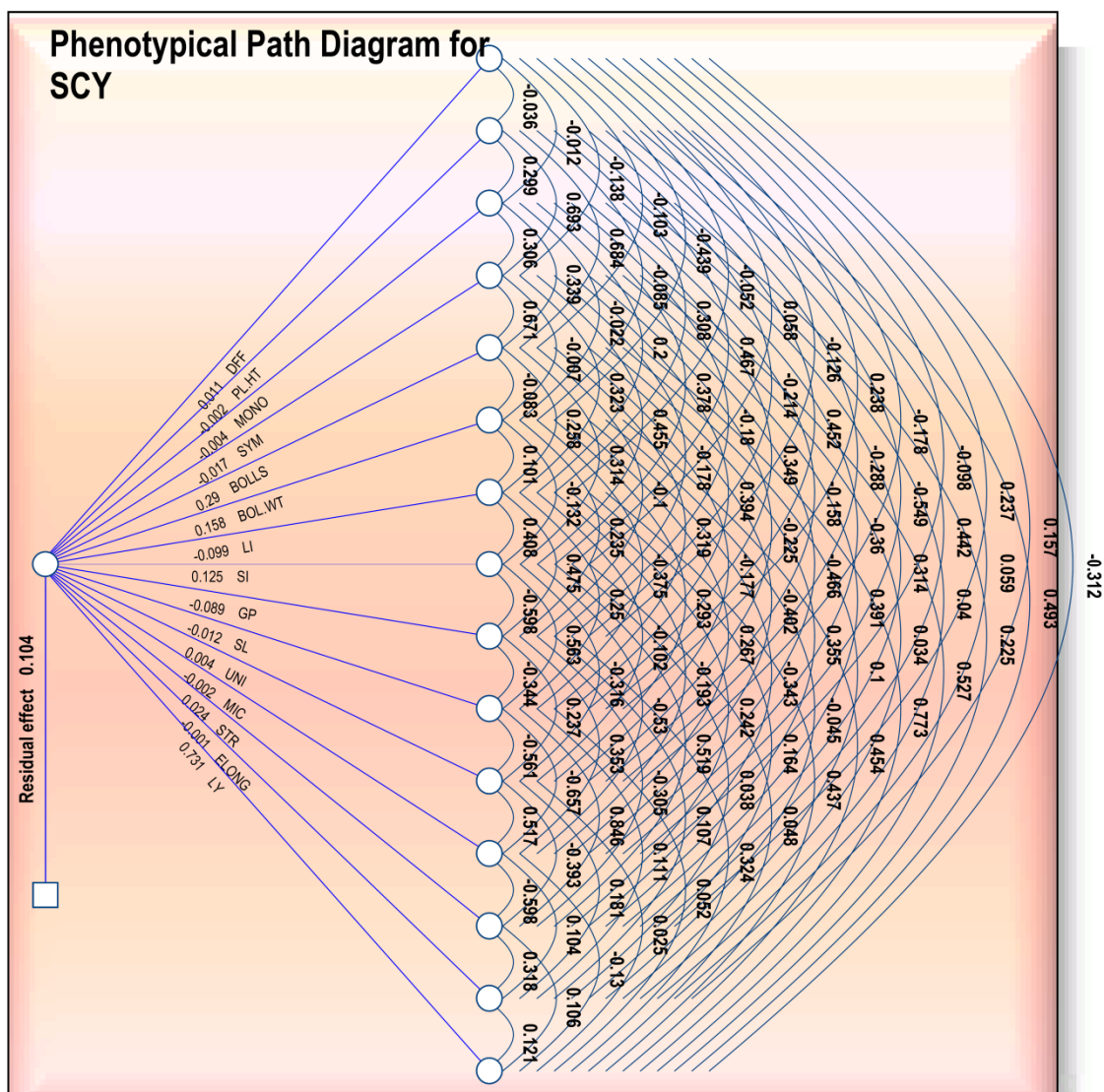


Fig. 4.9. Phenotypic path diagram showing cause- effect relationship of yield components with seed cotton yield plant⁻¹ in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.)

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ABSTRACT

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The present investigation was undertaken to elicit information on combining ability effects, heterosis and stability of inter-specific hybrids (*G. hirsutum* L. × *G. barbadense* L.) over environments for yield, yield components and quality characters and also to identify the donor parents having favorable alleles for 2.5 % span length and bundle strength for improving the target cross NDLH 1938 × MCU 5.

The first experiment was conducted during *kharif*, 2013-14 to select the parents for crossing programme by evaluating 70 *hirsutum* and 20 *barbadense* genotypes. The analysis of variance for both the groups of genotypes (*hirsutum* and *barbadense*) revealed significant differences among the genotypes for all the characters under study. Wider genetic variability was observed for number of monopodia plant⁻¹ in Egyptian cotton and was for number of monopodia plant⁻¹ and seed cotton yield plant⁻¹ in American cotton. High heritability coupled with high genetic advance as per cent of mean was observed for number of monopodia plant⁻¹, number of bolls plant⁻¹, lint index, seed index, micronaire value, seed cotton yield plant⁻¹ and lint yield plant⁻¹ in *hirsutum* while it was for number of monopodia plant⁻¹, number of sympodia plant⁻¹, number of bolls plant⁻¹, lint index, seed cotton yield plant⁻¹ and lint yield plant⁻¹ in *barbadense*. This indicates the operation of additive gene action in the inheritance of these traits. Simple selection could be profitably applied on these traits in the genetically diverse material.

D² analysis grouped the 70 American cotton genotypes into thirteen clusters and 20 Egyptian cotton genotypes into seven clusters. The traits *viz.*, micronaire value, lint index, days to 50% flowering and number of monopodia plant⁻¹ in *hirsutum* while seed index, fibre elongation and 2.5% span length, in *barbadense* contributed maximum towards genetic divergence. For both the genotype groups principal component analysis identified six principal components (PCs), which contributed 74.62 and 92.05 per cent of cumulative variance in *hirsutum* and *barbadense*, respectively.

Based on divergence studies, *per se* performance and cluster mean values, twelve *hirsutum* lines *viz.*, NDLH 1938, H 1442, ADB 542, ADB 532, WGCV 48, MR 786, TSH 0250, BS 37, SCS 793, MCU 5, L 1058, L 762 and six *barbadense* testers *viz.*, GSB 40, DB 16, DB 11, GSB 41, TCB 37 and SUVIN were selected and crossed in line × tester fashion to get 72 inter-specific hybrids during 2014-15 off-season. Pooled analysis of variance for 90 genotypes (72 hybrids + 12 lines + 6 testers) revealed presence of

significant variability among the genotypes. Wider variability was observed for number of monopodia plant⁻¹, number of bolls plant⁻¹, seed cotton yield plant⁻¹ and lint yield plant⁻¹. High heritability coupled with high genetic advance as per cent of mean was exhibited by micronaire value, seed cotton yield plant⁻¹ and lint yield plant⁻¹ which suggests the role of additive gene action in the inheritance of these traits and directional selection could be profitably exploited.

The character association and path analysis indicated plant height, number of bolls plant⁻¹, boll weight, lint index, ginning out-turn, 2.5% span length, bundle strength, fibre elongation and lint yield plant⁻¹ showed significant positive correlation and direct positive effects with seed cotton yield plant⁻¹ revealing their importance in direct selection.

The pooled combining ability analysis of variance showed significant differences due to locations, parents, hybrids and various interactions indicating the existence of sufficient variation in the material under study. The *gca* and *sca* variances indicated the presence of additive gene action for number of bolls plant⁻¹, seed index, 2.5% span length, uniformity ratio and seed cotton yield plant⁻¹ whereas, days to 50% flowering, plant height, number of monopodia plant⁻¹, number of sympodia plant⁻¹, lint index, ginning out-turn, micronaire value, bundle strength, fibre elongation and lint yield plant⁻¹ were controlled by non-additive gene action. Both additive and non-additive gene actions were involved in the inheritance of boll weight.

In pooled analysis, none of the line and tester was found to exhibit significant *gca* effects for all the characters studied. The lines, NDLH 1938, H 1442, ADB 542, ADB 532, MR 786, BS 37, L 762 and testers, GSB 40, DB 16, DB 11 and GSB 41, were found to be promising general combiners for seed cotton yield plant⁻¹ and other traits. Significant and desirable *sca* effects for seed cotton yield plant⁻¹ were exhibited by 22 hybrids. Based on *per se* performance, *sca* effects and standard heterosis, three cross combinations viz., H 1442 × GSB 41, H 1442 × DB 16 and TSH 0250 × GSB 40, were identified as superior for seed cotton yield plant⁻¹.

Genotype × environment interaction studies with 72 hybrids at different locations for yield, yield attributing and quality traits by Eberhart and Russell and AMMI model revealed one hybrid, ADB 542 × GSB 41, was stable for seed cotton yield plant⁻¹. Eight hybrids viz., NDLH 1938 × GSB 41, ADB 542 × GSB 41, ADB 532 × DB 16, WGCV 48 × DB 16, MR 786 × DB 16, MR 786 × SUVIN, TSH 0250 × GSB 40 and SCS 793 × DB 11, were stable for seed cotton yield plant⁻¹ with high mean and zero IPCA score in AMMI model.

Thus, the hybrid, ADB 542 × GSB 41, may be thoroughly tested over large number of environments for further confirmation before it is being exploited commercially. The hybrid, TSH 0250 × GSB 40, was identified as stable hybrid in AMMI analysis and suitable for poor environments as per Eberhart and Russell model and had significant *per se* performance, *sca* effect and standard heterosis for seed cotton yield plant⁻¹ with desirable 2.5% span length and micronaire value. Hence, this hybrid may also be considered for evaluation over environments before it is being exploited commercially.

For improving the target cross NDLH 1938 × MCU 5, the donor parent SUVIN contributed favourable alleles for 2.5% span length while, GSB 40 contributed for bundle strength. The ($\mu C' + \mu F'$), ($\mu D' + \mu E'$) and $\mu F'$ values indicated that both the donor parents had high genetic affinity with NDLH 1938 (P_1) and presence of favourable alleles in MCU 5 (P_2) for both the characters. Hence, NDLH 1938 need to be improved for both the quality traits and improved parent can be used to get target cross with high seed cotton yield along with good quality fibre.

Chapter I

INTRODUCTION

Cotton (*Gossypium* spp.) popularly called “White Gold” and “King of Fibre Crops” is the most widely used renewable natural fibre crop of global importance. It occupies a pre-eminent place among cash crops as it guides the destiny of a large section of the farming community as well as that of a flourishing textile industry. Cotton plays a major role in India’s economy and an important agricultural commodity providing remunerative income to millions of farmers both in developed and developing countries. It caters to one of the important basic needs of human race, clothing, besides meeting various industrial needs of cellulose and medicated absorbent cotton. The seed oil is also edible and can be used for the culinary purpose as refined oil.

In India, all the four cultivated cotton species viz., *Gossypium arboreum* L., *Gossypium herbaceum* L., *Gossypium hirsutum* L. and *Gossypium barbadense* L. are grown on a commercial scale. Among these four species, *Gossypium hirsutum* L. and *Gossypium barbadense* L. are tetraploids ($2n = 4x = 52$) and are commonly called new world cottons. Whereas, *Gossypium herbaceum* L. and *Gossypium arboreum* L. are diploids ($2n = 2x = 26$) are known as old world cottons. Out of the four cultivated cotton species, *Gossypium barbadense* L. is the important species known for its fibre quality and source for production of extra-long staple (ELS) cotton.

In India, cotton is being grown over an area of 12.65 m ha with an annual production of 40 million bales (1 bale=170 kg) with a productivity of 537 kg lint ha⁻¹. In the unified state of Andhra Pradesh (Andhra Pradesh +Telangana) cotton is a crop of great economic value, playing significant role in the socio-economic status of the farmers. It occupies an area of about 0.74 m ha with an annual production of 2.11 million bales and productivity of 624 kg lint ha⁻¹ (AICCIP Annual Report, 2014-15).

Cotton improvement programmes primarily lay emphasis on the development of varieties/hybrids that have contributed to the improvement of productivity. The hybrid cotton era in India had started in 1970 with the release of world’s first intra-specific cotton hybrid ‘H4’ (Patel, 1971). Later, the world’s first inter-specific hybrid between *G. hirsutum* and *G. barbadense* was released under the name “Varalaxmi” (Katarki, 1971). With the success of these two hybrids, heterosis breeding programmes

got momentum in the country and several hybrids were released for commercial cultivation. Among the hybrids, maximum area is covered by intra-hirsutum hybrids (*G. hirsutum* L. × *G. hirsutum* L.) followed by inter-specific hybrids (*G. hirsutum* L. × *G. barbadense* L.).

In India as against the demand of 20 lakh bales of extra-long staple fibre only 5 lakh bales are available. There are number of long and medium staple hybrids being cultivated in South and Central Zones, but in extra-long staple category, hybrids are very limited and current production of extra-long staple cotton is not sufficient to meet the domestic textile requirement of our country. So, there is an urgent need to develop suitable high yielding extra-long staple hybrids with desirable fibre qualities to cater the needs of Indian Textile Industry.

Identification of superior parents from both the species (*G. hirsutum* L. and *G. barbadense* L.) is necessary to develop potential heterotic inter - specific hybrids in cotton. Selection of parents on the basis of phenotypic performance alone is not a sound procedure, since phenotypically superior genotypes may perform poorly so there is a need to study genetic diversity in cotton. Genetic diversity analysis played an important role, because hybrids between lines of high genetic diversity can display a great heterosis than those between closely related parents. Hybridization involving genetically diverse parents is known to provide an opportunity for pooling genes together to yield desirable transgressive segregants in advanced generations.

The information on the extent of genetic variability, heritability, combining ability and genetic advance present in the material, coupled with the details on character association and path-coefficient analysis of yield, yield components and quality traits would also assist the breeder in selection of suitable parents and to decide the appropriate breeding methodology for crop improvement.

The line × tester analysis can be used to estimate general and specific combining abilities in both self and cross pollinated crops (Kempthorne, 1957). It also provides information for detection of appropriate parents and crosses superior in terms of the investigated characters. Besides estimates of general (*gca*) and specific combining ability (*sca*), information pertaining to the different types of gene action and relative magnitude of genetic variance estimates are paramount and vital parameters to understand the genetic architecture of breeding material.

The performance of any crop hybrid/variety is the result effect of its genotype and environment in which it grows. The differential response of a genotype or cultivar for a given trait across environments is defined as the genotype $\times$ environment interaction ($G \times E$). $G \times E$ is an important and essential component of plant breeding programmes because the genotypes or hybrids performing well under a particular environment may or may not perform well over other environments due to genotype $\times$ environment interactions. Several methods of estimating phenotypic stability across environments by determining $G \times E$ interaction effects are available and Eberhart and Russell (1966) and Additive Main effects and Multiplicative Interaction (AMMI) models (Gauch, 1988) are widely used. Eberhart and Russell model is the most exploited for stability analysis while, the AMMI model has been revealed to be more efficient because it captures a large portion of the $G \times E$ sum of squares and separates main and interaction effects. Stable performance of varieties/ hybrids under different environments with regard to economic characters like seed cotton and lint yields is one of the focal endeavors of cotton breeding programmes.

One of the methods of the development of new hybrids is the improvement of existing hybrids, *i.e.*, the improvement of one or both parental lines of the elite hybrid (Dudley, 1987a). For which older cultivars, lines *etc.* may serve for the improvement of existing cotton hybrids as the donors of favourable alleles. The procedure involves the introduction of favourable alleles into the existing parental lines, which would be manifested through better agronomic properties of future hybrids.

Hence, the present investigation was carried out with 70 American and 20 Egyptian cotton genotypes for evaluating genetic divergence during *kharif*, 2013-14. Eighteen parents (12 lines + 6 testers) were chosen based on their performance from diversity studies and crosses were attempted in line $\times$ tester fashion. The resulted 72 inter- specific hybrids along with their parents and standard checks were evaluated for their seed cotton yield, yield contributing and quality traits over locations *viz.*, Regional Agricultural Research Station (RARS) Lam Farm; Agricultural Research Station (ARS), Jangamaheswarapuram and Agricultural College Farm, Bapatla during *kharif*, 2014-15 with the following objectives.

1. To assess the genetic divergence among the genotypes.
2. To estimate the character association among yield and yield components through correlation and to assess the magnitude of direct and indirect effects of component characters on fibre quality and seed cotton yield.

3. To study the type of gene action and combining ability effects in inter-specific hybrids of cotton.
4. To assess the heterosis in inter-specific hybrids of cotton.
5. To assess the phenotypic stability of yield in inter-specific hybrids of cotton across the environments.
6. To identify the parents with favourable alleles.

LITERATURE CITED

- Ahsan, M.Z., Majidano, M.S., Bhutto, H., Soomro, A.W., Panhwar, F.H., Channa, A.R and Sial, K.B. 2015. Genetic variability, coefficient of variance, heritability and genetic advance of some *Gossypium hirsutum* L. accessions. *Journal of Agricultural Science*. 7(2): 147-151.
- Ahuja, S.L and Tuteja, O.P. 2000. Variability and association analysis for chemical components imparting resistance in cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 14(1): 19-22.
- AICCIP Annual Report. 2014-15. All India Co-ordinated Cotton Improvement Project. Coimbatore, Tamil Nadu, India.
- Allard, R.W. 1960. *Principle of Plant Breeding*. John Wiley and Sons Inc., New York. 145-147.
- Allard, R.W and Bradshaw, A.P. 1964. Implications of genotype-environment interaction in applied plant breeding. *Crop Science*. 4: 503-507.
- Altaher, A.F and Singh, R.P. 2003a. Yield component analysis in upland cotton (*Gossypium hirsutum* L.). *Journal of the Indian Society for Cotton Improvement*. 28(3): 151-157.
- Altaher, A.F and Singh, R.P. 2003b. Genetic diversity studies in upland cotton (*Gossypium hirsutum* L.). *Journal of the Indian Society for Cotton Improvement*. 28(3): 158-163.
- Amalabalu, P., Kavithamani, P.D., Ravikesavan, R and Rajarathinam, S. 2012. Heterosis for seed cotton yield and its quantitative characters of *Gossypium barbadense* L. *Journal of Cotton Research and Development*. 26(1): 37-40.
- Ambhore, K.T., Pandit, S.P., Lodam, V.A and Patil, B.R. 2012. Diallel analysis for quantitative traits in *Gossypium hirsutum* L. *Journal of Cotton Research and Development*. 26(2): 167-171.
- Amir, S., Farooq, J., Ameer, B., Khan, S.H and Saleem, M.F. 2012. Genetic studies of earliness in *Gossypium hirsutum* L. *International Journal of Agriculture, Veterinary and Medical Sciences*. 6(3): 189-207.

- An, D.T.H., Ravikesavan, R and Iyanar, K. 2008. Genetic advance and heritability as a selection index for improvement of yield and quality in cotton. *Journal of Cotton Research and Development*. 22(1): 14-18.
- Anandan, A. 2009. Studies on choice of characters for breeding of seed cotton yield and fibre quality traits in cotton. *Crop Improvement*. 36(1): 35-37.
- Annapurve, S.N., Deshmukh, G.S., Kausale, S.P and Kale, U.V. 2007. Correlation study of yield contributing characters in American cotton. *Journal of Cotton Research and Development*. 21(1): 16-20.
- Araujo, L., Wener, S.D.A., Candida, H.C.M.B., Francisco, D.C and Vidal, N.E.B. 2014. The use of different clustering methods in the evaluation of genetic diversity in upland cotton. *Revista Cienicia Agronomica*. 45(2): 312-318.
- Asha, R., Ahmed, M.L., Ratnababu, D and Anil Kumar, P. 2013a. Studies on Genetic variability, Heritability and Genetic advance for seed cotton yield and quality traits in upland cotton. *The Andhra Agricultural Journal*. 60(4): 785-788.
- Asha, R., Ahamed, M.L., Ratnababu, D and Anil Kumar, P. 2013b. Multivariate analysis in upland cotton (*Gossypium hirsutum* L.). *Madras Agricultural Journal*. 100(4-6): 333-335.
- Ayrault, S., Gouesnard, B., Panouilli, A and Boyat, A. 1999. Evaluation of late inbred lines in order to improve early single maize crosses by the bi-additive model and predictive genetic models. *Maydica*. 44(3): 183-194.
- Baloch, M.J., Solangi, J.A., Jatoi, W.A., Rind, I.H and Halo, F.M. 2014. Heterosis and specific combining ability estimates for assessing potential crosses to develop F₁ hybrids in upland cotton. *Pakistan Journal of Agriculture, Agricultural Engineering and Veterinary Science*. 30(1): 8-18.
- *Banfield, C.F. 1978. Principal component analysis for genstat. *Journal of Statistics and Computer Simulation*. 6: 211-222.
- *Bartlett, M.S. 1937. Some examples of statistical methods of research in agriculture and applied biology. *Supplement to Journal of Royal Statistical Society*. 4: 137-170.

- Basal, H., Unay, A., Canavar, O and Yavas, I. 2009. Combining ability for fibre quality parameters and yield components in intra-specific and inter-specific cotton populations. *Spanish Journal of Agricultural Research*. 7(2): 364-374.
- Basanagouda, C.P., Vijay Kumar, N., Ratnakumari, S., Mishra, U.S., Sreekanth, S.P and Basavaraj, M.K. 2011. Stability of *G. hirsutum* genotypes for performance across Indian rainfed ecosystems. <https://www.icac.org/meetings/wcrc/wcrc4/presentations/Paper1607.pdf>.
- Basavaraddi, N and Katageri, I.S. 2011. Genetic diversity studies in recombinant lines from inter-specific cross of *G. hirsutum* × *G. barbadense*. *Karnataka Journal of Agricultural Sciences*. 24(3): 268-272.
- Basha, M. 1997. Genetic analysis of yield and yield components of intra-specific hybrid cotton (*Gossypium hirsutum* L.). *Ph.D Thesis*. Acharya N G Ranga Agricultural University, Hyderabad, India.
- Batool, S., Khan, N.U., Makhdoom, K., Bibi, Z., Hassan, G., Marwat, K.B.F., Mohammad, R.F and Khan, I.A. 2010. Heritability and genetic potential of upland cotton genotypes for morpho-yield traits. *Pakistan Journal of Botany*. 42(2): 1057-1064.
- Bazi, S.N.B. 2011. Genetic divergence based on metric and physiological traits in upland cotton (*Gossypium hirsutum* L.). *M.Sc (Ag) Thesis*. Acharya N G Ranga Agricultural University, Hyderabad, India.
- Bbebe, N., Siamasonta, B.M and Lungu, D.M. 2010. Combining ability among inter-specific (*G. hirsutum* × *G. barbadense*) and mutation derived lines of cotton in fibre quality and agronomic traits. *Second Ruforum Biennial Meeting*. 20-24th September, Uganda. 417-420.
- Bernardo, R. 1990. An alternative statistic for identifying lines useful for improving parents of an elite single cross. *Theoretical and Applied Genetics*. 80: 105-109.
- Bhailume, M.S., Borole, D.N., Magar, N.M., Shinde, P.Y and Patil, M.R. 2014. Genetic diversity in desi cotton (*Gossypium arboreum* L.). *Journal of Cotton Research and Development*. 28(2): 230-233.
- Bhaskaran, S and Ravikesavan, R. 2008. Combining ability analysis of yield related traits and fibre quality traits in cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 22(1): 23-27.

- Bhatade, S.S and Bhale, N.L. 1983. Studies on stability parameters in *Gossypium arboreum*. *Indian Journal of Agricultural Sciences*. 53: 519-524.
- *Breese, E.D. 1969. The measurement and significance of genotype-environment interaction in grasses. *Heredity*. 21: 27-44.
- *Burton, G.W. 1952. Quantitative inheritance in grasses. *Proceedings of 6th International Grassland Congress*. 277-283.
- Chitti, B.K., Rajesh, S.P., Katageri, I.S., Sekhar, L and Khadi, B.M. 2014. Direct and indirect effect of various traits on seed cotton yield in single, double and three way cross derivatives in upland cotton (*Gossypium arboreum* L.). *Journal of Cotton Research and Development*. 28(2): 195- 200.
- Cochran, G.W and Cox, M.G. 1950. *Experimental Designs*. John Wiley and Sons Inc., New York. 45-67.
- Comstock, R.E and Robinson, H.F. 1948. The components of genetic variance in populations of biparental progenies and their use in estimating the average degree of dominance. *Biometrics*. 4: 245-266.
- Dagaonkar, V.S and Malkhandale, S.D. 1993. Diallel analysis using fixed effect model in upland cotton. *Journal of the Indian Society for Cotton Improvement*. 18(1): 50-53.
- Dedaniya, A.D and Pethania, K.V. 1994. Genetic variability, correlation and path analysis in desi cotton (*Gossypium arboreum* L.). *Indian Journal of Genetics and Plant Breeding*. 54(3): 229-234.
- Deosarkar, D.B., Jadhav, D.S and Patil, S.G. 2009a. Heterosis study in cotton (*Gossypium hirsutum* L.) under rainfed conditions. *Journal of Cotton Research and Development*. 23(1): 36-40.
- Deosarkar, D.B., Jadhav, D.S and Patil, S.G. 2009b. Combining ability studies for yield and quality traits in cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 23(2): 183-187.
- Deosarkar, D.B., Deshmukh, J.D and Deshmukh, V.D. 2014. Combining ability analysis for yield and fibre quality traits in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 28(1): 18-23.

- Desai, K.D., Patel, R.M., Tikka, S.B.S and Kukadia, M.V. 1983. Phenotypic stability of some promising genotypes of grain sorghum. *Indian Journal of Agricultural Sciences*. 53(7): 485- 497.
- Deshmukh, J.D., Deosarkar, D.B and Deshmukh, V.D. 2014. Heterosis for fibre quality traits in cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 28(2): 217-219.
- Deshmukh, S.B., Missal, M.B and Bhongle, S.A. 2010. Combining ability studies on quantitative characters in cotton. *Annals of Plant Physiology*. 24(1): 58-61.
- Dewdar, M.D.H. 2013. Stability analysis and genotype $\times$ environment interactions of some Egyptian cotton cultivars. *African Journal of Agricultural Research*. 8(41): 5156-5160.
- *Dewey, D.R and Lu, K.H. 1959. A correlation and path coefficient analysis of components of crested wheat grass seed production. *Agronomy Journal*. 51(9): 515-518.
- Dhivya, R., Amalabalu, P., Pushpa, R and Kavithamani, D. 2014. Variability, heritability and genetic advance in upland cotton (*Gossypium hirsutum* L.). *African Journal of Plant Science*. 8(1): 1-5.
- Drazic, S., Prodanovic, S and Zivanovic, T. 2010. Identification of donor lines containing favorable alleles for quantitative traits in burley tobacco (*Nicotiana tabacum* L.). *Genetika*. 42(2): 287-297.
- Dudley, J.W. 1984. A method of identifying lines for use in improving parents of a single cross. *Crop Science*. 24: 355-357.
- Dudley, J.W. 1987a. Modification of methods for identifying populations to be used for improving parents of elite single crosses. *Crop Science*. 27: 940-943.
- Dudley, J.W. 1987b. Modification of methods for identifying inbred lines useful for improving parents of elite single crosses. *Crop Science*. 27: 944-947.
- Dudley, J.W. 1988. Evaluation of maize populations as source of favorable alleles. *Crop Science*. 28: 486-491.

- Dudley, J.W., Lamkey, K.R and Geadelman, J.L. 1996. Evaluation of populations for their potential to improve three maize hybrids. *Crop Science*. 36: 1553-1559.
- Dukre, V.B., Potdukhe, N.R., Neelam, D and Parmar, J.N. 2007. Heterosis for yield, economic and morphological traits in American cotton. *Annals of Plant Physiology*. 21(2): 236-239.
- Eberhart, S.A and Russell, W.A. 1966. Stability parameters for comparing varieties. *Crop Science*. 6: 36-40.
- Ehrenberg, A.S.C. 1985. *Data Reduction Analysis and Interpreting Statistical Data*. John Wiley and Sons Inc., New York. 54-56.
- Ekinci, R., Basag, S and Gencer, O. 2010. Path coefficient analysis between seed cotton yield and some characters in cotton (*Gossypium hirsutum* L.). *Journal of Environmental Biology*. 31(5): 861-864.
- Elango, D., Thirumeni, S and Paramasivam, K. 2012. Yield and fibre quality components analysis in upland cotton (*Gossypium hirsutum* L.). *Annals of Biological Research*. 3(8): 3910-3915.
- Erande, C.S., Kalpande, H.V., Deosarkar, D.B., Chavan, S.K., Patil, V.S., Deshmukh, J.D., Chinchane, V.N., Kumar, A., Utpal, D and Puttawar, M.R. 2014. Genetic variability, correlation and path analysis among different traits in desi cotton (*Gossypium arboreum* L.). *African Journal of Agricultural Research*. 9(29): 2278-2286.
- Falconer, D.S. 1964. *An Introduction to Quantitative Genetics*. Second Edition. Oliver and Boyd, Edinburgh, London. 312-324.
- Faqir, M.A and Muhammad, N. 2008. Assessment of cotton (*Gossypium hirsutum* L.) germplasm for combining ability in fibre traits. *Journal of Agriculture and Social Sciences*. 4(3): 129-131.
- Farooq, J., Anwar, M., Riaz, M., Farooq, A., Mahmood, A., Shahid, M.T.H., Rafiq, M.S and Ilahi, F. 2014. Correlation and path coefficient analysis of earliness, fiber quality and yield contributing traits in cotton (*Gossypium hirsutum* L.). *The Journal of Animal and Plant Sciences*. 24(3): 781-790.

- Farooq, J., Anwar, M., Riaz, M., Mahmood, A., Farooq, A., Saeed, M.I and Shahid, M.I. 2013. Association and path analysis of earliness, yield and fiber related traits under cotton leaf curl virus (CLCuV) intensive conditions in *Gossypium hirsutum* L. *Plant Knowledge Journal*. 2(1): 43-50.
- *Fatih, K and Eyup, H. 2006. Genotype $\times$ environment interaction and stability analysis of cotton yield in Aegean region of Turkey. *Journal of Environmental Biology*. 27(2): 427-430.
- *Finlay, K.W and Wilkinson, G.N. 1963. Analysis of adaptation in a plant breeding programme. *Australian Journal of Agricultural Research*. 14: 742-754.
- Fisher, R.A and Yates, F. 1963. *Statistical Tables for Biological, Agricultural and Medical Research*. Oliver and Boyd, Edinburgh, London. 46-63.
- Freeman, G.H and Perkins, J.M. 1971. Environmental and genotype-environmental components of variability VIII. Relation between genotypes grown in different environments and measures of these environments. *Heredity*. 27: 15-23.
- Gamal, I.A.M., Haleem, A.E and Ibrahim, E.M.A. 2009. Genetic analysis of yield and its components of Egyptian cotton (*Gossypium barbadense* L.) under divergent environments. *American-Eurasian Journal of Agriculture and Environmental Sciences*. 5(1): 5-13.
- Gauch, M.G. 1988. Model selection and validation for yield traits with interaction. *Biometrics*. 44: 705-715.
- Ghaffar, K., Nematzadeh, G.A., Kazemitabar, S.K and Omran, A. 2007. Combining ability in cotton cultivars for agronomic traits. *International Journal of Agriculture and Biology*. 9(3): 521-522.
- Gibri, R.K., Nirania, K.S., Yagya, D and Sangwan, R.S. 2006. Combining ability studies for yield and quality traits in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 20(2): 178-180.
- Girase, V.S and Mehetre, S.S. 2002. Variability, heritability and genetic advance studies in cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 16(1): 81-82.

- Gomez, K.W and Gomez, A.A. 1984. *Statistical Procedures for Agricultural Research*. John Wiley & Sons Inc., New York. 316-356.
- Gopinath, M., Rajamani, S., Naik, K.R and Rao, C.M. 2009. Genetic divergence for lint characters in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 23(1): 46-48.
- Goran, T., Secanski, M., Zivanovic, T., Protic, R., Kostic, M., Jovanovic, S and Bozovic, D. 2012. Inbred lines of different cycles of selection - donors of favourable alleles for the improvement of the kernel row number of F₁ maize hybrids. *Turkish Journal of Field Crops*. 17(2): 198-202.
- Gururajan, K.N and Manickam, S. 2002. Genetic divergence in Egyptian cotton (*Gossypium barbadense* L.). *Journal of the Indian Society for Cotton Improvement*. 27(2): 77-83.
- Gururajan, K.N and Sundar, S. 2004. Yield component analysis in American cotton. International Symposium on 'Strategies for Sustainable Cotton Production - A Global Vision'. University of Agricultural Sciences, Dharwad, 23rd - 25th November. 201-204.
- Gururajan, K.N. 2000. Yield component analysis in Egyptian cotton (*Gossypium barbadense* L.). *Journal of the Indian Society for Cotton Improvement*. 25(1): 17-22.
- Hafiz, G.A., Abid, M and Qurban, A. 2013. Genetic variability, heritability, genetic advance and correlation studies in cotton (*Gossypium hirsutum* L.). *International Research Journal of Microbiology*. 4(6): 156-161.
- Haleem, A.E.S.H.M., Metwali, E.M.R and Felay, A.A.M.M. 2010. Genetic analysis of yield and its components of some Egyptian cotton (*Gossypium barbadense* L.) varieties. *World Journal of Agricultural Sciences*. 6(5): 615-621.
- Haritha, T and Ahamed, M.L. 2013. Multivariate analysis in upland cotton (*Gossypium hirsutum* L.). *Crop Research*. 46(1, 2&3): 217-222.
- Haritha, T., Ahamed, M.L., Satyanarayanarao, V and Rani, Y.A. 2012. Studies on genetic variability, heritability and genetic advance in upland cotton. *The Andhra Agricultural Journal*. 59(2): 205-209.

- Haritha, T., Ahamed, M.L., Satyanarayanarao, V and Rani, Y.A. 2014. Genetic divergence for morpho physiological traits in upland cotton. *Journal of Cotton Research and Development*. 28(1): 34-36.
- Hayes, J.D and Foster, C.A. 1976. Heterosis in self-pollinated crops with particular reference to barley. *Proceedings of 7th Congress Eucarpia*. 239-256.
- Henry, A and Daulay, H.S. 1983. Genotype $\times$ environment interactions for seed yield in Cluster bean. *Indian Journal of Agricultural Sciences*. 53: 467-468.
- Horner, T.W and Frey, K.J. 1957. Method for determining natural areas for oat varietal recommendations. *Agronomy Journal*. 49: 315 - 317.
- Huseyin, B and Ismail, T. 2003. Heterosis and combining ability for yield components and fiber quality parameters in a half diallel cotton (*Gossypium hirsutum* L.) population. *Turkish Journal of Agriculture*. 27: 207-212.
- Hussain, A., Azhar, F.M., Ali, M., Ahmad, S and Mahmood, K. 2010. Genetic studies of fibre quality characters in upland cotton. *The Journal of Animal and Plant Sciences*. 20(4): 234-238.
- Ilyas, M., Naveed, M., Khan, T.M and Khan, I.A. 2007. Combining ability studies in some quantitative and qualitative traits of cotton (*Gossypium hirsutum* L.). *Journal of Agriculture and Social Sciences*. 3(2): 39-42.
- Imran, M., Shakeel, A., Azhar, F.M., Farooq, J., Saleem, M.F., Saeed, A., Nazeer, W., Riaz, M., Naeem, M and Javaid, A. 2012. Combining ability analysis for within boll yield components in upland cotton (*Gossypium hirsutum* L.). *Genetics and Molecular Research*. 11(3): 2790-2803.
- Iqbal, M., Hayat, K., Ahmad, R.T and Khan, N.I. 2007. Performance of F₁ and F₂ hybrids of cotton (*Gossypium hirsutum* L.). *Asian Journal of Plant Sciences*. 6(4): 678-683.
- Iraddi, V and Kajjidoni, S.T. 2009. Combining ability analysis for productivity and fibre quality traits in intra-herbaceum and inter-specific (*G. herbaceum* L. $\times$ *G. arboreum* L.) crosses of diploid cotton. *Journal of Research ANGRAU*. 37 (3&4): 13-21.
- *Jackson, J.E. 1991. *A User's Guide to Principal Components*. John Wiley and Sons Inc., New York.

- Jain, P.P and Yadav, I.S. 2001. Studies on genetic divergence in American cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 15(1): 81-83.
- Jatoi, W.A., Baloch, M.J., Veesar, N.F and Panhwar, S.A. 2011. Combining ability estimates from line $\times$ tester analysis for yield and yield components in upland cotton genotypes. *Journal of Agricultural Research*. 49(2): 165-172.
- Jesus, R.M., Abelardo, R., Jose, H and Jose, F.M. 2007. Genetic studies in upland cotton (*Gossypium hirsutum* L.). *Pakistan Journal of Botany*. 39(2): 385-395.
- Johnson, H.W., Robinson, H.F and Comstock, R.E. 1955. Estimates of genetic and environmental variability in soybean. *Agronomy Journal*. 47: 314-318.
- Jowett, D. 1972. Yield stability parameters for sorghum in East Africa. *Crop Science*. 12: 314-317.
- Jyothiba, S.S., Patil, B.R., Deshpande, S.K., Patil, S.S and Patil, R.S. 2010. Heterosis studies in GMS based diploid cotton. *Electronic Journal of Plant Breeding*. 1(4): 685-688.
- Kale, U.R., Kalpande, S., Annapurve, S.N and Gite, V.K. 2007. Yield components analysis in American cotton (*Gossypium hirsutum* L.). *Madras Agricultural Journal*. 94(7-12): 156-161.
- Kalpande, H.V., Mukeshwar, A.M and Kalpande, V.V. 2008. Combining ability analysis in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 22(1): 10-13.
- Kamboh, N., Baloch, M.J., Kumbhar, M.B., Khanzada, S and Jatoi, W.A. 2008. Diallel analysis for estimating combining ability in upland cotton (*Gossypium hirsutum* L.). *Pakistan Journal of Agriculture, Agricultural Engineering and Veterinary Sciences*. 24(1): 27-33.
- Kandalkar, V.S and Sanghi, A.K. 1982. Phenotypic stability of flowering and other quantitative characters in forage cowpea (*Vigna unguiculata* (L). Walp.). *Madras Agricultural Journal*. 69: 78-80.

- Karademir, C., Gencer, O and Karademir, E. 2007. Heterosis and combining ability for yield and fibre properties in cotton (*Gossypium hirsutum* L.) under drought stress conditions. *Asian Journal of Plant Sciences*. 6(4): 667-672.
- Karademir, C., Gencer, O., Karademir, E and Ekinici, R. 2009. Combining ability estimates and heterosis for yield and fibre quality of cotton in line $\times$ tester design. *Notulac Botanicae Horti Agrobotanici Cluj-Napoca*. 37(2): 228-233.
- Katarki, B.H. 1971. Varalaxmi- A high yielding hybrid cotton of quality. *Indian Farming*. 21: 35-36.
- Kaushik, S.K and Kapoor, C.J. 2006. Genetic variability and association study for yield and its component traits in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 20(2): 185-190.
- Kaushik, S.K., Kapoor, C.J and Koli, N.R. 2003. Association and path analysis in American cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 17(1): 24-26.
- Kavithamani, D., Amala Balu, P and Rajarathinam, S. 2011. Stability analysis of seed cotton yield and its components of *Gossypium barbadense* genotypes. *Madras Agricultural Journal*. 98(10-12): 321-326.
- Kavithamani, D., Amala Balu, P and Rajarathinam, S. 2013. Assessment of genetic diversity in *Gossypium barbadense* L. *Jounal of Cotton Research and Development*. 27(1): 20-25.
- *Kempthorne, O. 1957. *An Introduction to Genetic Statistics*. John Wiley and Sons Inc., New York. 458-471.
- Khan, F.Z., Rehman, S.U., Abid, M.A., Malik, W., Hanif, C.M., Bilal, M., Qanmber, G., Latif, A., Ashraf, J and Farhan, U. 2015. Exploitation of germplasm for plant yield improvement in Cotton (*Gossypium hirsutum* L.). *Journal of Green Physiology, Genetics and Genomics*. 1(1): 1-10.
- Kiani, G., Nematzadeh, G.A., Kazemitabar, S.K and Alishah, O. 2007. Combining ability in cotton cultivars for agronomic traits. *International Journal of Agriculture and Biology*. 9(3): 521-522.

- Kishore, K.D., Gopinath, M., Satyanarayana Rao, V and Srinivasa Rao, V. 2011. Genetic variability studies in upland cotton. *The Andhra Agricultural Journal*. 58(1): 17-21.
- *Kohel, R.J. 1999. Cotton germplasm resources and the potential for improved fibre production and quality. In: Basra AS (eds.). Cotton fibres, the Haworth Press, Inc., New York, USA. 167-182.
- Kowsalya, R and Raveendran, T.S. 1996. Correlation and path coefficient analysis in cotton. *Madras Agricultural Journal*. 83(11): 705-707.
- Kulkarni, A.A., Nanda, H.C and Patil, S.G. 2011. Study of genetic parameters on yield, yield contributing and fibre quality characters in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 25(1): 22-24.
- Kumar, P.R., Raveendran, T.S and Krishnan, V. 2000. Genetic diversity and association studies for fibre characters in cotton (*Gossypium hirsutum* L.). *Journal of the Indian Society for Cotton Improvement*. 14(1): 111-118.
- Kumar, M.V.N., Venkatesh, S., Satyanarayana, E. 2003. Comparison of methods to identify donor inbreds with favourable alleles for the improvement of elite maize single cross hybrids. *The Indian Journal of Genetics and Plant Breeding*. 63(3): 212-214.
- Kumar, R.K. 2004. Genetic divergence studies in introgressed material of upland cotton (*Gossypium hirsutum* L.). *M.Sc (Ag) Thesis*. Acharya N G Ranga Agricultural University, Hyderabad, India.
- Kumar, A.K and Ravikesavan, R. 2008. Genetic studies of combining ability estimates for seed oil, seed protein and fibre quality traits in upland cotton (*Gossypium hirsutum* L.). *Research Journal of Agriculture and Biological Sciences*. 4(6): 798-802.
- Kumar, A.K., Ravikesavan, R and Prince, K.S.J. 2010. Combining ability estimates for yield and fibre quality traits in line $\times$ tester crosses of upland cotton (*Gossypium hirsutum* L.). *International Journal of Biology*. 2(1): 179-183.
- Kumar, S.K., Ashok Kumar, K and Ravikesavan, R. 2013. Genetic effects of combining ability studies for yield and fibre quality traits in diallel crosses of upland cotton (*Gossypium hirsutum* L.). *African Journal of Biotechnology*. 13(1):119-126.

- Kumar, S.P., Siwach, S.S., Sangwan, R.S., Sangwan, O and Deshmukh, J. 2014. Correlation and path coefficient analysis for yield and fibre quality traits in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 28(2): 214-216.
- Ladole, M.Y and Meshram, L.D. 2000. Correlation and path coefficient analysis in naturally coloured cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 14(1): 89-92.
- Lakshmi, G.V., Reddy, V.C., Rao, C.P., Babu, J.S and Srinivasulu, R. 2009. Multivariate analysis of genetic diversity in upland cotton (*Gossypium hirsutum* L.). *The Andhra Agricultural Journal*. 56(2): 8-15.
- Lakshmi, P.D., Samba Murthy, J.S.V., Rama Kumar, P.V and Ratna Kumari, S. 2012. Genetic variability, correlation and path analysis in desi cotton (*Gossypium arboreum* L.). *The Andhra Agricultural Journal*. 59(3): 376-379.
- Laxman, S and Ganesh, M. 2003. Combining ability for yield components and fibre characters in cotton (*Gossypium hirsutum* L.). *Journal of Research ANGRAU*. 31(4): 19-23.
- *Legendre, L and Legendre, P. 1984. *Ecologia Numerique*. Presses de l'Universite du Quebec. Xv + 260p, viii+335p.
- Lewis, D. 1954. Genotype-environment interaction. A relationship between dominance, heterosis, phenotypic stability and variability. *Heredity*. 8: 333-356.
- *Lush, J.L. 1940. Intra-sire correlation on regression of offspring on dams as a method of estimating heritability of characters. *Proceedings of American Society for Animal Production*. 33: 392-401.
- *Mahalanobis, P.C. 1928. A statistical study at Chinese head measurement. *Journal of Asiatic Society of Bengal*. 25: 301-307.
- Mahantesh, P. 2009. Combining ability studies involving new *hirsutum* lines in cotton (*Gossypium hirsutum* L.). *M.Sc (Ag) Thesis*. Acharya N G Ranga Agricultural University, Hyderabad, India.

- Mahantesh, P., Lal Ahamed, M., Panduranga Rao, C and Samba Murthy, J.S.V. 2010. Combining ability studies involving new hirsutum lines in cotton (*Gossypium hirsutum* L.). *The Andhra Agricultural Journal*. 57(1): 75-79.
- Makhdoom, K., Khan, N.U., Batool, S., Bibi, Z., Farhatullah, S.K and Fida, M. 2010. Genetic aptitude and correlation studies in *Gossypium hirsutum* L. *Pakistan Journal of Botany*. 42(3): 2011-2017.
- Malik, W., Khan, A.A and Saida, B. 2013. *In situ* characterization of coloured cotton genotypes. *Australian Journal of Crop Sciences*. 7(3): 299-304.
- Malvar, R.A., Revilla, P., Cartea, M.E and Ordas, A. 1997. Field corn inbred to improve sweet corn hybrids for early vigour and adaptation to European conditions. *Maydica*. 42(3): 247-255.
- Malvar, R.A., Cartea, M.E., Revilla, P., Soengas, P and Ordas, A. 2004. Verification of predictions from estimators of favorable alleles to improve yield of sweet corn hybrids. *Maydica*. 49: 49-55.
- Mandloi, K.C., Holkar, S., Julka, R and Kotu, G. 2003. Character association studies in coloured cotton. *Journal of the Indian Society for Cotton Improvement*. 28(1): 45-47.
- Manickam, S and Gururajan, K.N. 2004. Combining ability analysis for fibre quality in upland cotton (*Gossypium hirsutum* L.). *Journal of the Indian Society for Cotton Improvement*. 8(1): 86-91.
- Mohammad, R.Z., Jelodar, N.B., Kazemitabar, S.K and Tabar, M.V. 2009. Cytoplasmic and combining ability on fibre quality traits in intra and inter-specific crosses of tetraploid cotton (*G.hirsutum* and *G. barbadense*). *American-Eurasian Journal of Agricultural and Environmental Sciences*. 5(4): 519-525.
- Mohammad, R.Z., Jelodar, N.B., Kazemitabar, S.K and Tabar, M.V. 2010. Cytoplasmic and combining ability effects on agro-morphological characters in intra and inter crosses of pima and upland cottons (*Gossypium barbadense* and *Gossypium hirsutum*). *International Journal of Biology*. 2(1): 94-102.
- Mohammad, M.R., Muneeb, M., Ghazanfar, H., Rasheda, A., Sajida, H and Amir, L. 2013. Genetic analysis of some metric plant traits in upland cotton (*Gossypium hirsutum* L.) through hybridization. *Universal Journal of Plant Sciences*. 1(1): 1-7.

- Mohan, K.M. 2011. Combining ability analysis for fibre quality in inter-specific hybrids of cotton. *M.Sc (Ag) Thesis*. Acharya N G Ranga Agricultural University, Hyderabad, India.
- Muhammad, A.A., Khan, I.A., Awan, S.I., Shiraz, A and Shahid, N. 2008. Genetics of fibre quality traits in cotton (*Gossypium hirsutum* L.). *Australian Journal of Crop Science*. 2(1): 10-17.
- Muhammad, I., Chang, M.A., Iqbal, M.Z., Mahmood, H., Abdul, N and Noor, U.I. 2003. Correlation and path coefficient analysis of earliness and agronomic characters of upland cotton in Multan. *Pakistan Journal of Agronomy*. 2(3): 160-168.
- Muraleedhar, S.A. 2005. Genetic divergence in tetraploid cotton (*Gossypium hirsutum* L.). *M.Sc (Ag) Thesis*. Acharya N G Ranga Agricultural University, Hyderabad, India.
- Murthy, J.S.V.S. 1997. Analysis of character association and component analysis in American cotton. *Annals of Agricultural Research*. 18(4): 573-576.
- Muthu, R., Kandasamy, G and Jayaramachandran, N. 2004. Correlation and path coefficient analysis for yield and fibre quality traits in cotton (*Gossypium hirsutum* L.). *Journal of the Indian Society for Cotton Improvement*. 29(1): 17-20.
- Muthuswamy, A and Vivekanandan, P. 2004. Correlation studies on seed yield and yield components in hirsutum cotton (*Gossypium hirsutum* L.). *Journal of the Indian Society for Cotton Improvement*. 29(1): 7-9.
- Naik, V.S. 2012. Genetic studies for improvement of single cross hybrids of maize (*Zea mays* L.) through identification of elite inbreds with favourable alleles for yield and yield components. *Ph.D Thesis*. Acharya N G Ranga Agricultural University, Hyderabad, India.
- Naphade, P.S., Khardes, R.P., Potdukhe, N.R and Meshram, L.D. 2004. Heterosis and combining ability for quality attributes in inter varietal crosses of diploid cotton. International Symposium on 'Strategies for Sustainable Cotton Production - A Global Vision'. University of Agricultural Sciences, Dharwad, 23rd-25th November. 267-269.

- Naqib, U.K., Marwat, K.B., Gul, H., Farhatullah., Sundas, B., Makhdoom, K., Waqas, A and Khan, H.U. 2010. Genetic variation and heritability for cotton seed, fibre and oil traits in *Gossypium hirsutum* L. *Pakistan Journal of Botany*. 42(1): 615-625.
- Narisireddy, A and Ratnakumari, S. 2004. Genetic components of variation of physiological attributes for drought screening of genotypes in American cotton (*Gossypium hirsutum* L.). *Annals of Agricultural Research*. 25(3): 412-414.
- Narisireddy, A and Satyanarayana, A. 2004. Combining ability studies for yield and yield components over environments in American cotton (*Gossypium hirsutum* L.). *Madras Agricultural Journal*. 91(1-3): 75-78.
- Natera, M.J.R., Rondon, A., Hernandez, J and Pinto, F.M.J. 2011. Genetic studies in upland cotton (*Gossypium hirsutum* L.). *Journal of Agricultural Science and Technology*. 14: 617-627.
- Neelam, G.D., Pankaj, K and Potdukhe, N.R. 2002. Studies on variability and correlations in upland cotton for yield and its components. *Journal of the Indian Society for Cotton Improvement*. 27(3): 148-152.
- Neelima, S., Chenga Reddy, V and Narisireddy, A. 2005. Association and path analysis in American cotton (*Gossypium hirsutum* L.). *Journal of the Indian Society for Cotton Improvement*. 30(1): 53-58.
- Neelima, S., Reddy, V.C and Narisireddy, A. 2008. Genetic parameters of yield and fibre quality traits in American cotton (*Gossypium hirsutum* L.). *Indian Journal of Agricultural Research*. 42(1): 67-70.
- Nidagundi, J.M., Patil, S.S., Salimath, P.M., Kajjidi, P.M., Patil, B.C and Hegde, M.G. 2012. Heterobeltosis in multiple environments for seed cotton yield and yield attributes in cotton (*Gossypium hirsutum* L.). *Karnataka Journal of Agricultural Sciences*. 25(3): 301-304.
- Nimbalkar, R.D., Mehetre, S.S., Shinde, G.C and Mokate, A.S. 2014. Genetic analysis of seed cotton yield and yield components in intra-specific diploid cotton. *Journal of Cotton Research and Development*. 28(2): 230-233.
- Nirania, K.S., Jain, P.P and Yadav, N.K. 2014. Genetic improvement for seed cotton yield and its component traits through heterosis breeding in *Gossypium hirsutum* L. *Journal of Cotton Research and Development*. 28(2): 220-222.

- Padmavathi, A. 2008. Characterization of cotton germplasm (*Gossypium hirsutum* L.). *M.Sc (Ag) Thesis*. Acharya N G Ranga Agricultural University, Rajendranagar, Hyderabad, India.
- Panhwar, S.A., Baloch, M.J., Jatoi, W.A., Veesar, N.F and Majeedano, M.S. 2008. Combining ability estimates from line $\times$ tester mating design in upland cotton. *Proceedings of Pakistan Academy of Sciences*. 45(2): 69-74.
- Panse, V.G. 1957. Genetics of quantitative characters in relation to plant breeding. *Indian Journal of Genetics and Plant Breeding*. 17: 318-328.
- Panse, V.G and Sukhatme, P.V. 1978. *Statistical Methods for Agricultural Workers*. Indian Council of Agricultural Research, New Delhi. 103-108.
- Paramjit, S and Buttar, G.S. 2013. Study of heritability, correlation and path coefficient analysis among yield components in *Bt* cotton hybrids (*Gossypium hirsutum* L.). *Cotton Research Journal*. 4(1): 46-50.
- Patel, C.T. 1971. Release of hybrid-4 cotton. *Cotton Reviews*. 1(2): 1-5.
- Patel, K.G., Patel, U.G., Patel J.C., Patel, D.H and Patel, R.B. 2005. Line $\times$ tester analysis for combining ability of introgressed Asiatic cotton. *Journal of the Indian Society for Cotton Improvement*. 11(1): 105-109.
- Patel, A.D., Patel, U.G and Kumar, V. 2009. Diallel analysis for combining ability for seed cotton yield and its component traits in upland cotton. *Journal of Cotton Research and Development*. 23(2): 222-225.
- Patel, M.C., Patel, U.G and Bagade, A.B. 2011. $G \times E$ interactions in CMS and conventional based hybrids in upland cotton. *Cotton Research Journal*. 2(2): 19-30.
- Patel, N.A., Patel, B.N., Bhatt, J.P and Patel, J.A. 2012. Heterosis and combining ability for seed cotton yield and component traits in inter-specific cotton hybrids (*Gossypium hirsutum* L. $\times$ *Gossypium barbadense* L.). *Madras Agricultural Journal*. 99(10-12): 649-656.
- Patel, N.N., Patel, K.G and Kumar, V. 2013a. Genotype $\times$ environment interaction and stability analysis for yield and its component traits in BG II cotton hybrids. *Cotton Research Journal*. 4(1): 51-56.

- Patel, S.M., Patel, N.A., Parmar, M.B., Patel, M.P and Patel, J.A. 2013b. Studies on variability parameters, correlation and path coefficient analysis in *Bt* cotton hybrids (H × H). *Crop Research*. 46(1, 2 &3): 212-216.
- Patel, B.N., Patel, N.A., Soni, N.V and Dave, V.D. 2014. Genetic studies of quantitative traits in inter-specific hybrids of tetraploid cotton (*Gossypium hirsutum* L. × *Gossypium barbadense* L.). *Electronic Journal of Plant Breeding*. 5(4): 708-715.
- Patel, T.T and Jadon, B.S. 2014. Combining ability studies in *Gossypium herbaceum*. *Cotton Research Journal*. 6: 28-31.
- Patil, H.E and Patel, K.G. 2010. Stability analysis of seed cotton yield and its components of released *Bt* cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 24(1): 17-22.
- Patil, S.A., Naik, M.R., Chougule, G.R., Pathak, V.D and Patil, A.B. 2011. Combining ability analysis for yield and fibre quality traits in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 25(2): 171-175.
- Patil, S.A., Naik, M.R., Pathak, V.D and Kumar, V. 2012. Heterosis for yield and fibre properties in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 26(1): 26-29.
- Patil, S.S., Magar, N.M and Pawar, V.Y. 2014. Heterosis and combining ability for yield and its components in desi cotton (*Gossypium arboreum* L.). *Journal of Cotton Research and Development*. 28(2): 211-213.
- Patnaik, R.K and Sial, P. 2010. Genetic variability, character association and component analysis in upland cotton (*Gossypium hirsutum* L.) under rainfed condition. *Journal of Cotton Research and Development*. 24(2): 155-159.
- Patnaik, R.K., Sial, P., Patil, S.A., Khadi, B.M and Patil, S.S. 2004. Heterosis for fibre quality parameters in intra-hirsutum crosses of cotton (*Gossypium hirsutum* L.). International Symposium on 'Strategies for Sustainable Cotton Production - A Global Vision'. University of Agricultural Sciences, Dharwad, 23rd-25th November.
- Paul, N.K. 1978. Genetic architecture of yield and components of yield in mustard (*Brassica juncea* L.). *Theoretical and Applied Genetics*. 53: 233-237.

- Paulo, D.A., Julio, C.V.P., Eleusio, C.F and Leonardo, C.M. 2007. Diallel analysis of upland cotton cultivars. *Crop Breeding and Applied Biotechnology*. 7: 353-359.
- Perkins, M.J and Jinks, J.L. 1968. Environmental and genotype-environment components of variability III. Multiple lines and crosses. *Heredity*. 23: 339-356.
- Plaisted, R.L and Peterson, L.C. 1959. A technique for evaluating the ability of selection to yield consistently in different seasons or locations. *American Potato Journal*. 36: 381-385.
- Pole, S.P., Kamble, S.K., Madrap, I.A and Saranga, D.H. 2008. Diallel analysis for combining ability of seed cotton yield and its components in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 22(1): 19-22.
- Potdukhe, N.R. 2002. Level of heterosis for quantitative traits in upland cotton. *Journal of the Indian Society for Cotton Improvement*. 27(3): 200-214.
- Pradeep, T and Sumalini, K. 2005. Studies on the performance and pattern of genetic variability for plant type and productive traits in multiple crosses of cotton (*Gossypium hirsutum* L.). *Journal of the Indian Society for Cotton Improvement*. 30(1): 59-66.
- Pratap, K.L., Chenga Reddy, V., Rama Kumar, P.V and Srinivasa Rao, V. 2007. Correlation and path coefficient analysis for yield and yield component traits in cotton (*Gossypium hirsutum* L.). *The Andhra Agricultural Journal*. 54(1&2): 31-35.
- Preetha, S and Raveendran, T.S. 2008. Combining ability studies for yield and fibre quality traits in line $\times$ tester crosses of upland cotton (*Gossypium hirsutum* L.). *International Journal of Plant Breeding and Genetics*. 2(2): 64-67.
- Punitha, D., Gunasekaran, M., Vinodhana, K., Puspha, R and Vindhavarman, P. 2012. Yield and fibre quality improvement in cotton (*Gossypium* spp.) using inter-specific hybridisation. *Madras Agricultural Journal*. 99(7-9): 461-464.
- Rajamani, S and Rao, Ch.M. 2009. Genetic divergence in upland cotton (*Gossypium hirsutum* L.). *The Andhra Agricultural Journal*. 56(2): 181-185.
- Rajamani, S., Mallikarjuna Rao, Ch and Krishna Naik, R. 2009. Heterosis for yield and fibre properties in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 23(1): 43-45.

- Rajamani, S., Gopinath, M and Reddy, K.H.P. 2012. Genetic analysis of boll weight in cotton (*Gossypium hirsutum* L.). *Journal of Research ANGRAU*. 40(4): 75-78.
- Rajamani, S., Sumalatha, P and Gopinath, M. 2013. Correlation and path coefficient analysis in *Gossypium hirsutum* L. *Journal of Cotton Research and Development*. 27(2):188-190.
- Rajamani, S., Gopinath, M and Reddy, K.H.P. 2014. Combining ability for seed cotton yield and fibre characters in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 28(2): 207- 210.
- Rajan, S.G.A. 1997. Studies on heterosis and combining ability in cotton (*Gossypium hirsutum* L.). *M.Sc (Ag) Thesis*. Tamil Nadu Agricultural University, Coimbatore, India.
- Rajanna, B. 2010. Combining ability studies involving new *hirsutum* lines in cotton (*Gossypium hirsutum* L.). *M.Sc (Ag) Thesis*. Acharya N G Ranga Agricultural University, Hyderabad, India.
- Rajanna, B., Samba Murthy, J.S.V., Lal Ahamed, M and Srinivasa Rao, V. 2011. Correlation and path coefficient analysis in upland cotton (*Gossypium hirsutum* L.). *The Andhra Agricultural Journal*. 58(2): 151-155.
- Ranjan, R., Sangwan, R.S., Siwach, S.S., Sangwan, O and Sah, M.K. 2014. Correlation and path analysis studies in *Gossypium arboreum* L. *Journal of Cotton Research and Development*. 28(1): 37-39.
- Rao, C.R. 1952. *Advanced Statistical Methods in Biometrical Research*. John Wiley and Sons Inc., New York. 236-272.
- Rao, G.N and Reddy, M.S.S. 2001. Studies on heritability and variability for yield and its components in *hirsutum* cotton. *Journal of Cotton Research and Development*. 15(1): 84-86.
- Rao, G.E., Chenga Reddy, V., Lal Ahamed, M., Srinivasa Rao, V., Panduranga Rao, C and Bali Reddy, V. 2009a. Correlation and path coefficient analysis in cotton (*Gossypium hirsutum* L.). *The Andhra Agricultural Journal*. 56(2): 192-195.
- Rao, G.E., Chenga Reddy, V., Lal Ahamed, M., Srinivasa Rao, V., Panduranga Rao, C and Bali Reddy, V. 2009b. Genetic divergence in upland cotton (*Gossypium hirsutum* L.). *The Andhra Agricultural Journal*. 56(2): 309-314.

- Rathore, P., Garg, H.R., Varma, P.K and Pathak, D. 2004. Genetics of seed cotton yield and some other traits in American cotton using triple test cross analysis. *Journal of the Indian Society for Cotton Improvement*. 30(1): 67-70.
- Ravikesavan, R., Do, T.H and Iyanar, K. 2008. Genetic advance and heritability as a selection index for improvement of yield and quality in cotton. *Journal of Cotton Research and Development*. 22(1): 14-18.
- Ravikesavan, R., Venkatesan, S., Sathish, S., Kavitha, P and Boopathi, N.M. 2014. Unlocking the genetic potential for improvement of economic traits in large collection of cotton (*Gossypium* spp.). *Journal of Cotton Research and Development*. 28(2): 175-184.
- Reddy, A.N. 2001. Heterosis, combining ability and stability analysis of hybrids for yield and yield components in cotton (*Gossypium hirsutum* L.). *Ph.D Thesis*. Acharya N G Ranga Agricultural University, Hyderabad, India.
- Reddy, D.M., Ahuja, V.P and Mukherjee, B.K. 2003. Identification of favourable alleles in inbred parents for the improvement of single cross hybrids in maize (*Zea mays* L.). *Indian Journal of Genetics and Plant Breeding*. 63(3): 253-254.
- Reddy, D.M., Ahuja, V.P and Mukherjee, B.K. 2004. Selection of recycled inbreds through identification of favourable alleles for the improvement of an elite single cross hybrid in maize (*Zea mays* L.). *Indian Journal of Genetics and Plant Breeding*. 64(1): 31-34.
- Reddy, D.M., Ahuja, V.P and Mukherjee, B.K. 2005. Comparison of various statistics for identification of maize inbreds with favourable alleles useful for the improvement of single cross hybrid in maize (*Zea mays* L.). *Indian Journal of Genetics and Plant Breeding*. 65(4): 253-256.
- Reddy, R.Y and Sarma, A.S.R. 2014. Stability analysis of diploid cotton (*Gossypium arboreum* L.). *Plant Archives*. 14(1): 593-596.
- Reshmi, J.A., Raveendran, T.S and Ravikesavan, R. 2007. Evaluation of genetic potential of newly developed restorers in upland cotton. *Journal of the Indian Society for cotton Improvement*. 32(3): 82-86.
- Riaz, M., Naveed, M., Farooq, J., Farooq, A., Mahmood, A., Rafiq, Ch.M., Nadeem, M and Sadiq, A. 2013. AMMI analysis for stability, adaptability and GE interaction studies in cotton (*Gossypium hirsutum* L.). *The Journal of Animal and Plant Sciences*. 22(3): 865-871.

- Rodriguez, V.M., Romay, M.C., Ordas, A and Revilla, P. 2007. Evaluation of European maize germplasm under cold conditions. *Crop Science*. 47: 1467-1474.
- Saini, D.P., Rianwaha, B.R and Rokodia, P. 2008. Stability parameters in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 22(1): 28-30.
- Sakthi, A.R., Kumar, M and Ravikesavan, R. 2007. Variability and association analysis using morphological and quality traits in cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 21(2): 148-152.
- Salahuddin, S., Abro, S., Kandhro, M.M., Salahuddin, L and Laghari, S. 2010. Correlation and path analysis for yield components in upland cotton (*Gossypium hirsutum* L.). *World Applied Sciences Journal*. 8: 71-75.
- Salman, S.C. 1951. Analysis of variance and long term variety test of wheat. *Agronomy Journal*. 43: 562-570.
- *Samanc, B and Ozkaynak, E. 2000. Determination of some agronomic traits of cotton (*Gossypium hirsutum* L.) cultivars and lines under antalya conditions. *Ziraat Fakultesi Dergisi Akdemiz Universitesi*. 13(2): 113-122.
- Sambamurthy, J.S.V., Chamundeswari, N and Udayasree, P. 2006. Assessment of genetic variability and relationship of yield attributes in introgressed lines of American cotton. *The Andhra Agricultural Journal*. 53(3&4): 129-132.
- *Sandison, A and Bartlett, B.O. 1958. Comparison of varieties for yield. *Journal of National and International Agricultural Botany*. 8: 351-357.
- Sangeetha, K. 1998. Character association of quality traits on yield and yield components in cotton (*Gossypium hirsutum* L.). *M.Sc (Ag) Thesis*. Acharya N G Ranga Agricultural University, Hyderabad, India.
- Sarada, B., Ahamed, M.L., Rao, V.S and Sreekanth, B. 2010. Genetic variability, character association and path coefficient analysis in *Gossypium hirsutum* L. *The Andhra Agricultural Journal*. 57(4): 352-356.
- Satish, Y., Jain, P.P and Chhabra, B.S. 2009a. Studies on genetic diversity in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 23(1): 18-22.

- Satish, Y., Jain, P.P and Chhabra, B.S. 2009b. Stability analysis for yield and its component traits in American cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 23(2): 175-182.
- Seoudy, E.A.A., Ghaffar, A.N.Y., Awad, H.Y., Hady, A.A and Darweesh, S.I.M. 2014. Evaluation of some crosses for economic traits in cotton (*Gossypium barbadense* L.). *Egyptian Journal of Agricultural Research*. 92(1): 183-192.
- Shaarawy, S.A, Abdel Bary, A.M.R., Hamoud, H.M and Yehia, W.M.B. 2013. Use of high efficient AMMI method to evaluate new Egyptian cotton genotypes. <https://www.icac.org/meetings/wcrc/wcrc4/presentations/Paper1704.pdf>.
- Shabana, M., Piar, A.S., Abdel, G.S., Sadaf, M., Saima, M., Mohammad, A.M and Akhtar, H.S. 2014. Biometrical analysis of some quantitative traits of cotton (*Gossypium hirsutum* L.). *International Journal of Science, Environment and Technology*. 3(6): 2069-2075.
- Sharma, P.K., Gupta, P.K and Govila, O.P. 1998. AMMI analysis of a pearl millet yield trial. *Indian Journal of Genetics and Plant Breeding*. 58(2): 183-192.
- Sharma, S.M., Jain, K.K., Rai, R.C and Neelam, S. 1980. Evaluation of yield and stability performance of some greengram varieties. *Indian Journal of Agricultural Sciences*. 47: 303-304.
- Sheraz, A.K., Naqib, U.K., Fida, M., Mushtaq, A., Ijaz, A.K., Zarina, B and Imdad, U.K. 2011. Combining ability analysis in intra-specific F₁ diallel cross of upland cotton. *Pakistan Journal of Botany*. 43(3): 1719-1723.
- Shinde, G.C., Mehtre, S.S and Jagtap, P.K. 2012. Combining ability and heterosis for seed cotton yield and its component traits in CGMS based hybrids of cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 23-32.
- *Shull, G.H. 1914. What is "heterosis"? *Genetics*. 33: 439-446.
- Simon, S.Y., Kadams, A.M and Aliyu, B. 2013. Combining ability analysis in F₁ hybrids of cotton (*Gossypium hirsutum* L.) by diallel method in Northern Nigeria. *Greener Journal of Agricultural Sciences*. 3(2): 90-96.
- Singh, R.K and Chaudhary, B.D. 1977. *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, New Delhi. 215-218.

- Singh, R.K and Chaudhary, B.D. 1985. *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani Publishers, New Delhi. 205-214.
- Singh, P., Dinesh, K.A and Loknathan, T.R. 2004. Stability analysis in Asiatic cotton (*Gossypium arboreum*). *Journal of the Indian Society for Cotton Improvement*. 29: 158-161.
- Singh, S.B and Singh, P. 2006. Heterosis and combining ability in GMS intra-hirsutum crosses under rainfed condition. *Journal of Soils and Crops*. 16(1): 25-32.
- Singh, S., Singh, V.V and Choudhary, A.D. 2010. Combining ability estimates for oil content, yield components and fibre quality traits in cotton (*G. hirsutum*) using an 8×8 diallel mating design. *Tropical and Subtropical Agroecosystems*. 12: 161-166.
- Sivaprasad, U., Chenga Reddy, V and Narisireddy, A. 2004. Combining ability studies for yield and yield components in American cotton. International symposium on 'Strategies for Sustainable Cotton Production - A Global Vision'. University of Agricultural Sciences, Dharwad 23rd - 25th November.
- Sivasubramaniam, P and Menon, P.M. 1973. Inheritance of short stature in rice. *Madras Agricultural Journal*. 60: 1129-1133.
- Snedecor, G.W and Cochran, W.G. 1967. *Statistical Methods*. The Iowa State College Press, Ames, Iowa. U.S.A. 160-413.
- *Sprague, G.F and Tatum, L.A. 1942. General vs Specific combining ability in single crosses of corn. *Journal of American Society for Agronomy*. 34: 923-932.
- Srinivasulu, P. 2009. Genetic divergence in upland cotton (*Gossypium hirsutum* L.) *M.Sc (Ag) Thesis*. Acharya N G Ranga Agricultural University, Hyderabad, India.
- Srinivasulu, P., Murthy, J.S.V.S., Kumar, P.V.R and Rao, V.S. 2010a. Character association and path coefficient analysis for yield and yield component traits in upland cotton (*Gossypium hirsutum* L.). *The Andhra Agricultural Journal*. 57(1): 69-74.
- Srinivasulu, P., Murthy, J.S.V.S., Kumar, P.V.R and Rao, V.S. 2010b. Multivariate analysis of genetic diversity in upland cotton (*Gossypium hirsutum* L.). *The Andhra Agricultural Journal*. 57(2): 148-155.

- Subramanian, A., Ravikesavan, R., Iyanar, K., Thangaraj, K and Vindhyavarman, P. 2005. Combining ability analysis in upland cotton (*Gossypium hirsutum* L.). *Plant Archives*. 5(1): 23-28.
- Sundaravadivelu, K., Reddy, V.R.K and Rathinavel, K. 2005. Heterosis and inbreeding depression in intervarietal crosses of cotton (*Gossypium hirsutum* L.) selfed progenies. *Crop Research*. 29(3): 474-479.
- Swarup, T and Chaugle, B.S. 1962. Studies on genetic variability in sorghum; phenotypic variation and heritable component in some quantitative characters contributing towards yield. *Indian Journal of Genetics and Plant Breeding*. 22: 31-36.
- Syed, A.H.S and Sajid, M.S. 2008. Heterosis in some intraspecific crosses of *Gossypium hirsutum* L. *Pakistan Journal of Agricultural Research*. 21(1): 1-4.
- Taranjit, S., Sohu, R.S., Paramjit, S., Rathore, P., Sekhon, P.S., Buttar, G.S., Hassan, H and Gurpreet, S. 2012. Stability analysis of *Bt* transgenic cotton hybrids of *Gossypium hirsutum* L. for lint yield and fibre quality traits. *Journal of Cotton Research and Development*. 26(2): 163-166.
- Tariq, M.K and Uzair, Q.M. 2012. Genetic studies of yield traits in cotton (*Gossypium hirsutum* L.). *Journal of Agricultural Research*. 50(1): 21-29.
- Tomar, S.K and Singh, S.P. 1996. Genetics of yield and yield components over locations in desi cotton (*Gossypium arboreum* L.). *Indian Journal of Genetics and Plant Breeding*. 56(1): 89-93.
- Tulasi, J., Ahamed, M.L., Murthy, J.S.V.S and Rani, Y.A. 2014. Multivariate analysis in upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 28(2): 191-194.
- Tuteja, O.P., Sunil, K., Hamid, H and Mahendar, S. 2005. Heterosis and inter-relationship between seed cotton yield and quantitative characters in upland cotton (*Gossypium hirsutum* L.). *Indian Journal of Agricultural Sciences*. 75(3): 169-171.
- Tuteja, O.P., Sunil, K and Mahendar, S. 2006. Selection parameters and yield enhancement of upland cotton (*Gossypium hirsutum* L.) under irrigated ecosystem of North India. *Indian Journal of Agricultural Sciences*. 76(2): 77-80.

- Tuteja, O.P and Banga, M. 2013. Combining ability estimates for yield and quality characters of parents and crosses based on genetic male sterility in cotton (*Gossypium hirsutum* L.). *Indian Journal of Agricultural Sciences*. 83(9): 987-991.
- Tuteja, O.P., Manju, B and Hamid, H. 2013. Heterosis for seed cotton yield component and fibre properties of American cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 27(2): 184-187.
- Tuteja, O.P. 2014. Studies on heterosis for yield and fibre quality traits in GMS hybrids of upland cotton (*Gossypium hirsutum* L.). *Journal of Cotton Research and Development*. 28(1): 1-6.
- Tyagi, A.P. 1994. Association of yield components and fibre traits and their functions in upland cotton (*Gossypium hirsutum* L.). *Indian Journal of Agricultural Research*. 28(3): 159-165.
- Usharani, K.S., Vindhyavarman, P and Amala Balu, P. 2014. Combining ability analysis in intra-specific F₁ diallel cross of upland cotton (*Gossypium hirsutum* L.). *Electronic Journal of Plant Breeding*. 5(3): 467-474.
- Valarmathi, M and Jehangir, K.S. 1998. Studies on genetic parameters for yield and fibre quality traits in intra-varietal crosses of cotton (*Gossypium hirsutum* L.). *Journal of the Indian Society for Cotton Improvement*. 23(1): 103-109.
- Venkatesh, P. 2012. Heterosis and combining ability in inter-specific cotton hybrids (*G. hirsutum* L. × *G. barbadense* L.). *M.Sc (Ag) Thesis*. Acharya N G Ranga Agricultural University, Hyderabad, India.
- Venkateswarlu, K., Chenga Reddy, V., Samba Murthy, J.S.V., Srinivasa Rao, V., Panduranga Rao, C., Siva Reddy, K.V and Sateesh Babu, J. 2010a. Character association and path coefficient analysis for yield and yield component traits in upland cotton (*Gossypium hirsutum* L.). *The Andhra Agricultural Journal*. 57(2): 173-176.
- Venkateswarlu, K., Chenga Reddy, V., Samba Murthy, J.S.V., Srinivasa Rao, V., Panduranga Rao, C., Siva Reddy, K.V and Sateesh Babu, J. 2010b. Multivariate analysis of genetic diversity in upland cotton (*Gossypium hirsutum* L.). *The Andhra Agricultural Journal*. 57(3): 240-247.

- Verma, S.K., Ahuja, S.L., Tuteja, O.P., Kumar, S., Singh, M., Monga, D and Prakash, R. 2004. Line $\times$ tester analysis of yield, its components and fibre quality traits in cotton (*Gossypium hirsutum* L.). *Journal of the Indian Society for Cotton Improvement*. 16 (1): 151-157.
- Verma, S.K., Tuteja, O.P., Koli, N.R., Jal, S and Monga, D. 2006. Assessment of genetic variability, nature and magnitude of character association in cytotype genotypes of upland cotton (*Gossypium hirsutum* L.). *Journal of the Indian Society for Cotton Improvement*. 31(3): 129-133.
- Verma, S.K., Tuteja, O.P and Monga, D. 2013. Studies on stability parameters and sustainability index for selecting stable genotypes in Asiatic cotton (*Gossypium hirsutum* L.). *Indian Journal of Agricultural Sciences*. 83(12): 1377-1380.
- Vijayalaxmi, G., Chenga Reddy, V., Panduranga Rao C., Satish Babu, J and Srinivasulu, R. 2008. Character association and path coefficient analysis in cotton (*Gossypium hirsutum* L.). *The Andhra Agricultural Journal*. 55(2): 156-160.
- Vineela, N., Samba Murthy, J.S.V., Rama Kumar, P.V and Ratna Kumari, S. 2012. Combining ability estimates for yield and fibre quality traits in line $\times$ tester crosses of intra-hirsutum hybrids of cotton (*Gossypium hirsutum* L.). *The Andhra Agricultural Journal*. 59(4): 545-555.
- Vinodhana, K.N., Gunasekaran, M and Vindhavarman, P. 2013. Genetic studies of variability, correlation and path coefficient analysis in cotton genotypes. *International Journal of Pure and Applied Bioscience*. 1(5): 6-10.
- Wajid, A.J., Baloch, M.J., Veesar, N.F and Panhwar, S.A. 2011. Combining ability estimates from line $\times$ tester analysis for yield and yield components in upland cotton genotypes. *Journal of Agricultural Research*. 49(2): 165-172.
- Wandhare, M.R., Patil, B.R., Ambhore, K.T and Bhongle, S.A. 2010. Diallel analysis for estimating combining ability of quantitative traits in upland cotton. *Annals of Plant Physiology*. 24(1): 62-64.
- Wankhade, S.N., Patil, S.P., Kayande, N.V and Burghate, S.K. 2008. Diallel analysis for estimating combining ability of quantitatively inherited traits in upland cotton. *Journal of Cotton Research and Development*. 22(2): 147-149.

- Wankhade, S.N., Patil, S.P., Burghate, S.K and Chikhale, N.J. 2009. Heterosis for seed cotton yield and its quantitative characters of *Gossypium hirsutum* L. *Journal of Cotton Research and Development*. 23(1): 27-31.
- *Wricke, O. 1962. Über eine Method Zur Erfassung der ökologischen Streubreite in Feldversuchen. *Zpflanz Zucht* 47: 92-96.
- *Wright, S. 1921. Correlation and causation. *Journal of Agricultural Research*. 20: 557-585.
- Yanal, A., Patil, S.S., Manjula, S.M., Patil, B.C., Nadaf, H.L., Nandihali, B.S. 2013. Development of heterotic groups (*G. hirsutum* vs *G. barbadense*) based on combining ability and inter-specific hybrids performance for yield and fiber quality traits. *Molecular Plant Breeding*. 4(24): 196-208.
- Yates, F and Cochran, W.G. 1938. The analysis of groups of experiments. *Journal of Agricultural Sciences*. 28: 556-558.
- Zanoni, U and Dudley, J.W. 1989a. Comparison of different methods of identifying inbreds useful for improving elite maize hybrids. *Crop Science*. 29: 577-582.
- Zanoni, U and Dudley, J.W. 1989b. Testcross evaluation of F₂ populations from maize inbreds selected for unique favourable alleles. *Crop Science*. 29: 589-595.

* Original not seen

Note: The literature is cited according to thesis guidelines prescribed by Acharya N. G. Ranga Agricultural University, Guntur, Andhra Pradesh.

Chapter III

MATERIAL AND METHODS

The present investigation entitled “**Genetic analysis of yield and fibre quality traits in inter-specific hybrids of cotton (*Gossypium hirsutum* L. × *Gossypium barbadense* L.)**” was taken up by selecting twelve *G. hirsutum* lines viz., NDLH 1938, H 1442, ADB 542, ADB 532, WGCV 48, MR 786, TSH 0250, BS 37, SCS 793, MCU 5, L 1058, L 762 and six *G. barbadense* testers viz., GSB 40, DB 16, DB 11, GSB 41, TCB 37 and SUVIN based on their performance in genetic divergence study carried out with 70 *G. hirsutum* and 20 *G. barbadense* genotypes during *kharif*, 2013-14 and 72 inter-specific cross combinations were made in line × tester fashion during off season (2014-15) at Regional Agricultural Research Station (RARS), Lam Farm, Guntur, Andhra Pradesh. The evaluation of hybrids along with parents and standard checks was done at three locations i.e., Regional Agricultural Research Station (RARS), Lam Farm, Agricultural Research Station (ARS), Jangamaheswarapuram (J M Puram) and Agricultural College Farm, Bapatla during *kharif*, 2014-15. RARS, Lam Farm, Guntur is located at an altitude of 35.10 m above MSL. Geographically this location is at latitude of 16° 21' N and longitude of 80° 26' E. The soils here were black cotton type with clay texture. ARS, J M Puram is located at latitude of 16° 13' N, longitude of 79° 38' E and at an altitude of 105.75 m above MSL. The soils are black cotton type with clay texture. Agricultural College Farm, Bapatla is located at latitude of 15° 54' N, longitude of 80° 3' E and at an altitude of 5.49 m above MSL. The soils are black cotton type with clay texture.

3.1 EXPERIMENT-I

The experimental material used in the present study during *kharif*, 2013-14 comprised 70 *Gossypium hirsutum* and 20 *Gossypium barbadense* genotypes. The list of genotypes used for the study is presented in Tables 3.1 and 3.2. The detailed experimental techniques followed in the present investigation are furnished in Table 3.3.

Table 3.3. Experimental details of genetic diversity analysis of cotton genotypes during *kharif*, 2013-14

Location	: RARS, Lam Farm, Guntur
Season	: <i>Kharif</i> , 2013-14
Design	: Randomized Complete Block Design
Genotypes	: 70 <i>G. hirsutum</i> and 20 <i>G. barbadense</i> genotypes
Replications	: 3
No. of rows/ genotype	: 2
No. of plants /row	: 10
Row length	: 6 m
Spacing	: 105 cm × 60 cm
Plot size	: 2.10 m × 6 m
Fertilizers	: 120 N: 60 P ₂ O ₅ : 60 K ₂ O kg/ha
Plant protection	
Seed treatment	: Imidacloprid 70 WS @ 5 g/kg followed by Carbendazim 50 WP @ 2 g / kg
Stem application	: At 30 & 45 DAS with monocrotophos (1:4)
Leafhoppers / aphids / thrips	: Monocrotophos 36 SL @ 1.6 ml/l or Acephate 75 SP @ 1.5g/l or Acetamiprid 20 SP @ 0.2 g/l
Whitefly	: Triazophos 40 EC @ 2.0 ml/l or Profenophos 50 EC @ 2.0 ml/l or NSKE @ 5%
Bacterial blight	: Copper oxy chloride 3.0 g/l + streptocycline 100 mg/l
Leaf spots	: Carbendazim @ 2.0g or mancozeb @ 3.0 g/l
Fusarium / Verticillium wilts	: Soil drenching with copper oxy chloride @3.0 g/l
Boll worms	: Chlorantraniliprole 18.5% SC @ 0.3 ml/ lt

3.2 EXPERIMENT-II

The list of parents, hybrids and checks used for the study are presented in the Table 3.4. The detailed experimental techniques followed in the present investigation are furnished in Tables 3.5 and 3.6.

3.2.1 Generation of Cotton Hybrid Seed

Hybridization

Seventy two inter-specific crosses were obtained involving twelve *hirsutum* lines and six *barbadense* testers in a line × tester fashion during off season (2014). Three staggered sowings of the parents (females and males) were undertaken to ensure synchronous flowering to produce adequate crossed seed, with a spacing of 120 cm × 60 cm. The plots were periodically irrigated, top dressed with urea. The need based cultural practices and plant protection measures were carried out timely.

Emasculation

Healthy flower buds of female parents were selected between 3.00 PM and 5.00 PM one day before anthesis. Corolla was removed along with anther column by giving shallow cut at base of the bud with thumb finger nail and twisting in one jerk action. If any anthers were present they were carefully removed without causing any damage to ovary. The emasculated flower bud was bagged and labelled properly.

Pollination

On the subsequent morning between 8.00 AM and 11.00 AM fully opened flowers ready for anthesis were selected from healthy male parents. The ripen anthers of one male flower were dusted sufficiently on 3-4 emasculated stigmas of female parents. A coloured thread was tied for marking of crossing. The pollinated bud was bagged again.

Harvesting

The fully opened crossed bolls were picked and stored in paper bags and labelled properly. The harvested bolls were Sun dried properly; seed was separated and stored in seed covers.

Seed Treatment

The fuzz seed of crossed bolls was subjected to seed treatment with sulphuric acid, washed with sufficient water and the delinted seed was shade dried properly. The delinted seed was treated with Imidacloprid and shade dried. Then the seed was collected in seed covers and used for further study of combining ability and stability over three locations.

3.3 EXPERIMENT-III

The experimental material for identification of favourable alleles consisted of two lines, NDLH 1938 and MCU 5 parents of target cross (NDLH 1938 $\times$ MCU 5) and six testers viz., GSB 40, DB 16, DB 11, GSB 41, TCB 37 and SUVIN. These eight parents mated in line $\times$ tester fashion to get 12 F_1 s during off season (2014-15). The parents and crosses were evaluated at three locations *i.e.*, RARS, Lam Farm; ARS, J M Puram and Agricultural College Farm, Bapatla during *kharif*, 2014-15. The list of genotypes used for the study is presented in the Table 3.7. The detailed experimental techniques followed in the present investigation are furnished in Table 3.8. Data was collected on 2.5% span length (mm) and bundle strength (g/tex).

Table 3.4. List of hybrids along with the parents

S.No.	Lines	S.No.	Testers
1	NDLD 1938	1	GSB 40
2	H 1442	2	DB 16
3	ADB 542	3	DB 11
4	ADB 532	4	GSB 41
5	WGCV 48	5	TCB 37
6	MR 786	6	SUVIN
7	TSH 0250		
8	BS 37		
9	SCS 793		
10	MCU 5		
11	L 1058		
12	L 762		
Crosses			
1	NDLH 1938 × GSB 40	37	TSH 0250 × GSB 40
2	NDLH 1938 × DB 16	38	TSH 0250 × DB 16
3	NDLH 1938 × DB 11	39	TSH 0250 × DB 11
4	NDLH 1938 × GSB 41	40	TSH 0250 × GSB 41
5	NDLH 1938 × TCB 37	41	TSH 0250 × TCB 37
6	NDLH 1938 × SUVIN	42	TSH 0250 × SUVIN
7	H 1442 × GSB 40	43	BS 37 × GSB 40
8	H 1442 × DB 16	44	BS 37 × DB 16
9	H 1442 × DB 11	45	BS 37 × DB 11
10	H 1442 × GSB 41	46	BS 37 × GSB 41
11	H 1442 × TCB 37	47	BS 37 × TCB 37
12	H 1442 × SUVIN	48	BS 37 × SUVIN
13	ADB 542 × GSB 40	49	SCS 793 × GSB 40
14	ADB 542 × DB 16	50	SCS 793 × DB 16
15	ADB 542 × DB 11	51	SCS 793 × DB 11
16	ADB 542 × GSB 41	52	SCS 793 × GSB 41
17	ADB 542 × TCB 37	53	SCS 793 × TCB 37
18	ADB 542 × SUVIN	54	SCS 793 × SUVIN
19	ADB 532 × GSB 40	55	MCU 5 × GSB 40
20	ADB 532 × DB 16	56	MCU 5 × DB 16
21	ADB 532 × DB 11	57	MCU 5 × DB 11
22	ADB 532 × GSB 41	58	MCU 5 × GSB 41
23	ADB 532 × TCB 37	59	MCU 5 × TCB 37
24	ADB 532 × SUVIN	60	MCU 5 × SUVIN
25	WGCV 48 × GSB 40	61	L 1058 × GSB 40
26	WGCV 48 × DB 16	62	L 1058 × DB 16
27	WGCV 48 × DB 11	63	L 1058 × DB 11
28	WGCV 48 × GSB 41	64	L 1058 × GSB 41
29	WGCV 48 × TCB 37	65	L 1058 × TCB 37
30	WGCV 48 × SUVIN	66	L 1058 × SUVIN
31	MR 786 × GSB 40	67	L 762 × GSB 40
32	MR 786 × DB 16	68	L 762 × DB 16
33	MR 786 × DB 11	69	L 762 × DB 11
34	MR 786 × GSB 41	70	L 762 × GSB 41
35	MR 786 × TCB 37	71	L 762 × TCB 37
36	MR 786 × SUVIN	72	L 762 × SUVIN
standard checks			
1	DCH 32		
2	Mahalakshmi (ZCHB-550)		

Table 3.5. Details of crossing programme during off season, 2014

Location	:	RARS, Lam Farm, Guntur
Season	:	Off season crossing of parents (Jan - June, 2014)
No. of lines	:	12
No. of testers	:	6
No. of rows/ parent	:	10
No. of plants /row	:	10
Row length	:	6 m
Spacing	:	120 cm × 60 cm
Plot size	:	12 m × 6 m
Fertilizers	:	120 N: 60 P ₂ O ₅ : 60 K ₂ O kg/ha
Plant protection		
Seed treatment	:	Imidacloprid 70 WS @ 5 g/kg followed by Carbendazim 50 WP @ 2 g / kg
Stem application	:	At 30 & 45 DAS with monocrotophos (1:4)
Leafhoppers / aphids / thrips	:	Monocrotophos 36 SL @ 1.6 ml/l or Acephate 75 SP @1.5g/l or Acetamiprid 20 SP @ 0.2 g/l
Whitefly	:	Triazophos 40 EC @ 2.0 ml/l or Profenophos 50 EC @ 2.0 ml/l or NSKE @ 5%
Bacterial blight	:	Copper oxy chloride 3.0 g/l + streptocycline 100 mg/l
Leaf spots	:	Carbendazim @2.0g or mancozeb @3.0 g/l
Fusarium / Verticillium wilts	:	Soil drenching with copper oxy chloride @3.0 g/l
Boll worms	:	Chlorantraniliprole 18.5% SC @0.3 ml/ lt

Table 3.6. Experimental details of stability analysis in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) over three locations during *kharif*, 2014-15

Locations	: RARS, Lam Farm, Guntur ARS, Jangamaheswarapuram Agricultural College Farm, Bapatla
Season	: <i>Kharif</i> , 2014-15
Design	: Randomized Complete Block Design
Genotypes	: 92 (18 parents + 72 hybrids + 2 standard checks)
Replications	: 3
No. of rows/ genotype	: 3
No. of plants /row	: 10
Row length	: 6 m
Spacing	: Parents: 105 cm × 60 cm Hybrids: 120 cm × 60 cm
Plot size	: Parents: 3.15 m × 6 m Hybrids: 3.6 m × 6 m
Fertilizers	: 120 N: 60 P ₂ O ₅ : 60 K ₂ O kg/ha
Plant protection	
Seed treatment	: Imidacloprid 70 WS @ 5 g/kg followed by Carbendazim 50 WP @ 2 g / kg
Stem application	: At 30 & 45 DAS with monocrotophos (1:4)
Leafhoppers / aphids / thrips	: Monocrotophos 36 SL @ 1.6 ml/l or Acephate 75 SP @ 1.5g/l or Acetamiprid 20 SP @ 0.2 g/l
Whitefly	: Triazophos 40 EC @ 2.0 ml/l or Profenophos 50 EC @ 2.0 ml/l or NSKE @ 5%
Bacterial blight	: Copper oxy chloride 3.0 g/l + streptocycline 100 mg/l
Leaf spots	: Carbendazim @ 2.0g or mancozeb @ 3.0 g/l
Fusarium / Verticillium wilts	: Soil drenching with copper oxy chloride @3.0 g/l
Boll worms	: Chlorantraniliprole 18.5% SC @ 0.3 ml/ lt

Table 3.7. Experimental material used in identification of favourable alleles in donor parents analysis

S.No.	Genotype	S.No.	Genotype
TARGET CROSS			
1	NDLH 1938 × MCU 5		
	LINES		TESTERS
1	NDLH 1938	1	GSB 40
2	MCU 5	2	DB 16
		3	DB 11
		4	GSB 41
		5	TCB 37
		6	SUVIN
CROSSES			
1	NDLH 1938 × GSB 40	7	MCU 5 × GSB 40
2	NDLH 1938 × DB 16	8	MCU 5 × DB 16
3	NDLH 1938 × DB 11	9	MCU 5 × DB 11
4	NDLH 1938 × GSB 41	10	MCU 5 × GSB 41
5	NDLH 1938 × TCB 37	11	MCU 5 × TCB 37
6	NDLH 1938 × SUVIN	12	MCU 5 × SUVIN

Table 3.8. Experimental details of identification of favourable alleles in donor parents analysis during *kharif*, 2014-15

Locations	: RARS, Lam Farm, Guntur ARS, Jangamaheswarapuram Agricultural College Farm, Bapatla
Season	: <i>Kharif</i> , 2014-15
Design	: Randomized Complete Block Design
Genotypes	: 21 (8 parents + 12 hybrids + 1 target cross)
Replications	: 3
No. of rows/genotype	: 3
No. of plants /row	: 10
Spacing	: Parents: 105 cm × 60 cm Hybrids: 120 cm × 60 cm
Plot size	: Parents: 3.15 m × 6 m Hybrids: 3.6 m × 6 m
Fertilizers	: 120 N: 60 P ₂ O ₅ : 60 K ₂ O kg/ha
Plant protection	
Seed treatment	: Imidacloprid 70 WS @ 5 g/kg followed by Carbendazim 50 WP @ 2 g / kg
Stem application	: At 30 & 45 DAS with monocrotophos (1:4)
Leafhoppers / aphids / thrips	: Monocrotophos 36 SL @ 1.6 ml/l or Acephate 75 SP @ 1.5g/l or Acetamiprid 20 SP @ 0.2 g/l
Whitefly	: Triazophos 40 EC @ 2.0 ml/l or Profenophos 50 EC @ 2.0 ml/l or NSKE @ 5%
Bacterial blight	: Copper oxy chloride 3.0 g/l + streptocycline 100 mg/l
Leaf spots	: Carbendazim @ 2.0g or mancozeb @ 3.0 g/l
Fusarium / Verticillium wilts	: Soil drenching with copper oxy chloride @3.0 g/l
Boll worms	: Chlorantraniliprole 18.5% SC @ 0.3 ml/ lt

3.4 RECORDING OBSERVATIONS

Five plants of each genotype in each replication were selected at random and labelled for recording observations. The mean of the five plants was subjected to statistical analysis. For estimating fibre quality parameters a composite sample of 300 g of kapas were obtained from each entry from each replication and ginned for seed and lint. The cleaned lint sample was used for estimating the fibre properties. The data on the following seed cotton yield, yield components and quality parameters were recorded.

3.4.1 Days to 50% Flowering

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

3.4.2 Plant Height (cm)

Plant height was measured from the base of the plant to apex of the plant at maturity for all the selected plants. The average of these measurements was then calculated and expressed in centimeters (cm).

3.4.3 Number of Monopodia Plant⁻¹

The total number of vegetative branches on the main stem were counted and recorded at the time of harvest for each selected plant.

3.4.4 Number of Sympodia Plant⁻¹

The total number of fruiting branches present in the plant at maturity was counted.

3.4.5 Number of Bolls Plant⁻¹

The total number of fully opened bolls per plant from all the pickings was counted by maintaining records for each selected plant. The average number of bolls per plant was then calculated for each genotype.

3.4.6 Boll Weight (g)

Seed cotton obtained from a random sample of 25 bolls per plant was used to determine boll weight.

3.4.7 Lint index (g)

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

3.4.8 Seed index (g)

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

3.4.9 Ginning out-turn (%)

A random sample of 300 g seed cotton from each entry was ginned and the lint obtained was utilized for working out the ginning out-turn in the following manner.

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

3.4.10 2.5% span length (mm)

2.5% span length is the distance from the clamp on a fibre board to a point up to which only 2.5% of the fibres extends. It is expressed as span length in mm and was estimated by using HVT Expert 1201 high volume fibre tester instrument.

3.4.11 Uniformity ratio

The ratio between two span lengths (2.5% and 50%) expressed as a percentage of the longer length and was determined by using HVT Expert 1201 high volume fibre tester instrument.

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

Micronaire value is a physical property indicating the cross-sectional thickness of fibre, which determines the spinning value of a variety. The fibre fineness was estimated by using HVT Expert 1201 high volume fibre tester instrument.

3.4.13 Bundle strength (g/tex)

Bundle strength is a measure of the tensile strength of the fibre using the principle of constant rate of loading. This was measured by using HVT Expert 1201 high volume fibre tester instrument.

3.4.14 Fibre elongation (%)

It is fibre extensibility measured with the help of HVT Expert 1201 high volume fibre tester instrument.

3.4.15 Seed cotton yield Plant⁻¹ (g)

Total weight of seed cotton obtained from five plants were recorded and averaged.

3.4.16 Lint yield Plant⁻¹ (g)

Total weight of lint obtained from five plants was recorded and averaged.

3.5 STATISTICAL ANALYSIS

The data recorded on various characters were subjected to following statistical analysis by using Windostat Version 9.2 software.

3.5.1 Analysis of Variance

The data for different characters was statistically analyzed on the basis of the model given by Cochran and Cox (1950) for Randomized Complete Block Design.

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

Where,

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

μ = General mean

b_i = Effect of i^{th} block

t_j = Effect of j^{th} genotype

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

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

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

Where,

r	=	Number of replications
t	=	Number of genotypes
d.f	=	Degrees of freedom
SS	=	Sum of squares
MSS	=	Mean sum of squares
σ^2_e	=	Error variance
σ^2_g	=	Variance due to genotypes
σ^2_r	=	Variance due to replications
Mr	=	Mean sum of squares due to replications
Mt	=	Mean sum of squares due to treatments
Me	=	Mean sum of squares due to error

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

3.5.2 Estimation of Genetic Parameters

3.5.2.1 Co-efficient of variation

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

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

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

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

Low	=	Less than 10 per cent
Moderate	=	10-20 per cent
High	=	More than 20 per cent

3.5.2.2 Heritability in broad sense ($\hat{h}_{(bs)}^2$)

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

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

As suggested by Johnson *et al.* (1955), $\hat{h}_{(bs)}^2$ estimates were categorized into

Low	=	0-30 per cent
Moderate	=	31-60 per cent
High	=	60 per cent and above

3.5.2.3 Genetic advance (GA)

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

$$GA = k \times \sigma_p \times \hat{h}_{(bs)}^2$$

Where,

K	=	Selection differential at 5% selection intensity which accounts to a constant value of 2.06
$\hat{h}_{(b)}^2$	=	Heritability in broad sense
σ_p	=	Phenotypic standard deviation

3.5.2.4 Genetic advance as per cent of mean (GAM)

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

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

Low	=	Less than 10 per cent
Moderate	=	10-20 per cent
High	=	More than 20 per cent

3.5.3 Correlation Analysis

3.5.3.1 Analysis of co-variance

Analysis of co-variance was computed by following procedure.

$$Y_{ij} = M + t_i + b_j + b_{yx}(X_{ij} - X_{\dots}) + e_{ij}$$

Where,

- Y_{ij} = Performance of i^{th} genotype in the j^{th} replication
- M = General mean
- t_i = True effect of i^{th} treatment
- b_j = True effect of j^{th} block
- b_{yx} = Regression co-efficient of y on x
- X_{ij} = Concomitant variable on i^{th} genotype in j^{th} replication
- $X_{\dots}$ = Mean of concomitant variable based on its units
- e_{ij} = Random error

The structure of analysis of co-variance is as follows.

Source of variation	d.f	SSY	SSX	SPXY	MSSY	MSSX	MSPXY
Replications	(r-1)	RY	RX	RXY	ry	Rx	rx
Genotypes	(t-1)	TY	TX	TXY	ty	Tx	txy
Error	(r-1)(t-1)	EY	EX	EXY	ey	Ex	exy

Where,

- d.f = Degrees of freedom
- SS = Sum of squares
- SP = Sum of products
- MSS = Mean sum of squares
- MSP = Mean sum of products
- r = Number of replications
- t = Number of genotypes

3.5.3.1.1 Genotypic co-variance ($x_i.x_j$) $g = (MSPr - MSPe) / r$

$(x_i.x_j) g$ = Genotypic co-variance between i^{th} and j^{th} characters

MSPr = Mean sum of products of genotypes

MSPe = Error mean sum of products

3.5.3.1.2 Phenotypic co-variance ($x_i.x_j$) $p = (x_i.x_j) g + e_i e_j$

$(x_i.x_j) p$ = Phenotypic co-variance between i^{th} and j^{th} characters

$(x_i.x_j) g$ = Genotypic co-variance between i^{th} and j^{th} characters

$e_i e_j$ = Environmental co-variance between i^{th} and j^{th} characters

3.5.3.2 Analysis of co-efficient of correlation

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

3.5.3.2.1 Genotypic co-efficient of correlation (r_g)

$$r(X_i.X_j)g = \frac{\text{Cov}(X_i.X_j)g}{\sqrt{v(X_i)g.v(X_j)g}}$$

Where,

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

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

$v(X_i)g$ = Genotypic variance of i^{th} character

$v(X_j)g$ = Genotypic variance of j^{th} character

3.5.3.2.2 Phenotypic co-efficient of correlation (r_p)

$$r(X_i.X_j)p = \frac{\text{Cov}(X_i.X_j)p}{\sqrt{v(X_i)p.v(X_j)p}}$$

Where,

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

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

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

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

3.5.3.3 Test of significance

Significance of correlation co-efficient was tested by comparing phenotypic correlation co-efficient with the table values (Fisher and Yates, 1963) at (n-2) degrees of freedom at 5% and 1% level where 'n' denotes the number of paired observations used in the calculation where genotypic correlation co-efficient was tested for significance using 'Z' transformation.

3.5.4 Path co-efficient Analysis

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

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

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

Where,

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

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

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

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

$$\begin{pmatrix} A \\ r_{1y} \\ r_{2y} \\ \vdots \\ \vdots \\ r_{iy} \end{pmatrix} = \begin{pmatrix} C \\ 1 & r_{12} & r_{1i} \\ r_{21} & 1 & r_{2i} \\ \vdots & \vdots & \vdots \\ r_{i1} & r_{i2} & 1 \end{pmatrix} \begin{pmatrix} B \\ P_{1y} \\ P_{2y} \\ \vdots \\ \vdots \\ P_{iy} \end{pmatrix}$$

$$\text{then, } B = [C]^{-1} A$$

Where,

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

The direct effects were calculated as follows

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

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

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

3.5.4.1 Residual effect

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

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

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

3.5.5 Genetic Divergence

3.5.5.1 Mahalanobis' D^2 analysis

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

3.5.5.1.1 Test of significance

Variances were calculated for all the characters investigated and test of significance was done. Analysis of co-variance for the character pairs was estimated on the basis of mean values (Panse and Sukhatme, 1978). After testing the difference between genotypes for each of the characters, a simultaneous test of significance for

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

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

Where,

- $\hat{\Lambda}$ = Wilk’s criterion
 $|E|$ = Determinant of error matrix
 $|E+V|$ = Determinant of error + variety matrix

$$V_{(Stat)} = -m \log_e \hat{\Lambda} = -\left(n - \frac{p+q+1}{2}\right) \log_e \hat{\Lambda}$$

Where,

- m = $n - (p+q+1)/2 = 2.3026 \log_{10} \hat{\Lambda}$
 p = Number of variables (or) characters (16)
 q = Degrees of freedom for varieties (number of varieties –1)
 n = Degrees of freedom for error + varieties

$V_{(stat)}$ is distributed as χ^2 with pq (1104 and 304) degrees of freedom for *hirsutum* and *barbadense* genotypes, respectively.

Transformation of correlated variables

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

3.5.5.1.2 Computation of D^2 values

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

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

Where,

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

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

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

3.5.5.1.3 Testing the significance of D^2 values

The D^2 value obtained for a pair of population is taken as calculated value of χ^2 and is tested against the tabulated value of χ^2 for p degrees of freedom where p is the number of characters considered i.e., 16 in the present study which is equal to 7.962.

3.5.5.1.4 Contribution of individual characters towards divergence

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

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

Where,

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

M = All possible combinations of number of genotypes considered i.e., 2415 and 190 for *hirsutum* and *barbadense* genotypes, respectively in the present study

3.5.5.1.5 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.

3.5.5.1.6 Average intra- cluster distance

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

3.5.5.1.7 Average inter-cluster distance

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

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

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

Where,

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

n_1 and n_2 = Number of genotypes of two clusters

3.5.5.2 Principal component analysis and cluster analysis

Principal Component Analysis (PCA) was carried out according to the 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).

3.5.5.2.1 Eigen values and eigen vectors

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

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

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

The principal components were identified by following procedure.

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

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

Where,

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

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

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

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

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

Where, S_i is the standard deviation of X_i .

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

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

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

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

3.5.6 Combining Ability Analysis

Estimates of combining ability variances and effects were obtained using line $\times$ tester method suggested by Kempthorne (1957) and detailed by Singh and Chaudhary (1985). The mathematical model is given below

$$Y_{ijk} = \mu + g_i + g_j + s_{ij} + r_k + e_{ijk}$$

Where,

Y_{ijk} = Any measurable character of the cross $i \times j$ in the k^{th} replication

μ = Population mean effect

g_i = General combining ability effect of line or female parent

g_j = General combining ability effect of tester or male parent

s_{ij} = Specific combining ability effect of $i \times j^{\text{th}}$ cross

r_k = Effect due to k^{th} replication

e_{ijk} = Environmental effect on ijk^{th} individual

Table 3.9. Analysis of variance (ANOVA) for combining ability

Source of variation	d.f	Mean sum of squares	F test
Replications	r-1	M_r	M_r / M_e
Genotypes	(g-1)	M_g	M_g / M_e
Parents	(p-1)	M_p	M_p / M_e
Parents vs crosses	1	M_{pc}	M_{pc} / M_e
Crosses	(c-1)	M_c	M_c / M_e
Lines	(l-1)	M_l	M_l / M_{lt}
Testers	(t-1)	M_t	M_t / M_{lt}
Lines $\times$ testers	(l-1) (t-1)	M_{lt}	M_{lt} / M_e
Error	(r-1) (g-1)	M_e	

Where,

r = Number of replications

g = Number of genotypes

p = Number of parents

c = Number of crosses

l = Number of females

t = Number of males

M_r = Replication mean sum of squares

M_g = Genotype mean sum of squares

M_p = Parents mean sum of squares

M_c = Crosses mean sum of squares

M_{pc} = Mean sum squares due to parents and crosses

M_l = Mean sum of squares due to lines

M_t = Mean sum of squares due to testers

M_{lt} = Mean sum of squares due to lines $\times$ testers

M_e = Mean sum of squares due to error

d.f = Degrees of freedom

The significant differences between the variances of genotypes, replications, parents, crosses, lines, testers, parents vs crosses, lines × testers was tested by applying the F test of Fisher and Yates (1963).

The *gca* and *sca* effects were estimated as follows:

gca effects of lines

$$g_i = \frac{x_{i..}}{tr} - \frac{x_{...}}{ltr}$$

Where,

- $x_{i..}$ = Total of i^{th} line over all testers and replications
- x = Mean of lines, testers and replications
- i = Number of lines
- t = Number of testers
- r = Number of replications

While, the *gca* effects of testers were estimated as follows

$$g_j = \frac{x_{j.}}{lr} - \frac{x_{...}}{ltr}$$

Where, $x_{j.}$ = total of j^{th} tester over lines and replications

$$s_{ij} = \frac{x_{ij.}}{r} - \frac{x_{i.}}{tr} - \frac{x_{j.}}{lr} + \frac{x_{...}}{ltr}$$

Where,

$x_{ij.}$ = total of ij^{th} combination over replications

The standard errors (SE) pertaining to *gca* effects of lines and testers and *sca* effects of combinations were calculated as shown below:

$$SE (g_i) \text{ (gca for female)} = \sqrt{\frac{M_e}{r \times t}}$$

$$SE (g_j) \text{ (gca for males)} = \sqrt{\frac{M_e}{(r \times l)}}$$

$$SE (s_{ij}) \text{ (sca effects)} = \sqrt{\frac{M_e}{r}}$$

$$SE (g_i - g_j) \text{ female} = \sqrt{\frac{2 M_e}{r \times t}}$$

$$SE (g_i - g_j) \text{ male} = \sqrt{\frac{2 M_e}{r \times l}}$$

$$SE (s_{ij} - s_{kl}) = \sqrt{\frac{2 M_e}{r}}$$

The covariance of half sibs (H.S) and full sibs (F.S.) was used to obtain the estimates of general and specific combining ability and their variances.

$$\text{Cov H.S. (female)} = \frac{M_l - M_{lt}}{r \times t}$$

$$\text{Cov H.S. (male)} = \frac{M_t - M_{lt}}{r \times l}$$

$$\text{Cov H.S. (average)} = \frac{1}{r(2l + 2t - 1)} \left[\frac{(l-1)(M_l) + (t-1)(M_t)}{1 + (t-2)} - M_{lt} \right]$$

Covariance of (F.S.) =

$$\frac{(M_l - M_e) + (M_t - M_e) + (M_{lt} - M_e)}{3r} + \frac{6r \text{Cov HS} - r(1+t)\text{Cov. (H.S)}}{3r}$$

The *gca* and *sca* variances were obtained as follows:

$$\sigma^2 gca = \text{Cov. H.S. (average)}$$

$$\sigma^2 sca = \frac{M_{lt} - M_e}{r}$$

gca to *sca* ratio was calculated to know the type of gene action involved i.e., additive or non-additive. The *gca* and *sca* effects were tested against zero for significance by calculating t-value, by using the following formulae

$$t - cal = \frac{|g_i - 0|}{SE(g_i)}; t - cal. = \frac{|g_j - 0|}{SE(g_j)}; t - cal. = \frac{|s_{ij} - 0|}{SE(s_{ij})};$$

t- calculated value is compared with t-table value at error degrees of freedom.

Proportional contribution of lines, testers and their interactions

$$\text{Contribution of lines} = \frac{\text{SS (l)} \times 100}{\text{SS (crosses)}}$$

$$\text{Contribution of testers} = \frac{\text{SS (t)} \times 100}{\text{SS (crosses)}}$$

$$\text{Contribution of l} \times \text{t} = \frac{\text{SS (l} \times \text{t)} \times 100}{\text{SS (crosses)}}$$

(Where, SS is sum of squares)

3.5.7 Estimation of Heterosis

The heterotic effects were measured as deviation of F_1 mean from mid parent (relative heterosis), better parent (heterobeltiosis) and the standard check (standard heterosis) mean.

The per cent of heterosis was calculated as follows:

$$\text{Relative heterosis} = \frac{\overline{F_1} - \overline{MP}}{\overline{MP}} \times 100$$

Where,

$$\overline{MP} = \frac{\overline{P_1} + \overline{P_2}}{2}$$

$$\text{Heterobeltiosis} = \frac{\overline{F_1} - \overline{BP}}{\overline{BP}} \times 100$$

Where,

$\overline{F_1}$ = Mean value of F_1

$\overline{MP}$ = Mean value of mid parent

$\overline{BP}$ = Mean value of better parent

$\overline{P_1}$ = Mean of first parent

$\overline{P_2}$ = Mean of second parent

$$\text{Standard heterosis} = \frac{\overline{F_1} - \overline{SC}}{\overline{SC}} \times 100$$

Where,

$\bar{F}_1$ = Mean value of F_1

$\bar{SC}$ = Mean value of standard check

3.5.7.1 Test of significance of heterosis

The test of significance of heterosis over mid parent, better parent and standard check was done by 't' test as suggested by Snedecor and Cochran (1967) as follows.

$$\text{Heterosis 't'} = \frac{\text{Mean of } F_1 - \text{Mean of mid parent (or) better parent (or) standard check}}{\sqrt{\frac{2EMS}{f}}}$$

The estimated 't' value was compared with 't' value at error degrees of freedom.

3.5.8 Stability Analysis

Analysis of variance of genotype means was computed for each agronomic variable in each location. The data were pooled over environments as the co-efficient of variation values in each environment were generally low, though the Bartlett's chi-square values showed significance in case of certain characters (Gomez and Gomez, 1984).

Bartlett's test of homogeneity (Bartlett, 1937) as quoted by Panse and Sukhatme (1978).

$$S_p^2 = \sum_{I=1}^k S_i^2$$

$$\chi^2 = \frac{(2.3026)f \left[k \log S_p^2 - \sum_{I=1}^k \log S_i^2 \right]}{1 + [(k+1)/3kf]}$$

Where,

k = Number of environments

S_i^2 = Error mean squares of locations or environments

If calculated χ^2 value is non-significant, the experimental errors of trials may be regarded as being homogeneous.

3.5.8.1 Eberhart and Russell's (1966) model

Stability parameters were computed as given by Eberhart and Russell (1966). The model is

$$Y_{ij} = \mu + \beta_i I_j + S_{ij}$$

i varies from 1 to 72 genotypes (72 hybrids)

j varies from 1 to 3 environments

Where,

Y_{ij} = Mean of i^{th} genotype in j^{th} environment

μ = Mean of all the genotypes over all the environments

β_i = Regression co-efficient of i^{th} genotype on the environmental index which measures the response of this genotype to varying environments

I_j = The environmental index which is defined as the deviation of the mean of all the genotypes at a given location from the overall mean

S_{ij} = The deviation from regression of the i^{th} genotype at j^{th} environment

3.5.8.1.1 Analysis of variance for stability

The analysis of variance as proposed by Eberhart and Russell (1966) is given in Table 3.10.

Table 3.10. Analysis of variance as proposed by Eberhart and Russell (1966)

Source of variation	Degrees of freedom	Sum of squares	Mean squares
Total	(ge-1)	$\sum_i \sum_j Y_{ij}^2 - C.F$	
Genotypes	(g-1)	$1/e \sum_i Y_{i.}^2 - C.F$	MS ₁
Environment+ (Genotype × Environment)	g(e-1)	$\sum_i \sum_j Y_{ij}^2 - \sum_i Y_{i.}^2 / e$	
Environment (linear)	1	$1 / g \left(\sum_j Y_{.j} \cdot I_j \right)^2 \bigg/ \sum_j I_j^2$	
Genotype × Environment (linear)	(g-1)	$\sum_j \left(\left(\sum_i Y_{ij} I_j \right)^2 \bigg/ \sum_i I_j^2 \right) - \text{Environment (linear) SS}$	MS ₂

Table 3.10 (cont.)

Pooled deviations	g(e-2)	$\sum_i \sum_j S_{ij}^2$	MS ₃
Deviation due to genotype 1	(e-2)	$\left[\sum_j Y_{ij}^2 - \left(Y_{i.} \right)^2 / e \right]$ $- \left(\sum_j Y_{ij}^2 I_j \right)^2 / \sum_j I_j^2$ $= \sum_j S_{ij}^2$	
Pooled error	e(g-1) (r-1)		

Where,

g = Genotype e = Environment r = Replication

3.5.8.1.2 Estimation of stability parameters

The regression co-efficient (b) and the deviation from the line of regression (S²d) were estimated as follows.

3.5.8.1.2.1 Regression co-efficient

$$b = \sum_j Y_{ij} I_j / \sum_j I_j^2$$

Where,

$\sum_j Y_{ij} I_j$ = The sum of products of environmental index (I_j) with corresponding mean of that genotype at each environment (Y_{ij})

$\sum_j I_j^2$ = The sum of squares of the environmental index (I_j)

3.5.8.1.2.2 Mean square deviations (S²d) from linear regression

$$S^2d = \frac{\sum_j S_{ij}^2}{(e-2)} - \frac{S_e^2}{r}$$

Where,

$$\sum_j S_{ij}^2 = \left[\sum_j Y_{ij}^2 - \frac{Y_{i.}^2}{g} \right] - \frac{\left(\sum_j Y_{ij} I_j \right)^2}{\sum_j I_j^2}$$

Where,

$$\sum_j S_{ij}^2 = \text{Variance due to deviation from regression for a genotype}$$

$$\sum_j Y_{ij}^2 - \frac{Y_{i.}^2}{g} = \text{Variance due to dependent variable}$$

$$\sum_j (Y_{ij} I_j)^2 / \sum_j I_j^2 = \text{Variance due to regression}$$

$$S_e^2 = \text{The estimate of pooled error}$$

e = Number of environments

g = Number of genotypes

r = Number of replications

The various computational steps involved in the estimation are as follows:

3.5.8.1.3 Computation of environmental index (I_j)

$$I_j = \frac{\sum_i Y_{ij}}{g} - \frac{\sum_i \sum_j Y_{ij}}{ge}$$

$$\text{With } \sum_j I_j = 0$$

3.5.8.1.4 Computation of regression co-efficient (b) for each genotype

$$b = \frac{\sum_j Y_{ij} I_j}{\sum_j I_j^2}$$

- For each value of regression co-efficient, $\sum_j I_j^2$ is common.
- $\sum_j Y_{ij} I_j$ for each genotype is the sum of products of environmental index (I_j) with the corresponding mean ($\bar{X}$) of that genotype in each environment.

These values may be obtained in the following manner

$$[\bar{X}][I_j] = \left[\sum_j Y_{ij} I_j \right] = [S]$$

Where

$\left[\overline{X}\right]$ = Matrix of means

$\left[I_j\right]$ = Vector for environmental index

$\left[S\right]$ = Vector for sum of products, i.e., $\sum_j Y_{ij} I_j$

3.5.8.1.5 Computation of S^2_d

In a regression analysis, it is possible to partition the variance of the dependent variable (Y) into two parts, the one which explains the linearity between dependent and independent variables (variance due to regression) and the other which explains the variance due to deviations from linearity.

$$\sigma_y^2 = \sigma^2_{\text{regression}} + \sigma^2_{\text{deviation from the regression}}$$

The variance of mean over different locations with regard to individual genotype may be obtained in the following way.

$$\sigma_{g_i}^2 = \sum_j Y_{ij}^2 - (Y_{i.}^2 / g)$$

The variance due to deviations from regression $\left(\sum_j S_{ij}^2\right)$ for a genotype being

$$\sum_j S_{ij}^2 = \left[\sum_j Y_{ij}^2 - \frac{Y_{i.}^2}{g} \right] - \frac{\left(\sum_j Y_{ij} I_j \right)^2}{\sum_j I_j^2}$$

Where,

$$\sum_j Y_{ij}^2 - \frac{Y_{i.}^2}{g} = \text{Variance due to dependent variable and}$$

$$(\sum_j Y_{ij} I_j)^2 / \sum_j I_j^2 = \text{The variance due to regression}$$

because

$$\frac{\left(\sum_j Y_{ij} I_j \right)^2}{\sum_j I_j^2} = \frac{\left(\sum_j Y_{ij} I_j \right) \left(\sum_j Y_{ij} I_j \right)}{\sum_j I_j^2} = b \sum_j Y_{ij} I_j$$

From $\sum_j S_{ij}^2$ values, the stability parameter S^2_d for each variety is computed as follows

$$S^2_d = \left[\sum_j S_{ij}^2 / (e-2) \right] - (S_e^2 / r)$$

$$\text{Mean square} = \frac{\text{Deviation from regression}}{\text{Degrees of freedom for environment}} = \frac{\text{Pooled error}}{\text{Number of replications}}$$

The variance due to genotypes, environments and the pooled error were the same as those calculated in the pooled analysis of data, except that the total sum of squares was mainly partitioned into 3 main components namely (1) sum of squares due to genotypes (2) sum of squares due to environments + (genotype $\times$ environment) and (3) pooled error. Again sum of squares due to genotype $\times$ environment was further partitioned into 2 parts namely (a) sum of squares due to genotype $\times$ environment (linear) which is in fact sum of squares due to regression and (b) sum of squares due to deviations from linearity of response (*i.e.*, sum of squares due to deviation).

Sum of squares due to environment + (Genotype $\times$ environment)

$$= \sum_i \sum_j Y_{ij}^2 - \left(\sum_j Y_{i.}^2 / e \right)$$

Sum of squares due to environment (linear)

$$= \frac{1}{g} \left(\sum_j Y_{.j} I_j \right)^2 / \left(\sum_j I_j^2 \right)$$

Sum of squares due to genotype $\times$ environment (linear)

$$= \sum_j \left[\left(\sum_i Y_{ij} I_j \right)^2 / \left(\sum_j I_j^2 \right) \right] - \text{SS environment (linear)}$$

Where,

$$\left(\sum_j Y_{ij} I_j \right)^2 / \left(\sum_j I_j^2 \right) = b \sum_j Y_{ij} I_j \text{ for each genotype}$$

3.5.8.1.6 Test of significance

The following tests of significance were carried out:

1. To test the significance of the differences among genotype means namely

$$H_o = \mu_1 = \mu_2 = \mu_3 = \dots \mu_{10}$$

the 'F' test used was

$$F = \frac{\text{Mean square due to genotypes}}{\text{Mean square due to pooled deviation}} = \frac{MS_1}{MS_3}$$

2. To test that the genotypes did not differ due to regression on environmental index, *i.e.*, $H_o = b_1 = b_2 = \dots b_{10}$,

the 'F' test used was

$$F = \frac{\text{Mean square due to genotype} \times \text{environment (linear)}}{\text{Mean square due to pooled deviation}} = \frac{MS_2}{MS_3}$$

3. Individual deviation from linear regression was tested as follows

$$F = \left[\left(\sum_j S_{ij}^2 \right) / (e - 2) \right] / \text{pooled error mean sum of squares}$$

t-value at (g-2) d.f at P=0.05 and 0.01 levels.

4. The hypothesis that any regression co-efficient does not differ from unity or from zero was tested by the appropriate 't' test, *i.e.*,

$$t = \frac{|1 - b|}{SE(b)} \quad SE(b) = \sqrt{\left[\sum_j S_{ij}^2 / (e - 2) \right] / \sum_j I_j^2}$$

t -value at (g-2) d.f at p = 0.05 and 0.01 levels

3.5.8.2 Additive Main effects and Multiplicative Interaction (AMMI) model (Gauch, 1988)

AMMI model is a useful technique to capture non-linear interaction, when traditional stability modeling techniques fail to perceive important effects in studies of G × E interaction. Even a single Principal Component Analysis (PCA) axis can capture much large amount of G × E interaction when compared to the variation captured by the linear component of the traditional stability models. Due to the above salient features, for the present study, AMMI modeling methodology is employed for the identification of elite genotypes.

3.5.8.2.1 Additive model

The model of yield response of the i^{th} variety in the j^{th} environment is

$$Y_{ij} = \mu + g_i + e_j + d_{ij}$$

Where,

μ = Overall mean yield

g_i = Deviation of the mean of genotype i from μ

e_j = Deviation of environment j from μ

d_{ij} = Residual deviation not explained by the components μ , g_i and e_j

Y_{ij} = Yield response of i^{th} variety in the j^{th} environment.

d_{ij} partitioned as $d_{ij} = C_{ij} + \varepsilon_{ij}$ ----- (1)

Where,

C_{ij} = Random variable representing interaction between the n genotypes and the p environments with zero means and variance σ^2_e

ε_{ij} = Residual errors with zero mean and variance σ^2

The expectation of the variety by environments mean squares ($G \times EMS$) is a linear combination of these two parameters:

$$E(G \times EMS) = \sigma_e^2 + \sigma^2 / r$$

The percentage of structural variability in the deviations from the additive model, d_{ij} , is estimated by

$$100(G \times EMS - PEMS / r) / G \times EMS$$

3.5.8.2.2 Multiplicative interactions

In principal component analysis (PCA), the elements in a matrix D , say d_{ij} , ($D = [d_{ij}]$) are decomposed as a sum of multiplicative terms.

$$d_{ij} = \sum_{k=1}^q \lambda_k \mu_{ik} V_{jk}$$

Where,

q = Rank of the matrix D

$\lambda_1, \lambda_2, \dots, \lambda_q$ = Decreasing sequence of singular values of D.

μ_{ik} = i^{th} component of the k^{th} left singular vector of D

V_{jk} = j^{th} component of the k^{th} right singular vector of D.

The decomposition in above equation is exact and complete, so the problem of finding a partition of d_{ij} like equation - (1) is to choose a value 'm' less than 'q' such that

$$d_{ij} = \sum_{k=1}^m \lambda_k \mu_{ik} V_{jk} + \varepsilon_{ij}$$

Where the sum of products is e_{ij} of equation - (1) which should account for a large part of the structural variability in D.

The combination of all above equations has become known as the Additive Main Effects and Multiplicative Interaction model of order m (AMMI) which can be written as

$$Y_{ij} = \mu + g_i + e_j + \sum_{k=1}^m \lambda_k \mu_{ik} V_{jk} + \varepsilon_{ij}$$

Where,

Y_{ij} = Mean yield of the i^{th} genotype in the j^{th} environment

μ = Grand mean

g_i = i^{th} genotype

e_j = j^{th} environment

k = Number of PCA axes retained in the model

λ_k = Singular value for the PCA axis, k

u_{ik} = i^{th} genotype PCA score for the axis, k

v_{jk} = j^{th} environment PCA score for the axis, k

ε_{ij} = Residual

3.5.9 Methods for Identification of Favourable Alleles in the Donor Parents

3.5.9.1 Identification of favourable alleles (Dudley, 1984)

This model has not been utilized in the present investigation for analysis. However, this has been explained to elucidate the basic concept on which the modified model (Dudley, 1987b) was built upon.

3.5.9.1.1 Basic concept

For any three homozygous lines, only eight classes of loci exist viz., A to H (Table 3.13). Consider an elite single cross $P_1 \times P_2$, and a third line P_w , which might be used to improve either P_1 or P_2 for the production of a new hybrid superior to $P_1 \times P_2$. Among the eight classes of loci A and H indicates all three lines are homozygous *i.e.*, either + or – type of alleles. The most interest class is G, because for this class, P_w contains favourable alleles which are not present in either P_1 or P_2 .

Let A, B, C, D, E, F, G and H be the number of loci in their respective classes. Let the genotypic values of the three possible genotypes (++ , + – , – –) at a single locus be μ , $a\mu$ and $-\mu$, respectively (Comstock and Robinson, 1948).

Table 3.11. Genetic status of classes of loci possible for three homozygous lines

Class of loci	Line		
	P_1	P_2	P_w
A	+	+	+
B	+	+	–
C	+	–	+
D	+	–	–
E	–	+	+
F	–	+	–
G	–	–	+
H	–	–	–

where,

+ = Loci homozygous for favourable allele

– = Loci homozygous for unfavourable allele

A, B,.... H = Number of loci in their respective classes.

3.5.9.1.2 Estimation of μ_B to μ_G

Assume μ is constant for all loci, $a = 1$ (complete dominance), no epistasis and that $\mu_A = \mu_H$. Under these assumptions, the genotypic values for each line and for each of the possible F_1 's among the three lines can be written in terms of B, C, D, E, F, G and μ (Table 3.12) and which subsequently gives six equations with seven unknowns. The equation can be solved in terms of $\mu_B, \mu_C, \dots, \mu_G$ (Table 3.13).

Table 3.12. Genotypic values of inbreds and F_1 's assuming complete dominance ($a=1$) and $\mu_A - \mu_H = 0$

P_1	=	$(B + C + D - E - F - G) \mu$
P_2	=	$(B - C - D + E + F - G) \mu$
P_w	=	$(-B + C - D + E - F + G) \mu$
$P_1 \times P_2$	=	$(B + C + D + E + F - G) \mu$
$P_1 \times P_w$	=	$(B + C + D + E - F + G) \mu$
$P_2 \times P_w$	=	$(B + C - D + E + F + G) \mu$

Table 3.13. Solutions to equations in Table 3.12

μ_B	=	$[(P_2 \times P_w) + (P_1 \times P_w) + P_2 + P_1 - P_w - (P_1 \times P_2)] / 4$
μ_C	=	$[(P_2 \times P_w) + P_w \times P_1 + (P_1 + P_2) - P_2 - P_1 \times P_w] / 4$
μ_D	=	$[(P_1 \times P_w) + (P_1 \times P_2) - P_1 - P_2 - P_w - (P_2 \times P_w)] / 4$
μ_E	=	$[(P_2 \times P_w) + (P_1 \times P_2) + (P_1 + P_w) - P_1 - (P_2 \times P_w)] / 4$
μ_F	=	$[(P_1 \times P_2) + (P_2 \times P_w) - P_1 - P_2 - P_w - (P_1 \times P_w)] / 4$
μ_G	=	$[(P_2 \times P_w) + (P_1 \times P_w) - P_w - P_2 - P_1 - (P_1 \times P_2)] / 4$

3.5.9.2 Identification of favourable alleles without major assumptions

3.5.9.2.1 Basic concept

Dudley (1984), under the assumptions of complete dominance ($a=1$) μ constant for all loci, $\mu_A - \mu_H = 0$ and $z = -\mu$ obtained estimators for $\mu_B, \mu_C, \dots, \mu_G$. If $\mu_A \neq \mu_H$ and $z \neq \mu$, then the expectations of $\mu_B, \dots, \mu_G$ as estimated from expressions in Table 3.13 are as shown in Table 3.14.

Table 3.14. Expectations of estimates of $\mu_B, \dots, \mu_G$ when values of ++, +- and -- genotypes are $z + 2\mu$, $z + \mu + a\mu$ and z , respectively

$\mu_B = \mu_{B'} + \frac{\mu(A - H)}{2} + \frac{N(z + \mu)}{2}$
$\mu_C = \mu_{C'} + \frac{\mu(A - H)}{2} + \frac{N(z + \mu)}{2}$
$\mu_D = \mu_{D'} + \frac{\mu(A - H)}{2} + \frac{N(z + \mu)}{2}$
$\mu_E = \mu_{E'} + \frac{\mu(A - H)}{2} + \frac{N(z + \mu)}{2}$
$\mu_F = \mu_{F'} + \frac{\mu(A - H)}{2} + \frac{N(z + \mu)}{2}$
$\mu_G = \mu_{G'} + \frac{\mu(A - H)}{2} + \frac{N(z + \mu)}{2}$

So in order to obtain unbiased estimates of $\mu_B, \dots, \mu_G$ an estimate of $\mu(A - H)/2 + N(z + \mu)/2$ is needed. If an estimate of μ_G not containing this bias, say $\mu_{G'}$, could be obtained then $\mu_{G'} - \mu_G = \mu(A - H)/2 + N(z + \mu)/2$.

With two homozygous lines (I_1 and I_2) four classes of loci exist, which Dudley (1984, 1987a) designated as i, j, k and l (Table 3.15). If i, j, k, and l are numbers of loci then $i = A + B$, $j = C + D$, $k = E + F$, and $l = G + H$. Let p_l be the average frequency of favourable alleles in I_w at class l loci. Because of $l = G + H$ and $p_l = G/G + H$, $lp_l\mu$ is an estimate of μ_G . Dudley (1987b) describes estimators (designated $lp_l\mu$) for $lp_l\mu$ that are free of the assumption that $z = -\mu$ and $A=H$. If estimates of μ_G (e.g. $\mu_{G'}$) are obtained using the estimator $lp_l\mu$ then $\mu_{G'} - \mu_G$ where μ_G is calculated as shown in Table 3.13 is an estimate of $[N(z + \mu) + \mu(A - H)]/2$. By adding or subtracting, as appropriate (Table 3.14), this estimate from the $\mu_B, \dots, \mu_F$ values obtained from the expressions in Table 3.13, modified estimates of $\mu_B, \dots, \mu_F$ ($\mu_{B'}, \dots, \mu_{F'}$) are obtained.

Table 3.15. Genetic status of classes of loci possible for two homozygous lines

Class of loci	Lines	
	I_1	I_2
i	+	+
j	+	-
k	-	+
l	-	-

As derived in Dudley (1987a) and shown in Table 3.17 four estimators of $lpl\mu$ exist depending on the combination of q_j and q_k (frequency of recessive alleles in I_w at class j and k loci, respectively) used to estimate average values of q_j and q_k from the expression (I).

$$(I_1 \times I_w) - (I_2 \times I_w) = [(I_1 \times I_2) - I_2] q_j - [(I_1 \times I_2) - I_1] q_k$$

So, if $(I_1 \times I_w) - (I_2 \times I_w)$ is positive and $< (I_1 \times I_2) - I_2$ then q_k is set equal to zero (designated as q_{ko}) to estimate minimum values of q_j and q_k . If $(I_1 \times I_w) - (I_2 \times I_w)$ is negative and $< (I_1 \times I_2) - I_1$ then q_j (designated as q_{jo}) is set equal to zero. If $(I_1 \times I_w) - (I_2 \times I_w) + (I_1 \times I_2) - I_1$ is positive and $< (I_1 \times I_2) - I_2$ then q_k is set equal to one (q_{k1}) and Eq.(1) solved for q_j . If $(I_1 \times I_w) - (I_2 \times I_w) - (I_1 \times I_2) - I_2$ is negative and $< (I_1 \times I_2) - I_1$, then q_j is set equal to one (q_{j1}) and Eq. (1) is solved for q_k . Thus, four estimators of $lpl\mu$ exist, designated as: q_{jo} , q_{kl} , q_{j1} , q_{k1} , q_{ko} , and q_{kl} , q_{ko} as shown in Table 3.16.

Using the estimators for $lpl\mu$ to estimate $\mu G'$, algebraic solutions for $[\mu (A - H) + N (z + \mu)]/2$, were obtained and used to derive estimators for $\mu B', \dots, \mu F'$ for each case (Table 3.15).

Table 3.16. Estimators for $lpl\mu$ for different combinations of q_j and q_k .

Case	Estimator
q_{jo}, q_{kl}	$\frac{1}{4} [(I_1 \times I_w) + (I_2 \times I_w) - I_1 \times I_2 - I_1]$
q_{jo}, q_{j1}	$\frac{1}{4} [2(I_2 \times I_w) - (I_1 \times I_2) - I_2]$
q_{j1}, q_{ko}	$\frac{1}{4} [(I_1 \times I_w) + (I_2 \times I_w) - I_1 \times I_2 - I_2]$
q_{kl}, q_{ko}	$\frac{1}{4} [2(I_1 \times I_w) - (I_1 \times I_2) - I_1]$

3.3.9.2.2. Estimation of $\mu B'$ to $\mu G'$

Table 3.17. Estimators for $\mu B', \dots, \mu G'$ for different cases

$q_{jo}q_{kl}$		
$\mu B'$	=	$[(I_1 \times I_w) + (I_2 \times I_w) - (I_1 \times I_2) + I_1 - 2 I_w]/4$
$\mu C'$	=	$[-(I_1 \times I_w) + (I_2 \times I_w) + (I_1 \times I_2) + I_1 - 2 I_w]/4$
$\mu D'$	=	$[(I_1 \times I_w) - (I_2 \times I_w) + (I_1 \times I_2) - I_1]/4$
$\mu E'$	=	$[(I_1 \times I_w) - (I_2 \times I_w) + (I_1 \times I_2) - I_1]/4$
$\mu F'$	=	$[-(I_1 \times I_w) + (I_2 \times I_w) + (I_1 \times I_2) - I_1]/4$
$\mu G'$	=	$[(I_1 \times I_w) + (I_2 \times I_w) - (I_1 \times I_2) - I_1]/4$

q_{jb}, q_{ko}		
$\mu B'$	=	$[(I_1 \times I_w) + (I_2 \times I_w) - (I_1 \times I_2) + I_2 - 2 I_w]/4$
$\mu C'$	=	$[- (I_1 \times I_w) + (I_2 \times I_w) + (I_1 \times I_2) - I_2]/4$
$\mu D'$	=	$[(I_1 \times I_w) - (I_2 \times I_w) + (I_1 \times I_2) - I_2]/4$
$\mu E'$	=	$[(I_1 \times I_w) - (I_2 \times I_w) + (I_1 \times I_2) - 2 I_1 + I_2]/4$
$\mu F'$	=	$[- (I_1 \times I_w) + (I_2 \times I_w) + (I_1 \times I_2) - I_2]/4$
$\mu G'$	=	$[(I_1 \times I_w) + (I_2 \times I_w) - (I_1 \times I_2) - I_2]/4$
q_{jo}, q_{jl}		
$\mu B'$	=	$[2(I_1 \times I_w) - (I_1 \times I_2) + I_2 - 2 I_w]/4$
$\mu C'$	=	$[(I_1 \times I_2) - I_2]/4$
$\mu D'$	=	$[I_1 \times I_2 - I_2]/4$
$\mu E'$	=	$[2 (I_1 \times I_2) - 2 (I_2 \times I_w) + (I_1 \times I_2) - 2 I_1 + I_2]/4$
$\mu F'$	=	$[- 2 (I_1 \times I_w) + 2 (I_2 \times I_w) + (I_1 \times I_2) - I_2]/4$
$\mu G'$	=	$[2 (I_2 \times I_w) - (I_1 \times I_2) - I_2]/4$
q_{ko}, q_{k1}		
$\mu B'$	=	$[2 (I_2 \times I_w) - (I_1 \times I_2) + I_1 - 2 I_w]/4$
$\mu C'$	=	$[2 (I_1 \times I_w) + 2 (I_2 \times I_w) + (I_1 \times I_2) + I_1 - 2 I_2]/4$
$\mu D'$	=	$[2 (I_1 \times I_w) - 2 (I_2 \times I_w) + (I_1 \times I_2) - I_1]/4$
$\mu E'$	=	$[(I_1 \times I_2) - I_1]/4$
$\mu F'$	=	$[(I_1 \times I_2) - I_1]/4$
$\mu G'$	=	$[2 (I_1 \times I_w) - (I_1 \times I_2) - I_1]/4$

3.3.9.2.3 Test of significance of different estimates ($\mu B'$ to $\mu G'$)

The standard error (SE) of the estimators for $\mu B'$ to $\mu G'$ were calculated as the square root of the variance of the linear function associated with each estimator ignoring co-variance. All estimates were considered different from zero if they exceeded twice their standard error.

Table 3.1. Name and source of American cotton (*Gossypium hirsutum* L.) genotypes studied for genetic divergence during *kharif*, 2013-14

S.No.	Genotype	Source
1	BGDS 1063	University of Agricultural Sciences, Bheemarayangudi
2	GISV 267	Navsari Agricultural University, Surat
3	SCS 1062	University of Agricultural Sciences, Raichur
4	RAH 1065	University of Agricultural Sciences, Raichur
5	CCH 12-2	Central Institute for Cotton Research, Coimbatore
6	TSH 0499	Tamil Nadu Agricultural University, Srivilliputtur
7	LH 2306	Punjab Agricultural University, Ludhiana
8	GJHV 514	Junagadh Agricultural University, Junagadh
9	P 5430	Indian Agricultural Research Institute, New Delhi
10	L 1801	Regional Agricultural Research Station, Lam
11	RAH 1066	University of Agricultural Sciences, Bheemarayangudi
12	LH 2232	Punjab Agricultural University, Ludhiana
13	RS 266	Agricultural Research Station, Sriganganagar
14	LH 2298	Punjab Agricultural University, Ludhiana
15	TCH 1705	Tamil Nadu Agricultural University, Coimbatore
16	GJHV 04/13	Junagadh Agricultural University, Junagadh
17	RS 2718	Agricultural Research Station, Sriganganagar
18	CCH 12-6	Central Institute for Cotton Research, Coimbatore
19	GSHV 167	Navsari Agricultural University, Surat
20	ARBH 702	University of Agricultural Sciences, Dharwad
21	ARBH 701	University of Agricultural Sciences, Dharwad
22	Su-Flum	Shaktivardhak hybrid seeds
23	MCU 5	Tamil Nadu Agricultural University, Coimbatore
24	L 1060	Regional Agricultural Research Station, Lam
25	L 1058	Regional Agricultural Research Station, Lam
26	L 761	Regional Agricultural Research Station, Lam
27	L 1008	Regional Agricultural Research Station, Lam
28	P 72-9-37	Indian Agricultural Research Institute, New Delhi
29	L 1569	Regional Agricultural Research Station, Lam
30	L 604	Regional Agricultural Research Station, Lam
31	GISV 103	Navsari Agricultural University, Surat
32	L 389	Regional Agricultural Research Station, Lam
33	HYPS 152	Regional Agricultural Research Station, Lam
34	RHC 0811	Mahatma Phule Krishi Vidyapeeth, Rahuri
35	HS 289	Chaudhary Charan Singh Haryana Agricultural University, Sirsa
36	H 1442	Chaudhary Charan Singh Haryana Agricultural University, Hisar

Table 3.1 (cont.)

Table 3.1 (cont.)

S.No.	Genotype	Source
37	F 2310	Punjab Agricultural University, Faridkot
38	CPD 867	University of Agricultural Sciences, Dharwad
39	GISV 272	Navsari Agricultural University, Surat
40	RS 2669	University of Agricultural Sciences, Sriganganagar
41	SCS 1002	University of Agricultural Sciences, Raichur
42	GJHV 44	Junagadh Agricultural University, Junagadh
43	SHS 2-4	Southern India Mills Association, Cotton Development and Research Association
44	GSHV 162	Navsari Agricultural University, Surat
45	CCH 11-2	Central Institute for Cotton Research, Coimbatore
46	CCH 11-1	Central Institute for Cotton Research, Coimbatore
47	CA 105	Dr. PunjabraoDeshmukhKrishiVidyapeeth, Akola
48	CNH 50	Central Institute for Cotton Research, Nagpur
49	CNH 44	Central Institute for Cotton Research, Nagpur
50	RAH 1004	University of Agricultural Sciences, Bheemarayangudi
51	GJHV 08/70	Junagadh Agricultural University, Junagadh
52	KH 1101	RajamathaVijayaRajeScindiaKrishiViswavidyalaya, Khandwa
53	TCH 1741	Tamil Nadu Agricultural University,Coimbatore
54	LH 2256	Punjab Agricultural University, Ludhiana
55	PUSA 5760	Indian Agricultural Research Institute, New Delhi
56	L 799	Regional Agricultural Research Station, Lam
57	L 804	Regional Agricultural Research Station, Lam
58	L 762	Regional Agricultural Research Station, Lam
59	L 808	Regional Agricultural Research Station, Lam
60	MR 786	MR Seeds
61	NDLH 1938	Regional Agricultural Research Station, Nandyal
62	BS 51	Orissa University of Agriculture and Technology, Bhawanipatna
63	LH 2220	Punjab Agricultural University, Ludhiana
64	SCS 1001	University of Agricultural Sciences, Raichur
65	ADB 542	Agricultural Research Station, Adilabad
66	ADB 532	Agricultural Research Station, Adilabad
67	WGCV 48	Regional Agricultural Research Station, Warangal
68	TSH 0250	Tamil Nadu Agricultural University, Srivilliputtur
69	BS 37	Orissa University of Agriculture and Technology, Bhawanipatna
70	SCS 793	University of Agricultural Sciences, Raichur

Table 3.2. Name and source of Egyptian cotton (*Gossypium barbadense* L.) genotypes studied for genetic divergence during *kharif*, 2013-14

S.No.	Genotype	Source
1	GSB 43	Navsari Agricultural University, Surat
2	ARBD 27	University of Agricultural Sciences, Dharwad
3	DB 40	University of Agricultural Sciences, Dharwad
4	CCB 30	Central Institute for Cotton Research, Coimbatore
5	SUVIN	Tamil Nadu Agricultural University, Coimbatore
6	CCB 33	Central Institute for Cotton Research, Coimbatore
7	DB 39	University of Agricultural Sciences, Dharwad
8	GSB 21	Navsari Agricultural University, Surat
9	DB 16	University of Agricultural Sciences, Dharwad
10	CCB 11	Central Institute for Cotton Research, Coimbatore
11	GSB 40	Navsari Agricultural University, Surat
12	TCB 37	Tamil Nadu Agricultural University, Coimbatore
13	DB 11	University of Agricultural Sciences, Dharwad
14	RAB 8	University of Agricultural Sciences, Raichur
15	GSB 41	Navsari Agricultural University, Surat
16	RhCB 011	Mahatma Phule Krishi Vidyapeeth, Rahuri
17	DB 14	University of Agricultural Sciences, Dharwad
18	GSB 39	Navsari Agricultural University, Surat
19	TCB 51	Tamil Nadu Agricultural University, Coimbatore
20	TCB 26	Tamil Nadu Agricultural University, Coimbatore

Chapter IV

RESULTS AND DISCUSSION

The present investigation was carried out with 70 *Gossypium hirsutum* and 20 *Gossypium barbadense* genotypes for genetic divergence studies during *kharif*, 2013-14. Based on cluster mean values and *per se* performance, twelve lines from *hirsutum* and six testers from *barbadense* group were selected and crossed in line $\times$ tester fashion to generate F₁s. The resulted 72 inter-specific hybrids along with 18 (12 lines + 6 testers) parents and two standard checks were evaluated at Regional Agricultural Research Station, Lam Farm; Agricultural Research Station, Jangamaheswarapuram and Agricultural College Farm, Bapatla during *kharif*, 2014-15 to know the combining ability, heterosis and stability of genotypes over locations. The data was recorded on five randomly selected competitive plants per entry per replication for plant height (cm), number of monopodia plant⁻¹, number of sympodia plant⁻¹, number of bolls plant⁻¹, boll weight (g), lint index (g), seed index (g), seed cotton yield plant⁻¹ (g) and lint yield plant⁻¹ (g). Whereas, the data on days to 50% flowering, ginning out-turn (%), bundle strength (g/tex), uniformity ratio, 2.5% span length (mm), micronaire value (10⁻⁶g/inch) and fibre elongation (%) were recorded on plot basis and were subjected to statistical analysis. The results are presented and discussed under the following headings.

4.1 Analysis of variance

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

4.3 Genetic divergence

4.4 Pooled analysis of variance

4.5 Genetic variability, heritability and genetic advance as per cent of mean (pooled)

4.6 Character association

4.7 Path coefficient analysis

4.8 Combining ability and gene action

4.9 Heterosis

4.10 Stability analysis

4.11 Identification of favourable alleles in the donor parents

4.1 ANALYSIS OF VARIANCE

The mean performance of 70 *hirsutum* and 20 *barbadense* genotypes is presented in Appendices I and II. The analysis of variance (ANOVA) of both the species genotypes for seed cotton yield and yield components is presented in Tables 4.1 and 4.2. The results revealed existence of significant differences among the genotypes for 16 characters indicating the presence of genetic variability in the genotypes evaluated.

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

4.2.1 *G. hirsutum* Genotypes

Genetic variability together with the heritability estimates would give a better idea on the amount of genetic gain expected out of selection (Burton, 1952 and Swarup and Chaugle, 1962). Further, the magnitude of heritable variability is the most important aspect (Panse, 1957), which is directly proportional to response to selection. Heritability estimates along with genetic advance are more helpful in predicting the genetic gain under selection than heritability estimates alone. However, it is not necessary that a character showing high heritability will always exhibit high genetic advance (Johnson *et al.*, 1955).

The estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ($h^2_{(b)}$) in broad sense and genetic advance as per cent of mean (GAM) pertaining to 70 *hirsutum* genotypes were calculated and are presented in the Table 4.3 and described character- wise here under.

4.2.1.1 Days to 50% flowering

The number of days to 50 % flowering varied from 52.00 (CCH 12-6) to 71.00 (KH 1101) days with a mean of 60.22 days. The estimates of PCV and GCV (6.95 and 6.76) were low indicating less variation for days to 50% flowering among the genotypes studied. These findings are similar to the results of Sarada *et al.* (2010), Kulkarni *et al.* (2011), Dhivya *et al.* (2014) and Erande *et al.* (2014).

High heritability (94.60) coupled with moderate genetic advance as per cent of mean (13.56) was observed for this trait indicating the presence of both additive and non-additive gene actions. Desired results may not be obtained by simple selection. However,

Kale *et al.* (2007), An *et al.* (2008), Rajanna (2010), Patel *et al.* (2013b) and Dhivya *et al.* (2014) reported high heritability coupled with low genetic advance as per cent of mean. This may be due to differences in the material and environments studied.

4.2.1.2 Plant height (cm)

The range varied from 104.22 (L 389) to 140.99 cm (PUSA 5760) with a mean value of 127.77 cm. Low phenotypic (7.74) and genotypic (5.83) coefficients of variation were observed for plant height indicating less variation among the genotypes evaluated. These results are in agreement with the findings of Kulkarni *et al.* (2011), Erande *et al.* (2014), Farooq *et al.* (2014) and Ahsan *et al.* (2015).

Moderate heritability (56.70) coupled with low genetic advance as per cent of mean (9.04) was observed indicating the role of non-additive type of gene action in the inheritance of this character. Further improvement of this trait would be possible through heterosis breeding. Kaushik and Kapoor (2006), Verma *et al.* (2006) and Mahantesh (2009) reported high heritability coupled with low genetic advance. This may be due to differences in the material and environments studied.

4.2.1.3 Number of monopodia plant⁻¹

Number of monopodia plant⁻¹ varied from 0.67 (LH 2306, RAH 1066, RS 2669 and PUSA 5760) to 2.33 (CCH 12-6, L 1569 and GJHV 44) with a mean value of 1.33. The estimates of PCV and GCV (34.37 and 33.37) were high revealing wider variation among the genotypes studied. These results are supported by Kulkarni *et al.* (2011), Hafiz *et al.* (2013), Paramjit and Buttar (2013) and Khan *et al.* (2015).

High heritability (94.30) and high genetic advance as per cent of mean (66.75) were observed for this trait making selection effective due to preponderance of additive gene action. Similar findings were also reported by Lakshmi *et al.* (2012), Hafiz *et al.* (2013), Paramjit and Buttar (2013), Patel *et al.* (2013b) and Erande *et al.* (2014).

4.2.1.4 Number of sympodia plant⁻¹

The range of variation was from 10.44 (GISV 267) to 18.22 (LH 2232) with a mean value of 14.96. Both PCV (11.88) and GCV (10.16) estimates were moderate and there is large difference between them indicating the influence of environment. These results are in accordance with the reports of Girase and Mehetre (2002), Vinodhana *et al.* (2013) and Farooq *et al.* (2014).

High heritability (73.10) coupled with moderate genetic advance as per cent of mean (17.90) was noticed for number of sympodia plant⁻¹. Desired results may not be obtained by simple selection due to the operation of both additive and non-additive gene actions. However, Reddy (2001), Kulkarni *et al.* (2011), Vinodhana *et al.* (2013) and Farooq *et al.* (2014) reported high heritability coupled with low genetic advance. This may be due to differences in the material and environments studied.

4.2.1.5 Number of bolls plant⁻¹

The variation for this character ranged from 20.90 (GISV 267) to 54.20 (SCS 793) with a mean value of 37.25. The estimates of PCV (18.00) and GCV (17.14) were moderate and there is less difference between them indicating less influence of environment. These results are in conformity with the research findings of An *et al.* (2008), Mahantesh (2009), Rajanna (2010) and Hafiz *et al.* (2013).

High heritability (90.70) coupled with high genetic advance as per cent of mean (33.64) indicating the role of additive gene action in the inheritance of this trait and further improvement would be possible through selection. Elango *et al.* (2012), Asha *et al.* (2013a), Hafiz *et al.* (2013), Paramjit and Buttar (2013), Ahsan *et al.* (2015) and Khan *et al.* (2015) also reported similar results like present investigation for number bolls plant⁻¹.

4.2.1.6 Boll weight (g)

Boll weight recorded a range of variation from 3.45 (L 762) to 5.36 g (HYPS 152) with a mean value of 4.20 g. Moderate PCV (10.28) and low GCV (9.53) were observed and difference between them is low indicating less influence of environment and similar results were also reported by the earlier workers Bazi (2011), Vinodhana *et al.* (2013), Dhivya *et al.* (2014) and Erande *et al.* (2014).

High heritability (86.00) with moderate genetic advance as per cent of mean (18.22) was observed indicating the presence of both additive and non-additive gene actions. Further improvement of this trait may not be possible by simple selection. Elango *et al.* (2012), Asha *et al.* (2013a), Paramjit and Buttar (2013), Erande *et al.* (2014), Ahsan *et al.* (2015) and Khan *et al.* (2015) recorded high heritability accompanied with high genetic advance as per cent of mean for the same character. This may be due to differences in the material and environments studied.

4.2.1.7 Lint index (g)

The range of variation for this character varied from 2.36 (GJHV 08/70) to 6.27 g (SCS 1062) with a mean value of 4.37 g. Moderate PCV (17.42) and GCV (17.06) were recorded and there is less difference between them indicating negligible influence of environment. These findings are similar to the findings of Naqib *et al.* (2010), Kulkarni *et al.* (2011) and Vinodhana *et al.* (2013).

High heritability (95.90) and high genetic advance as per cent of mean (34.42) were observed for this trait indicating presence of additive gene action and further improvement of this trait would be easier through simple selection. Haritha *et al.* (2012), Lakshmi *et al.* (2012), Vinodhana *et al.* (2013), Dhivya *et al.* (2014) and Ahsan *et al.* (2015) also reported similar results.

4.2.1.8 Seed index (g)

The variation for this character ranged from 5.80 (GIHV 08/70) to 11.35 g (L 1008) with a mean value of 8.51 g. The estimates of PCV (14.16) and GCV (13.70) were moderate and there is less difference between them revealing negligible influence of environment. Similar results were earlier reported by Paramjit and Buttar (2013), Vinodhana *et al.* (2013), Erande *et al.* (2014) and Ahsan *et al.* (2015).

Both heritability (93.70) and genetic advance as per cent of mean (27.34) were high for this character indicating the operation of additive gene action. Selection would be gainful for this character. This is in conformity with the observations of Ravikesavan *et al.* (2008), Mahantesh (2009), Bazi (2011), Paramjit and Buttar (2013), Dhivya *et al.* (2014), Erande *et al.* (2014) and Ahsan *et al.* (2015).

4.2.1.9 Ginning out-turn (%)

Ginning out-turn recorded a range of variation from 27.41 (RHC 0811) to 41.06 per cent (GSHV 167) with a mean value of 33.87 per cent. Moderate PCV (10.23) and GCV (10.00) estimates were observed. The difference between PCV and GCV is less revealing less influence of environment. These results are in accordance with those of Vinodhana *et al.* (2013), Dhivya *et al.* (2014), Erande *et al.* (2014), Farooq *et al.* (2014) and Khan *et al.* (2015).

High heritability (87.50) and moderate genetic advance as per cent of mean (18.44) were observed for this trait. This indicates the presence of both additive and non-additive gene actions and further improvement of this character may not be possible by simple selection. In contrary to this, Ravikesavan *et al.* (2008), Elango *et al.* (2012), Haritha *et al.* (2012) and Ahsan *et al.* (2015) noticed high heritability coupled with high genetic advance as per cent of mean. This may be due to differences in the material and environments studied.

4.2.1.10 2.5% span length (mm)

2.5% span length was in the range of 20.84 (GSHV 167) to 33.05 mm (L 604) with a mean value of 26.93 mm. The estimates of PCV (7.73) and GCV (7.23) were low revealing less variation among the genotypes studied. These results are in agreement with the findings of Kishore *et al.* (2011), Asha *et al.* (2013a), Vinodhana *et al.* (2013), Dhivya *et al.* (2014) and Erande *et al.* (2014).

High heritability (87.50) coupled with moderate genetic advance as per cent of mean (13.93) was observed for this character indicating desired results may not be obtained by simple selection due to the operation of both additive and non-additive gene actions. However, Ravikesavan *et al.* (2008), Mahantesh (2009), Rajamani and Rao (2009) and Kulkarni *et al.* (2011) recorded high heritability coupled with low genetic advance as per cent of mean. This clearly indicates that inheritance pattern of same trait depends on the material and environments studied.

4.2.1.11 Uniformity ratio

This trait ranged from 43.22 (GISV 267) to 51.63 (RAH 1065) with a mean value of 48.44. Both PCV (5.17) and GCV (4.13) estimates were low. These results show that there is less variation among the genotypes studied for uniformity ratio. These findings were in accordance with the results of Sarada *et al.* (2010), Kishore *et al.* (2011), Asha *et al.* (2013a), Vinodhana *et al.* (2013), Erande *et al.* (2014) and Khan *et al.* (2015).

High heritability (63.90) coupled with low genetic advance as per cent of mean (6.81) was recorded for uniformity ratio indicating the importance of non-additive gene action. The high heritability is being exhibited due to favourable influence of environment rather than genotype. These findings were in supportive of Elango *et al.* (2012), Haritha *et al.* (2012), Asha *et al.* (2013a), Erande *et al.* (2014) and Khan *et al.* (2015).

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

The range of variation observed for micronaire value was from 2.55 (L 808) to 5.64 10^{-6} g/inch (RAH 1065) with a mean value of 3.62 10^{-6} g/inch. The estimates of PCV (15.55) and GCV (15.20) were moderate and there is less difference between them indicating negligible influence of environment. These results are in conformity with the reports of Sarada *et al.* (2010), Kulkarni *et al.* (2011), Vinodhana *et al.* (2013) and Khan *et al.* (2015).

High heritability (95.50) associated with high genetic advance as per cent of mean (30.61) was observed for this trait which makes selection effective due to additive gene action. These results are in agreement with the findings of Bazi (2011), Asha *et al.* (2013a), Vinodhana *et al.* (2013) and Erande *et al.* (2014).

4.2.1.13 Bundle strength (g/tex)

The range of variation among the genotypes for this trait was from 17.00 (GSHV 167) to 24.16 g/tex (BS 37) with a mean value of 20.39 g/tex. Low phenotypic (6.49) and genotypic (5.78) coefficients of variation were recorded. These results reveal that there is less variation among the genotypes studied for bundle strength. These findings were in accordance with those of Rajanna (2010), Sarada *et al.* (2010), Bazi (2011) and Asha *et al.* (2013a).

High heritability (79.40) and moderate genetic advance as per cent of mean (10.63) were recorded indicating the importance of both additive and non-additive gene actions. Further improvement of this character may not possible by simple selection. Rao and Reddy (2001), Sakthi *et al.* (2007), Rajanna (2010) and Kulkarni *et al.* (2011) recorded high heritability coupled with low genetic advance as per cent of mean for this trait. This may be due to differences in the material and environments studied.

4.2.1.14 Fibre elongation (%)

The variation for this character ranged from 4.30 (RHC 0811) to 5.55 per cent (RAH 1065) with a mean value of 5.03 per cent. Both PCV (5.11) and GCV (4.16) estimates were low indicating less variation among the genotypes studied. Similar results were reported by Rajanna (2010), Bazi (2011), Kulkarni *et al.* (2011), Elango *et al.* (2012) and Asha *et al.* (2013a).

High heritability (66.20) coupled with low genetic advance as per cent of mean (6.97) was observed for fibre elongation indicating the importance of non-additive gene action. Further improvement of this trait would be possible through heterosis breeding. These research findings were similar to those described by Vijayalakshmi *et al.* (2008), Kulkarni *et al.* (2011), Elango *et al.* (2012) and Asha *et al.* (2013a).

4.2.1.15 Seed cotton yield plant⁻¹ (g)

The range of variation observed for this character was from 89.32 (GISV 267) to 184.22 g (SCS 793) with a mean value of 130.79 g. The estimates of PCV (15.48) and GCV (13.52) were moderate and there is large difference between them indicating the influence of environment. The results were in conformity with findings of An *et al.* (2008), Mahantesh (2009), Rajanna (2010) and Bazi (2011).

High heritability (76.30) coupled with high genetic advance as per cent of mean (24.34) was observed for seed cotton yield plant⁻¹ making selection effective due to the preponderance of additive gene action. These findings were in accordance with those of Elango *et al.* (2012), Haritha *et al.* (2012), Paramjit and Buttar (2013), Vinodhana *et al.* (2013), Dhivya *et al.* (2014), Ahsan *et al.* (2015) and Khan *et al.* (2015).

4.2.1.16 Lint yield plant⁻¹ (g)

Lint yield plant⁻¹ ranged from 30.38 (GISV 267) to 60.64 g (WGCV 48) with a mean value of 44.33 g. The estimates of PCV (18.87) and GCV (16.81) were moderate and there is large difference between them revealing the influence of environment. Similar results were also reported by Mahantesh (2009), Rajanna (2010) and Lakshmi *et al.* (2012).

High heritability (79.40) coupled with high genetic advance as per cent of mean (30.86) was recorded indicating the importance of additive gene action in the inheritance of this trait and making selection effective. These results are in accordance with the findings of Mahantesh (2009), Rajanna (2010), Elango *et al.* (2012) and Erande *et al.* (2014).

Thus, in the present study, number of monopodia plant⁻¹ exhibited wide genetic variability while, number of sympodia plant⁻¹, number of bolls plant⁻¹, lint index, seed index, ginning out-turn, micronaire value, seed cotton yield plant⁻¹ and lint yield plant⁻¹ recorded moderate genetic variability. The other traits recorded low variability.

High heritability coupled with high genetic advance as per cent of mean was observed in case of number of monopodia plant⁻¹, number of bolls plant⁻¹, lint index, seed index, micronaire value, seed cotton yield plant⁻¹ and lint yield plant⁻¹ indicating the importance of additive gene action governing in the inheritance of these traits. Directional selection could be profitably applied on these traits in the genetically diverse material.

Days to 50% flowering, number of sympodia plant⁻¹, boll weight, ginning out-turn, 2.5% span length and bundle strength recorded high heritability coupled with moderate genetic advance as per cent of mean. This indicates involvement of both additive and non-additive gene actions in the inheritance of these traits. Improvement of these traits is possible by simultaneous exploitation of both additive and non-additive components of gene action by adopting breeding procedures like biparental mating, diallel selective mating system or cyclic hybridization.

Moderate heritability coupled with low genetic advance as per cent of mean was noticed for plant height whereas, uniformity ratio and fibre elongation showed high heritability coupled with low genetic advance as per cent of mean indicating operation of non-additive gene action. Further improvement of these characters can be possible through heterosis breeding.

4.2.2 *G. barbadense* Genotypes

The estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ($h^2_{(b)}$) in broad sense and genetic advance as per cent of mean (GAM) pertaining to 20 *barbadense* genotypes were calculated and are presented in the Table 4.4 and described character wise here under.

4.2.2.1 Days to 50% flowering

The range varied from 68.00 (GSB 41) to 77.00 days (DB 39) with a mean of 72.50 days after sowing was observed for this trait. The estimates of PCV (3.51) and GCV (3.17) were low indicating less variation among the genotypes studied. Similar results were earlier observed by Neelima *et al.* (2008), Asha *et al.* (2013a), Dhivya *et al.* (2014) and Erande *et al.* (2014).

High heritability (81.60) coupled with low genetic advance as per cent of mean (5.90) was observed for this trait indicating the presence of non-additive gene action and further improvement of this trait would be possible through heterosis breeding. These results are in accordance with the reports of Mahantesh (2009), Asha *et al.* (2013a), Patel *et al.* (2013b) and Dhivya *et al.* (2014).

4.2.2.2 Plant height (cm)

Plant height exhibited a range from 125.00 (ARBD 27) to 156.83 cm (DB 16) with a mean of 138.33 cm. Both PCV (8.65) and GCV (6.19) estimates were low revealing less variation among the genotypes evaluated. These results are in conformity with the findings of Rajanna (2010), Erande *et al.* (2014), Farooq *et al.* (2014) and Ahsan *et al.* (2015).

Moderate heritability (51.20) and low genetic advance as per cent of mean (9.13) was recorded for this trait indicating the importance of non-additive gene action and further improvement of this trait would be possible through heterosis breeding. However, Kaushik and Kapoor (2006), Verma *et al.* (2006) and Mahantesh (2009) reported high heritability coupled with low genetic advance. This may be due to differences in the material and environments studied.

4.2.2.3 Number of monopodia plant⁻¹

Number of monopodia plant⁻¹ varied from 0.67 (RhCB 011) to 2.00 (TCB 51) with a mean of 1.32. High PCV (26.73) and GCV (25.69) were observed. These results reveal that there is wider variability among the genotypes studied. Similar findings were also reported by Mohan (2011), Hafiz *et al.* (2013), Paramjit and Buttar (2013) and Khan *et al.* (2015).

High heritability (92.40) and high genetic advance as per cent of mean (50.87) was noticed for this trait indicating the operation of additive gene action and selection would be gainful. Asha *et al.* (2013a), Hafiz *et al.* (2013), Patel *et al.* (2013b) and Erande *et al.* (2014) also noted similar findings.

4.2.2.4 Number of sympodia plant⁻¹

The range of variation was from 12.21 (GSB 39) to 20.11 (GSB 41) with a mean of 16.49. The estimates of PCV (13.28) and GCV (11.39) were moderate and there is large difference between them indicating the influence of environment. These results are in agreement with the findings of Girase and Mehetre (2002), Vinodhana *et al.* (2013) and Farooq *et al.* (2014).

High heritability (73.60) coupled with high genetic advance as per cent of mean (20.14) was observed for this trait indicating making selection would be effective due to the preponderance of additive gene action. Verma *et al.* (2006), Sakthi *et al.* (2007), An *et al.* (2008), Ravikesavan *et al.* (2008), Dhivya *et al.* (2014) and Khan *et al.* (2015) also reported similar findings.

4.2.2.5 Number of bolls plant⁻¹

The mean number of bolls plant⁻¹ varied from 32.80 (DB 39) to 57.22 (RhCB 011) with an average of 44.18. The estimates of PCV (15.91) and GCV (14.48) were moderate and there is large difference between them indicating the influence of environment. The results are in broad agreement with the reports of Mahantesh (2009), Rajanna (2010) and Hafiz *et al.* (2013).

High heritability (82.80) associated with high genetic advance as per cent of mean (27.15) was observed for this trait indicating the operation of additive gene action and selection would be effective. Similar results were also reported by Elango *et al.* (2012), Vinodhana *et al.* (2013), Ahsan *et al.* (2015) and Khan *et al.* (2015).

4.2.2.6 Boll weight (g)

Boll weight ranged from 2.10 (SUVIN) to 3.10 g (RAB 8) with a mean of 2.61 g. Low phenotypic (9.87) and genotypic (8.84) coefficients of variation were recorded indicating less variation among the genotypes studied. These findings are in broad agreement with the reports of Vinodhana *et al.* (2013), Dhivya *et al.* (2014) and Erande *et al.* (2014).

High heritability (80.30) coupled with moderate genetic advance as per cent of mean (16.32) was observed for this trait indicating the operation of both additive and non-additive gene actions in the inheritance of boll weight. Desired results may not be

obtained by simple selection. However, Bazi (2011), Haritha *et al.* (2012), Lakshmi *et al.* (2012), Ahsan *et al.* (2015) and Khan *et al.* (2015) noticed high heritability coupled with high genetic advance. This may be due to differences in the material and environments studied.

4.2.2.7 Lint index (g)

This trait varied from 3.36 (DB 39) to 5.66 g (TCB 37) with a mean of 4.39 g. The estimates of PCV (14.13) and GCV (13.60) were moderate and difference between them is low revealing less influence of environment. The above findings are in conformity with the results of Neelima *et al.* (2008), Naqib *et al.* (2010), Kulkarni *et al.* (2011) and Vinodhana *et al.* (2013).

High heritability (92.60) and high genetic advance as per cent of mean (26.97) were recorded for lint index indicating making selection would be effective due to the preponderance of additive gene action. Similar results were earlier reported by Haritha *et al.* (2012), Asha *et al.* (2013a), Vinodhana *et al.* (2013), Dhivya *et al.* (2014) and Ahsan *et al.* (2015).

4.2.2.8 Seed index (g)

The range of variation recorded for this trait was from 7.40 (DB 39) to 11.20 g (TCB 37) with a mean of 9.31 g. Moderate PCV (10.45) and low GCV (10.00) were observed and there is less difference among them indicating negligible influence of environment. These results are in broad agreement with the reports of Paramjit and Buttar (2013), Vinodhana *et al.* (2013), Erande *et al.* (2014) and Ahsan *et al.* (2015).

High heritability (92.30) and moderate genetic advance as per cent of mean (19.86) were recorded indicating desirable results may not be obtained by simple selection due to operation of both additive and non-additive gene actions. Bazi (2011), Asha *et al.* (2013a), Paramjit and Buttar (2013), Dhivya *et al.* (2014), Erande *et al.* (2014) and Ahsan *et al.* (2015) noticed high heritability coupled with high genetic advance for this trait. This may be due to differences in the material and environments studied.

4.2.2.9 Ginning out-turn (%)

Ginning out-turn was in the range of 28.77 (CCB 33) to 34.75 per cent (RAB 8) with a mean of 31.96 per cent. Low PCV (6.22) and GCV (5.03) estimates were recorded revealing less variation among the genotypes studied. Mohan (2011), Dhivya *et al.* (2014), Erande *et al.* (2014), Farooq *et al.* (2014) and Khan *et al.* (2015) also reported similar findings in their studies.

High heritability (65.40) coupled with low genetic advance as per cent of mean (8.38) was observed for this trait. This clearly shows the operation of non-additive gene action and further improvement of this trait would be easier through heterosis breeding. These results are in conformity with previous reports of Patel *et al.* (2013b), Dhivya *et al.* (2014), Erande *et al.* (2014), Farooq *et al.* (2014) and Khan *et al.* (2015).

4.2.2.10 2.5% span length (mm)

The variation for this trait ranged from 28.27 (TCB 51) to 37.82 mm (TCB 37) with an average value of 32.58 mm. The estimates of PCV (8.35) and GCV (7.85) were low indicating less variation among the genotypes studied. The above findings are in agreement with the results of Mohan (2011), Dhivya *et al.* (2014) and Erande *et al.* (2014).

High heritability (88.40) coupled with moderate genetic advance as per cent of mean (15.20) was observed for 2.5% span length indicating the presence of both additive and non-additive gene actions. Further improvement of this character may not be possible by simple selection. However, Hafiz *et al.* (2013), Dhivya *et al.* (2014) and Erande *et al.* (2014) recorded high heritability coupled with high genetic advance. This clearly shows that inheritance pattern of a particular character depends on the material and environments studied.

4.2.2.11 Uniformity ratio

The variation for this character ranged from 44.18 (GSB 21) to 50.05 (ARBD 27) with a mean of 46.76. Low PCV (4.15) and GCV (3.02) were observed for uniformity ratio indicating less variation among the genotypes studied. Bazi (2011), Mohan (2011), Vinodhana *et al.* (2013) and Khan *et al.* (2015) also reported similar findings.

Moderate heritability (53.10) and low genetic advance as per cent of mean (4.54) revealed the preponderance of non-additive gene action and further improvement of this trait would be possible through heterosis breeding. These results are in agreement with the reports of Mahantesh (2009), Haritha *et al.* (2012), Asha *et al.* (2013a), Erande *et al.* (2014) and Khan *et al.* (2015).

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

Micronaire value varied from 2.40 (SUVIN) to 3.20 10^{-6} g/inch (RhCB 011) with an average value of 2.84 10^{-6} g/inch. Low estimates of PCV (7.27) and GCV (6.16) were observed revealing less variation among the genotypes studied. Similar results were earlier reported by Srinivasulu (2009), Rajanna (2010), Kulkarni *et al.* (2011), Vinodhana *et al.* (2013) and Khan *et al.* (2015).

High heritability (71.80) with moderate genetic advance as per cent of mean (10.75) indicates that desired results may not be obtained by simple selection due to presence of both additive and non-additive gene actions. In contrary to this, Mahantesh (2009), Elango *et al.* (2012), Haritha *et al.* (2012) and Khan *et al.* (2015) noticed high heritability coupled with low genetic advance for this trait. This may be due to differences in the material and environments studied.

4.2.2.13 Bundle strength (g/tex)

The range of variation was from 21.73 (TCB 51) to 29.49 g/tex (TCB 37) with a mean of 25.19 g/tex. Both PCV (7.60) and GCV (6.82) estimates were low showing less variation among the genotypes studied. The above findings are in conformity with the results reported by Srinivasulu (2009), Rajanna (2010), Sarada *et al.* (2010) and Bazi (2011).

High heritability (80.50) and moderate genetic advance as per cent of mean (12.62) were recorded for this trait indicating the operation of both additive and non-additive gene actions. Further improvement of this character may not be possible through simple selection. However, Ravikesavan *et al.* (2008), Asha *et al.* (2013a) and Vinodhana *et al.* (2013) observed high heritability coupled with high genetic advance. This may be due to differences in the material and environments studied.

4.2.2.14 Fibre elongation (%)

Fibre elongation ratio varied from 4.90 (TCB 51) to 5.53 per cent (TCB 37) with a mean of 5.25 per cent. Low estimates of PCV (3.96) and GCV (3.17) were recorded. These results revealed less variation among the genotypes studied. Similar results were earlier reported by Bazi (2011), Kulkarni *et al.* (2011), Elango *et al.* (2012) and Asha *et al.* (2013a).

High heritability (63.90) associated with low genetic advance as per cent of mean (5.22) was observed for this trait indicating further improvement of this trait would be possible through heterosis breeding due to operation of non-additive gene action. These findings are in conformity with the reports of Vijayalakshmi *et al.* (2008), Kulkarni *et al.* (2010), Elango *et al.* (2012) and Asha *et al.* (2013a).

4.2.2.15 Seed cotton yield plant⁻¹ (g)

The variation for this character ranged from 66.88 (DB 39) to 133.20 g (RhCB 011) with a mean of 98.52 g. The estimated values of PCV (19.59) and GCV (18.04) were moderate indicating wider variation for seed cotton yield plant⁻¹ among the genotypes studied. An *et al.* (2008), Mahantesh (2009), Rajanna (2010) and Bazi (2011) also reported similar results.

High heritability (84.80) coupled with high genetic advance as per cent of mean (34.23) was recorded for seed cotton yield plant⁻¹ indicating the preponderance of additive gene action and further improvement of this character would be possible through simple selection. These results are in agreement with the reports of Elango *et al.* (2012), Haritha *et al.* (2012), Asha *et al.* (2013a), Paramjit and Buttar (2013), Vinodhana *et al.* (2013), Farooq *et al.* (2014), Ahsan *et al.* (2015) and Khan *et al.* (2015).

4.2.2.16 Lint yield plant⁻¹ (g)

Lint yield plant⁻¹ was in the range of 20.86 (DB 39) to 41.59 g (RhCB 011) with a mean of 31.59 g. High PCV (21.49) and moderate GCV (19.88) were observed for this trait. The magnitude of PCV was higher than GCV revealing the influence of environment in inheritance of this trait. These results are in conformity with the findings of Patnaik *et al.* (2004), Rajanna (2010) and Erande *et al.* (2014).

High heritability (85.60) coupled with high genetic advance as per cent of mean (37.90) was observed indicating that making selection effective due to presence of additive gene action. Mahantesh (2009), Rajanna (2010), Elango *et al.* (2012) and Erande *et al.* (2014) also reported similar findings.

In the present study the magnitude of difference between PCV and GCV was relatively low for all the traits which revealed the least influence of environment on these traits. The traits viz., number of monopodia plant⁻¹ and seed cotton yield plant⁻¹ recorded wide genetic variability whereas, moderate genetic variability was exhibited by number of sympodia plant⁻¹, number of bolls plant⁻¹, lint index and lint yield plant⁻¹. The remaining characters showed low genetic variability.

Preponderance of additive gene action was noticed for number of monopodia plant⁻¹, number of sympodia plant⁻¹, number of bolls plant⁻¹, lint index, seed cotton yield plant⁻¹ and lint yield plant⁻¹ as these characters registered high heritability coupled with high genetic advance. Further improvement of these traits can be possible through simple selection procedures. Boll weight, seed index, 2.5% span length, micronaire value and bundle strength registered high heritability coupled with moderate genetic advance which indicates the operation of both additive and non-additive gene actions. Biparental mating, diallel selective mating system or cyclic hybridization can be used for further improvement of these characters.

High heritability coupled with low genetic advance as per cent of mean was observed for days to 50% flowering, ginning out-turn and fibre elongation whereas moderate heritability accompanied with low genetic advance as per cent of mean was noticed for plant height and uniformity ratio. This indicates operation of non-additive gene action in the inheritance of these traits and can be effectively exploited through heterosis breeding or population improvement through various forms of recurrent selection.

4.3 GENETIC DIVERGENCE

In hybridization programmes, the diversity of parents is of prime importance, since the crosses made between the genetically divergent parents are likely to throw desirable recombinants in the progenies. It is a difficult task for plant breeder to choose most suitable parents unless provided with the information on genetic variability present in the material.

The multivariate analysis using Mahalanobis' D^2 statistic and principal component analysis provides a very useful statistical tool for measuring the amount of genetic diversity in a given germplasm with respect to the characters considered together (Panse and Sukhatme, 1978). Further, the problem of selecting divergent parents for hybridization programme can be narrowed, if one can identify the characters responsible for the discrimination between populations.

The data was collected on 16 yield, yield contributing and quality characters from 70 *hirsutum* and 20 *barbadense* genotypes of cotton and were subjected to multivariate analysis like Mahalanobis' D^2 statistic, principal component and cluster analysis. The magnitude of values suggested that there was considerable variability in the material studied, which led to genetic diversity.

4.3.1 Mahalanobis' D^2 Analysis

4.3.1.1 Test with Wilk's criterion ' Λ '

Significant differences among the genotypes for individual characters were first determined and later the statistical significant differences between the genotypes based on the pooled effects of all the characters were carried out using the *Wilk's criterion ' Λ '*. The *Wilk's* criterion thus obtained was used in calculations of ' V ' statistic. The statistic was highly significant indicating that genotypes differed significantly when all the characters were considered simultaneously. The value of ' V ' statistic for *hirsutum* and *barbadense* genotypes was 4986.11 and 991.19, respectively, in the present study.

4.3.1.2 Mahalanobis' D^2 values

To estimate the D^2 values, correlated mean of characters were transformed into standardized uncorrelated characters by 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 possible 2415 and 190 combinations and the corresponding D^2 values were obtained for both American and Egyptian cotton genotypes.

4.3.1.2.1 *G. hirsutum* genotypes

The per cent contribution towards genetic divergence by all the 16 contributing characters is presented in the Table 4.5. The knowledge on characters influencing divergence is an important aspect to a plant breeder. Character-wise rank has shown that none of the character lonely had a greater contribution to total genetic divergence. The maximum contribution towards genetic divergence was by micronaire value (21.33) followed by lint index (19.30), days to 50% flowering (16.40), number of monopodia plant⁻¹ (13.94), seed index (13.29), number of bolls plant⁻¹ (5.88), boll weight (3.44), 2.5% span length (3.40), seed cotton yield plant⁻¹ (0.80), fibre elongation (0.58), number of sympodia plant⁻¹ (0.54), ginning out-turn (0.37), bundle strength (0.37), lint yield plant⁻¹ (0.33) and uniformity ratio (0.04).

4.3.1.2.1.1 Grouping of genotypes into various clusters

The 70 *hirsutum* genotypes were grouped into 13 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 (Table 4.6).

The distribution of 70 genotypes into 13 clusters was at random with maximum number of genotypes in cluster I (33 genotypes). Cluster IV was the second largest with 11 genotypes followed by cluster VII (7 genotypes), cluster III (6 genotypes), cluster X (5 genotypes). Clusters II, V, VI, VIII, IX, XI, XII and XIII were solitary clusters with nil intra- cluster D^2 values. The formation of distinct solitary clusters may be due to the fact that geographic barriers prevent gene flow or intensive natural and human selection for diverse and adoptable gene complexes.

This pattern of grouping has indicated that the diversity need not be necessarily be 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. 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. 4.1) was constructed based on clustering by Tocher's method.

4.3.1.2.1.2 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 Chowdhary (1977) are presented in the Table 4.7. The proximity and divergence among 13 clusters are indicated in the Table 4.8 and Fig. 4.2.

The maximum intra cluster distance was 124.02 for cluster X followed by 110.20 for cluster IV, 92.49 for cluster VII and 67.03 for cluster III, 48.38 for cluster I while, it was zero for clusters II, V, VI, VIII, IX, XI, XII and XIII.

Cluster I, with 33 genotypes, was the largest of all clusters. It was closest to cluster II (71.68) followed by Cluster V (72.11) and it was farthest from cluster X (180.17) followed by cluster XI (146.47).

Cluster II had only one genotype (RAH 1004). It was nearest to cluster IV (59.91) followed by cluster V (96.51) and it was farthest from cluster XI (155.92) followed by cluster XII (141.21).

Six genotypes were grouped in cluster III. It was nearest to cluster VIII (87.59) followed by cluster VI (92.43) and it was farthest from cluster XI (297.04) followed by XII (250.85).

Cluster IV comprised of 11 genotypes. It was nearest to the cluster II (59.91) followed by cluster I (84.43) and it was farthest from cluster X (185.31) followed by cluster VIII (155.86).

Cluster V was mono-genotypic (CCH 11-2). It was nearest to cluster I (72.11) followed by cluster VII (83.14) while it was farthest from cluster XI (260.37) followed by cluster IX (197.35).

Cluster VI had only one genotype (L 762). It was nearest to cluster I (72.38) followed by cluster III (92.43) and it was farthest from X (235.53) followed by XI (215.52).

Cluster VII comprised of 7 genotypes. It was nearest to cluster V (83.14) followed by cluster VI (99.21) and it was farthest from cluster XI (273.72) followed by cluster X (225.14).

Cluster VIII was mono-genotypic (P 72-9-37). It was closest to cluster XIII (57.85) followed by cluster V (85.62) and was farthest from cluster XI (266.12) followed by cluster XII (217.22).

Cluster IX was mono-genotypic (SHS 2-4). It was nearest to cluster XI (41.00) followed by cluster I (106.69) and was farthest from cluster X (315.66) followed by cluster XIII (236.30).

Cluster X consisted of five genotypes. It was closest to cluster II (107.25) followed by cluster VIII (143.64) and was farthest from cluster XII (317.26) followed by cluster IX (315.66).

Cluster XI was solitary (GJHV 08/70). It was nearest to cluster IX (41.00) followed by cluster IV (130.33) and was farthest from cluster X (315.32) followed by cluster III (297.04).

Cluster XII was mono-genotypic (L 604). It was closest to cluster IX (112.31) followed by cluster I (113.55) and was farthest from cluster X (317.26) followed by cluster III (250.85).

Cluster XIII was solitary (GTHV 04/13). It was nearest to cluster VIII (57.85) followed by cluster V (101.08) and was farthest from XI (254.97) followed by cluster IX (236.30).

The intra, inter cluster distance values revealed that inter-cluster distance values were greater than intra-cluster distance values. Cluster X (124.02) has maximum intra-cluster distance followed by cluster IV (110.20), cluster VII (92.49), cluster III (67.03) and cluster I (48.38). Eight clusters (cluster II, V, VI, VIII, IX, XI, XII and XIII) were solitary and had no intra-cluster distances. The high intra-cluster distance in cluster X indicates the presence of wide genetic diversity among the genotypes present within this cluster.

Genotypes grouped into the same cluster presumably differ little from one another as the aggregate of characters measured. General notion exists that the larger the divergence between the genotypes, the higher will be the heterosis (Falconer, 1964). Therefore, it would be desirable to attempt crosses between genotypes belonging to distant clusters for getting highly heterotic crosses which are likely to yield a wide range of segregants on which selection can be practiced.

In the present investigation, inter-cluster distances were worked out considering 16 characters and these distances ranged from 41.00 (between cluster IX and XI) to 317.26 (between X and XII).

The inter cluster-distance was maximum between cluster X and XII (317.26) followed by cluster IX and X (315.66), cluster X and XI (315.32), cluster III and XI (297.04), cluster VII and XI (273.72), cluster VIII and XI (266.12), cluster V and XI (260.37), cluster XI and XIII (254.97), cluster III and XII (250.85), cluster IX and XIII (236.60), cluster VI and X (235.53), cluster VII and X (225.14), cluster VIII and XII (217.22) and cluster VI and XI (215.52). This suggests 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 a particular genotype from selected cluster are the two important points to be considered before initiating the crossing programme.

4.3.1.2.1.3 Cluster mean values

The cluster mean values for 16 characters are presented in the Table 4.9. The data indicated a wide range of mean values between the clusters. Days to 50% flowering had a range of 53.00 for cluster XIII to 68.33 for cluster VI; plant height had a range of 107.11 for cluster IX to 135.55 for cluster II; number of monopodia plant⁻¹ ranged from 1.00 for cluster VI to 2.00 for cluster XIII; number of sympodia plant⁻¹ varied from 12.07 for cluster to 17.11 for cluster II; number of bolls plant⁻¹ ranged from 28.11 for cluster IX to 45.32 for cluster III; boll weight varied from 3.45 for cluster VI to 4.74 for cluster VII; lint index ranged from 2.37 for cluster XI to 5.86 for cluster VIII; seed index varied from 5.80 for cluster XI to 10.77 for cluster V; ginning out-turn ranged from 28.07 for cluster IX to 39.75 for cluster XIII; 2.5% span length varied from 19.01 for cluster VI to 22.99 for cluster XII ; micronaire value ranged from 3.03 for cluster XII to 4.09 for cluster II; uniformity ratio varied from 46.22 for cluster XII to 51.03 for cluster VIII; fibre elongation ranged from 4.53 for cluster XIII to 5.29 for cluster X; seed cotton yield plant⁻¹ varied from 99.59 for cluster XIII to 159.83 for cluster III; lint yield plant⁻¹ ranged from 30.76 for cluster XI to 54.79 for cluster III.

High mean values for number of bolls plant⁻¹ were seen in cluster III followed by clusters VI, IV and I and high means for boll weight were observed in cluster VII followed by clusters V, II and IX which are major contributors in improving seed cotton yield plant⁻¹ in cotton. Based on mean values genotypes from these clusters can be used in seed cotton yield improvement programmes.

4.3.1.2.2 *G. barbadense* genotypes

The per cent contribution towards genetic divergence by all the 16 contributing characters is presented in the Table 4.10. The maximum contribution towards genetic divergence was by seed index (18.37) followed by fibre elongation (12.63), 2.5% span length (12.11), seed cotton yield plant⁻¹ (10.60), number of monopodia plant⁻¹ (10.49), micronaire value (7.87), ginning out-turn (6.32), lint yield plant⁻¹ (4.74), lint index (4.21), number of sympodia plant⁻¹ (2.65), boll weight (2.63), uniformity ratio (2.63), days to 50% flowering (2.11) and number of bolls plant⁻¹ (2.11) while, the contribution of the remaining traits was less than one per cent towards genetic divergence.

4.3.1.2.2.1 Grouping of genotypes into various clusters

The 20 *barbadense* genotypes were grouped into seven clusters using the Tocher's method (Table 4.11). The mutual relationships among the clusters were presented diagrammatically in Fig. 4.3. The distribution of 20 genotypes into seven clusters was at random with maximum number of genotypes in cluster II (6 genotypes). Clusters I and IV were comprised of five genotypes each. Clusters III, V, VI and VII were solitary clusters with nil intra- cluster D² values.

4.3.1.2.2.2 Average intra and inter- cluster D² values

The average intra and inter- cluster D² values estimated as per the procedure given by Singh and Chowdhary (1977) are presented in the Table 4.12. Based on D² values, the twenty genotypes were grouped into seven clusters. The proximity and divergence among seven clusters are given in the Table 4.13 and Fig. 4.4.

Intra-cluster D² values ranged from zero (cluster III, V, VI and VII) to 55.49 (cluster IV), while the inter-cluster D² values ranged from 57.57 (cluster III and IV) to 263.35 (cluster III and VI).

Cluster I comprised of five genotypes. It was nearest to cluster VI (69.32) followed by cluster II (78.56) and farthest from cluster III (148.77) followed by cluster V (133.68).

Cluster II consisted of six genotypes was the largest of all clusters. It was nearest to cluster V (71.97) followed by cluster III (82.27) and farthest from cluster VI (168.26) followed by cluster IV (105.98).

Cluster III was mono-genotypic (GSB 39). It was closest to cluster IV (57.57) followed by cluster II (82.27) and farthest from VI (263.35) followed by cluster V (175.60).

Cluster IV comprised of five genotypes. It was nearest to the cluster III (57.57) followed by cluster IV (105.98) and farthest from VI (236.01) followed by cluster V (212.57).

Cluster V was solitary (TCB 51) and nearest to the cluster II (71.97) followed by cluster VII (132.23) while farthest from cluster IV (212.57) followed by cluster VI (208.17).

Cluster VI consisted of one genotype (TCB 37). It was closest to the cluster I (69.32) followed by cluster II (168.26) and farthest from cluster III (263.35) followed by cluster IV (236.01).

Cluster VII was solitary (RhCB 011) and nearest to cluster I (86.62) followed by cluster III (98.92) and farthest from V (203.82) followed by cluster VI (181.54).

The maximum intra-cluster distance was recorded by cluster IV (55.49) followed by cluster II (42.93) and cluster I (38.76). Clusters III, V, VI and VII had zero intra-cluster distances and mono-genotypic. Presence of high genetic diversity among the genotypes present in the cluster IV indicated by high intra-cluster distance.

The maximum inter-cluster distance (263.35) was observed between cluster III and VI followed by 236.01 (clusters IV and VI), 212.57 (clusters IV and V), 208.17 (clusters V and VI) and 203.82 (clusters V and VII). The minimum inter-cluster distance of 57.57 was recorded between cluster III and IV. These results revealed presence of wide genetic diversity between the clusters.

4.1.2.2.3 Cluster mean values

The clusters mean values for all the sixteen characters are presented in the Table 4.14. Cluster I exhibited high mean values for number of sympodia plant⁻¹ (18.58), boll weight (2.84) and ginning out-turn (33.63); Cluster III recorded high mean values for days to 50% flowering (73.00); cluster V recorded high mean for number of monopodia plant⁻¹ (2.00) and uniformity ratio (48.31); cluster VI recorded high mean for seed index (11.20), lint index (5.67), 2.5% span length (37.83), bundle strength (29.49) and fibre

elongation (5.54); cluster VII recorded high mean for plant height (149.34), number of bolls plant⁻¹ (57.22), micronaire value (3.20), seed cotton yield plant⁻¹ (133.20) and lint yield plant⁻¹ (41.59).

Cluster mean values revealed that cluster I had high mean values for number of sympodia plant⁻¹ and boll weight and cluster VII had high mean value for number of bolls plant⁻¹. So genotypes from these clusters can be used for cotton yield improvement. High mean values for 2.5% span length and bundle strength were observed in Cluster VI followed by clusters IV and I. So genotypes from these clusters can be used for cotton fibre quality improvement.

The success and usefulness of Mahalanobis' D² analysis in quantifying genetic divergence has been studied by Kumar *et al.* (2000), Jain and Yadav (2001), Gururajan and Manickam (2002), Altaher and Singh (2003b), Padmavathi (2008), Gopinath *et al.* (2009), Lakshmi *et al.* (2009), Rajamani and Rao (2009), Satish *et al.* (2009a), Srinivasulu *et al.* (2010b), Basavaraddi and Katageri (2011), Asha *et al.* (2013b), Haritha and Ahamed (2013), Kavithamani *et al.* (2013), Malik *et al.* (2013), Araujo *et al.* (2014), Bhailume *et al.* (2014), Ravikesan *et al.* (2014) and Tulasi *et al.* (2014).

4.3.2 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 D² 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 16 new variables for 70 *hirsutum* and 20 *barbadense* genotypes without changing their relative positions. These 16 new variables are the principal components (PC₁, PC₂,.....PC₁₆). Each principal component is a linear combination of the 16 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 PC₂ is as large as possible, subject to the constraint that PC₁ and PC₂ are uncorrelated. The process was continued to create 16 principal components, but PC's having eigen value less than one is not having any practical significance (Legendre and Legendre, 1984).

Principal components (eigen value greater than one), eigen values (Latent Root), per cent variability, cumulative per cent variability and component loading of different characters for 70 *hirsutum* and 20 *barbadense* genotypes are presented in Tables 4.15 and 4.16. Results of PCA are discussed here under.

4.3.2.1 *G. hirsutum* genotypes

Results obtained from PCA on the correlation matrix of the traits reduce the dimensionality of the data set by creating six significant principal components having eigen value more than one. In the present investigation, the first six principal components with eigen values more than one contributed 74.62 per cent towards the total variability. The principal component with eigen values less than one were considered as non-significant.

It was therefore inferred that the essential features of data set had been represented in the first six principal components. The first principal component (PC₁) contributed maximum towards variability (19.83). The characters viz., plant height (-0.34), number of monopodia plant⁻¹ (-0.24), number of sympodia plant⁻¹ (-0.32), seed index (0.23), 2.5% span length (0.43), micronaire value (-0.34), fibre elongation (-0.25), uniformity ratio (0.22) and lint yield plant⁻¹ (-0.43) explained the maximum variance in the first principal component (PC₁) signifying their importance in yield.

The second principal component (PC₂) described 13.79 per cent of total variance and the characters viz., plant height (0.24), number of sympodia plant⁻¹ (0.20), number of bolls plant⁻¹ (0.29), boll weight (0.40), lint index (0.26), seed index (0.41), 2.5% span

length (0.21), bundle strength (0.33), uniformity ratio (-0.31), fibre elongation (-0.21) and seed cotton yield plant⁻¹ (0.28) explained the maximum variance in the second principal component (PC₂) signifying their importance.

The third principal component (PC₃) described 13.17 per cent contribution towards the total variability. The characters viz., number of sympodia plant⁻¹ (0.23), number of bolls plant⁻¹ (0.36), lint index (-0.40), seed index (-0.38), micronaire value (-0.38), fibre elongation (-0.44) and lint yield plant⁻¹ (0.26) exhibited the maximum variance in this principal component.

The fourth principal component (PC₄) was characterized by 10.91 per cent contribution towards the total variability. The characters viz., number of bolls plant⁻¹ (0.24), lint index (0.38), ginning out-turn (-0.56), bundle strength (-0.33), uniformity ratio (0.22), seed cotton yield plant⁻¹ (-0.42) showed the maximum variance in this principal component.

The fifth principal component (PC₅) characterized by high loading of days to 50% flowering (0.53), number of monopodia plant⁻¹ (0.36), number of sympodia plant⁻¹ (0.27), number of bolls plant⁻¹ (-0.33), boll weight (0.43), 2.5% span length (0.21) and bundle strength (-0.26). Contribution of this principal component towards the total variability was 9.49 per cent.

The sixth principal component (PC₆) described 7.43 per cent of total variance. The characters viz., days to 50% flowering (0.41), number of monopodia plant⁻¹ (-0.27), number of sympodia plant⁻¹ (0.39), boll weight (-0.25), 2.5% span length (-0.25), uniformity ratio (0.23) and seed cotton yield plant⁻¹ (0.56) showed the maximum variance in this principal component.

The analysis thus identified the maximum contributing variables *i.e.*, number of monopodia plant⁻¹, number of sympodia plant⁻¹, number of bolls plant⁻¹, boll weight, lint index, seed index, 2.5% span length, bundle strength, uniformity ratio, fibre elongation and seed cotton yield plant⁻¹. It is important to study the variance as the relative contribution than the signs (indicative of direction) in principal component analysis.

4.3.2.2 *G. barbadense* genotypes

In the present study, the first six principal components with eigen values more than one contributed 92.05 per cent towards the total variability. It indicates the essential features of data set had been represented in the first six principal components.

The first principal component contributed maximum towards variability (30.22%). The characters viz., number of sympodia plant⁻¹ (-0.35), boll weight (-0.31), lint index (-0.41), seed index (-0.42), ginning out-turn (-0.27), bundle strength (-0.28), fibre elongation (-0.22), seed cotton yield plant⁻¹ (0.28) and lint yield plant⁻¹ (0.24) explained the maximum variance in the first principal component (PC₁).

The second principal component (PC₂) described 18.92 per cent of total variance. The characters viz., number of monopodia plant⁻¹ (0.39), ginning out-turn (0.39), uniformity ratio (0.27), plant height (-0.25), 2.5% span length (-0.49) and fibre elongation (-0.46) explained the maximum variance in the second principal component (PC₂) signifying their importance.

The third principal component (PC₃) was characterized by 14.29 per cent contribution towards the total variability. The characters viz., plant height (0.28), number of monopodia plant⁻¹ (-0.29), number of bolls plant⁻¹ (0.44), boll weight (0.33), 2.5% span length (-0.21), micronaire value (0.49), uniformity ratio (0.28), seed cotton yield plant⁻¹ (0.24) and lint yield plant⁻¹ (0.28) showed the maximum variance in this principal component.

The fourth principal component (PC₄) was characterized by high loading of days to 50% flowering (0.52), number of bolls plant⁻¹ (-0.28), bundle strength (0.32), micronaire value (0.26), seed cotton yield plant⁻¹ (0.38) and lint yield plant⁻¹ (-0.41). Contribution of this principal component towards the total variability was 13.56 per cent.

Similarly, principal component fifth (PC₅) and sixth (PC₆) contributed 8.88 and 6.20 per cent, respectively, towards total variability. High loading value of days to 50% flowering (0.34), plant height (-0.37), number of monopodia plant⁻¹ (0.24), number of sympodia plant⁻¹ (-0.26), number of bolls plant⁻¹ (0.31), lint index (0.23), bundle strength (0.34), uniformity ratio (-0.51) and lint yield plant⁻¹ (0.26) in PC₅ and plant height (0.51), boll weight (0.27), ginning out-turn (0.33), bundle strength (-0.38), micronaire value (-0.29), uniformity ratio (-0.32), seed cotton yield plant⁻¹ (0.26) and lint yield plant⁻¹ (-0.20) in PC₆ was observed.

The analysis thus identified the maximum contributing variables *i.e.*, plant height, number of monopodia plant⁻¹, number of bolls plant⁻¹, bundle strength, uniformity ratio, seed cotton yield plant⁻¹ and lint yield plant⁻¹.

The PCA scores for 70 *hirsutum* and 20 *barbadense* 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 Tables 4.17 and 4.18.

These three PCA scores for 70 *hirsutum* and 20 *barbadense* genotypes were plotted in graph to get two dimensional (2D) and three dimensional (3D) scatter diagrams (Fig. 4.5 and 4.6 and Fig. 4.7 and 4.8) which revealed diversity between the genotypes. Rajamani and Rao (2009), Lakshmi *et al.* (2009), Srinivasulu (2009), Venkateswarulu *et al.* (2010b), Asha *et al.* (2013b), Haritha and Ahamed (2013) and Tulasi *et al.* (2014) studied the utilization of principal component analysis in cotton.

Based on the cluster mean values and *per se* performance for important traits *viz.*, number of bolls plant⁻¹, boll weight and seed cotton yield plant⁻¹ the genotypes, NDLH 1938, H 1442, ADB 542, ADB 532, WGCV 48, MR 786, TSH 0250, BS 37, SCS 793, MCU 5, L 1058 and L762 were selected as female parents (lines) from *hirsutum* group. On the other hand *barbadense* genotypes, GSB 40, DB 16, DB 11, GSB 41, TCB 37 and SUVIN were identified as male parents (testers) as they have higher cluster mean and *per se* performance values for 2.5% span length and bundle strength. Hence, these genotypes (12 lines + 6 testers) were recommended to develop potential heterotic inter-specific hybrids by crossing in line × tester fashion.

4.4 POOLED ANALYSIS OF VARIANCE

The pooled mean performance of parents and 72 inter-specific hybrids is presented in Annexure III. Pooled analysis of variance over three locations showed highly significant mean sum of squares for all the characters studied indicating significant genetic differences among the genotypes. Pooled analysis of variance over three locations for 16 characters is presented in the Table 4.19.

4.5 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE AS PER CENT OF MEAN (POOLED)

The estimates of mean, range, phenotypic coefficient of variation (PCV), genotypic coefficient of variation (GCV), heritability ($h^2_{(b)}$) in broad sense and genetic advance as per cent of mean (GAM) were calculated over three locations and are presented in the Table 4.20 and described character- wise here under.

4.5.1 Days to 50% Flowering

The number of days to 50% flowering ranged from 53.66 (H 1442) to 75.22 days (DB 11) with a mean of 64.01 days. The estimates of PCV and GCV were low (6.87 and 5.56) indicating less variation among the genotypes studied. Higher PCV value over GCV revealed that variation is not only due to the genotypes but also due to the influence of environment and therefore selection will be misleading. Similar findings were also reported by Neelima *et al.* (2008), Sarada *et al.* (2010), Asha *et al.* (2013a) and Dhivya *et al.* (2014).

Moderate heritability (65.40) coupled with low genetic advance as per cent of mean (9.27) was observed for days to 50% flowering indicating the predominance of non-additive type of gene action in the inheritance of this trait. The desired results may not be obtained by simple selection. However, Muraleedhar (2005), Mahantesh (2009), Patel *et al.* (2013b), Dhivya *et al.* (2014) and Erande *et al.* (2014) noticed high heritability and low genetic advance as per cent of mean for this trait. This may be due to differences in the material and environments studied.

4.5.2 Plant Height (cm)

The range of variation for this character varied from 111.13 (ADB 542) to 194.53 cm (NDLH 1938 × GSB 40) with a mean of 163.19 cm. The estimates of PCV and GCV (14.83 and 11.47) were moderate and there is large difference between them indicating the influence of environment. These results are in conformity with the findings of Kulkarni *et al.* (2011), Erande *et al.* (2014), Farooq *et al.* (2014) and Ahsan *et al.* (2015).

Moderate heritability (59.80) coupled with moderate genetic advance as per cent of mean (18.28) was observed for plant height revealing the preponderance of non-additive gene action. It can be exploited through heterosis breeding rather than simple

selection procedures. In contrary to this, Dhivya *et al.* (2014), Erande *et al.* (2014), Farooq *et al.* (2014) and Khan *et al.* (2015) reported high heritability coupled with high genetic advance for this trait.

4.5.3 Number of Monopodia Plant⁻¹

The number of monopodia plant⁻¹ ranged from 1.00 (MCU 5) to 3.20 (ADB 532 × GSB 41) with a mean of 2.26. The estimates of PCV and GCV (33.36 and 21.37) were high indicating more variation among the genotypes evaluated. The difference between PCV and GCV is large indicating the influence of environment. These results were in accordance with the findings of Mohan (2011), Hafiz *et al.* (2013), Paramjit and Buttar (2013) and Khan *et al.* (2015).

Moderate heritability (41.10) and high genetic advance as per cent of mean (28.22) was registered for this trait which may be due to the operation of additive type of gene action. This character can be improved through simple selection procedures. Asha *et al.* (2013a), Paramjit and Buttar (2013), Patel *et al.* (2013b) and Erande *et al.* (2014) noticed high heritability coupled with high genetic advance for this character. This may be due to differences in the material and environments studied.

4.5.4 Number of Sympodia Plant⁻¹

The number of sympodia plant⁻¹ ranged from 13.77 (TSH 0250) to 31.42 (MR 786 × GSB 41) with a mean of 22.06. The estimates of PCV and GCV (18.53 and 14.16) were moderate and difference between them is high indicating the influence of environment. These results are in agreement with the reports of Girase and Mehetre (2002), Vinodhana *et al.* (2013) and Farooq *et al.* (2014).

Moderate heritability (58.40) coupled with high genetic advance as per cent of mean (28.56) was noticed for this trait indicating the role of additive type of gene action in the inheritance. In contrary to this, Kaushik and Kapoor (2006), Verma *et al.* (2006), An *et al.* (2008), Ravikesavan *et al.* (2008), Lakshmi *et al.* (2012), Hafiz *et al.* (2013), Dhivya *et al.* (2014) and Khan *et al.* (2015) recorded high heritability coupled with high genetic advance for this character. This may be due to differences in the material and environments studied.

4.5.5 Number of Bolls Plant⁻¹

The number of bolls plant⁻¹ ranged from 33.98 (MCU 5) to 79.98 (BS 37 × SUVIN) with an average of 61.01. The estimates of PCV and GCV (25.20 and 19.04) were high and moderate. The difference between PCV and GCV is high indicating the influence of environment. Similar results were also observed by Kaushik and Kapoor (2006), Kishore *et al.* (2011), Mohan (2011), Dhivya *et al.* (2014), Ahsan *et al.* (2015) and Khan *et al.* (2015).

Moderate heritability (57.10) associated with high genetic advance as per cent of mean (29.65) revealing the preponderance of additive type of gene action. Mahantesh (2009), Bazi (2011), Elango *et al.* (2012), Hafiz *et al.* (2013), Ahsan *et al.* (2015) and Khan *et al.* (2015) noticed high heritability and high genetic advance as per cent of mean for this trait.

4.5.6 Boll Weight (g)

The boll weight ranged from 2.40 (TCB 37) to 4.21 g (TSH 0250 × GSB 40) with a mean of 3.33 g. The estimates of PCV and GCV (14.76 and 11.76) were moderate and difference between them is high indicating the role of environment in the existing variation. These results are in agreement with the results of Vinodhana *et al.* (2013), Dhivya *et al.* (2014) and Erande *et al.* (2014).

High heritability (63.50) and moderate genetic advance as per cent of mean (19.32) were recorded for this trait indicating the operation of both additive and non-additive gene actions in the inheritance of this trait. Further improvement of this trait may not be possible through simple selection. In contrary to this, Ravikesavan *et al.* (2008), Bazi (2011), Haritha *et al.* (2012), Ahsan *et al.* (2015) and Khan *et al.* (2015) recorded high heritability coupled with high genetic advance. This clearly demonstrates that inheritance pattern of same trait varies based on the material and environments studied.

4.5.7 Lint index (g)

The range of variation observed for this character was from 3.91 (SCS 793) to 6.07 g (L 1058 × DB 16) with a mean of 5.03 g. The estimates of PCV and GCV (12.49 and 9.49) were moderate and low and variation between them is high exhibiting major

role of environment in the existing variation. These findings are in accordance with the reports of Neelima *et al.* (2008), Naqib *et al.* (2010), Rajanna (2010), Kulkarni *et al.* (2011) and Vinodhana *et al.* (2013).

Moderate heritability (57.70) coupled with moderate genetic advance as per cent of mean (14.85) was observed for lint index indicating the preponderance of non-additive gene action. Improvement of this character would be possible through heterosis breeding rather than simple selection. Similar findings were also reported by Sakthi *et al.* (2007), Rajanna (2010), Kulkarni *et al.* (2011) and Khan *et al.* (2015).

4.5.8 Seed index (g)

Seed index ranged between 8.27 (TSH 0250) and 14.33 g (ADB 532 × GSB 40) with a mean of 12.17 g. The estimates of PCV and GCV (13.48 and 9.64) were moderate and low and difference between them is high revealing the predominant role of environment in the existing variation. Srinivasulu (2009), Rajanna (2010), Vinodhana *et al.* (2013), Erande *et al.* (2014) and Ahsan *et al.* (2015) also reported similar results.

Moderate heritability (51.20) and moderate genetic advance as per cent of mean (14.22) were observed revealing the role of non-additive type of gene action in the expression of this character and may be exploited through heterosis breeding. These results are in conformity with the findings of Kulkarni *et al.* (2011), Haritha *et al.* (2012), Vinodhana *et al.* (2013) and Khan *et al.* (2015).

4.5.9 Ginning out-turn (%)

The variation among the genotypes for this trait ranged from 23.80 (BS 37 × TCB 37) to 33.48 per cent (TSH 0250 × GSB 40) with a mean of 29.52 per cent. The estimates of PCV and GCV (9.90 and 7.50) were low indicating less variation among the genotypes studied. The difference between PCV and GCV is high indicating the influence of environment in the existing variation. These results are in harmony with the reports of Mohan (2011), Dhivya *et al.* (2014), Farooq *et al.* (2014) and Khan *et al.* (2015).

Moderate heritability (57.40) coupled with moderate genetic advance as per cent of mean (11.72) was recorded for this trait indicating the preponderance of non-additive gene action. Further improvement of this character would be possible through heterosis breeding. These findings are in accordance with the results of Bazi (2011), Asha *et al.* (2013a), Vinodhana *et al.* (2013), Farooq *et al.* (2014) and Khan *et al.* (2015).

4.5.10 2.5% span length (mm)

The mean 2.5% span length ranged from 26.48 (SCS 793) to 37.96 mm (MCU 5 × SUVIN) with a mean of 33.92 mm. The estimates of PCV and GCV (8.82 and 7.92) were low indicating less variation among the genotypes evaluated. Similar results were also noticed by Neelima *et al.* (2008), Kishore *et al.* (2011), Kulkarni *et al.* (2011), Asha *et al.* (2013a), Vinodhana *et al.* (2013), Dhivya *et al.* (2014) and Erande *et al.* (2014).

High heritability (80.60) and moderate genetic advance as per cent of mean (14.66) was observed for this trait indicating the operation of both additive and non-additive gene actions. Further, improvement of this character may not be possible through simple selection. Rao and Reddy (2001), Bazi (2011), Elango *et al.* (2012), Dhivya *et al.* (2014) and Erande *et al.* (2014) noticed high heritability coupled with high genetic advance as per cent of mean for 2.5% span length. This may be due to differences in the material and environments studied.

4.5.11 Uniformity ratio

The range of variation was from 43.87 (MCU 5 × DB 16) to 50.07 per cent (MR 786) with a mean of 46.13 per cent for this character. The estimates of PCV and GCV (3.93 and 2.70) were low. These results are in agreement with the findings of Kishore *et al.* (2011), Mohan (2011), Vinodhana *et al.* (2013), Erande *et al.* (2014) and Khan *et al.* (2015).

Moderate heritability (47.10) coupled with low genetic advance as per cent of mean (3.81) was observed for uniformity ratio indicating the role of non-additive type of gene action. Further improvement of this trait would be possible through heterosis breeding. Elango *et al.* (2012), Haritha *et al.* (2012), Asha *et al.* (2013a), Erande *et al.* (2014) and Khan *et al.* (2015) observed high heritability with low genetic advance as per cent of mean for this trait.

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

The range of variation for this character was from 2.53 (TSH 0250 $\times$ GSB 41) to 4.49 10^{-6} g/inch (L 762) with a mean of 3.02 10^{-6} g/inch. The estimates of PCV and GCV (15.71 and 14.13) were moderate. These results are in harmony with the findings of Sarada *et al.* (2010), Vinodhana *et al.* (2013) and Khan *et al.* (2015).

High heritability (80.90) coupled with high genetic advance as per cent of mean (26.20) was recorded for this trait making selection effective due to additive gene action. Similar findings were also reported by Bazi (2011), Asha *et al.* (2013a), Vinodhana *et al.* (2013) and Erande *et al.* (2014).

4.5.13 Bundle strength (g/tex)

The range of variation for bundle strength was from 19.34 (H 1442) to 30.17 g/tex (MCU 5 $\times$ GSB 40) with a mean of 26.29 g/tex. The estimates of PCV and GCV (9.70 and 8.57) were low indicating less variation among the genotypes studied. Higher PCV value than GCV revealed that variation is not only due to the genotypes but also due to the influence of environment and therefore selection will be misleading. Neelam *et al.* (2002), Altaher and Singh (2003a), Srinivasulu (2009), Rajanna (2010) and Asha *et al.* (2013a) also reported similar findings for this character.

High heritability (78.10) coupled with moderate genetic advance as per cent of mean (15.60) was recorded for this trait indicating the operation of both additive and non-additive gene actions in the inheritance of this character and desired results may not be obtained by simple selection. However, Sambamurthy *et al.* (2006), An *et al.* (2008), Asha *et al.* (2013a) and Vinodhana *et al.* (2013) recorded high heritability coupled with high genetic advance as per cent of mean for this trait. This may be due to differences in the material and environments studied.

4.5.14 Fibre elongation (%)

The range of variation was from 4.54 (TSH 0250 $\times$ SUVIN) to 5.29 per cent (DB 11) with a mean of 4.93 per cent for this character. The estimates of PCV and GCV (4.43 and 2.80) were low indicating less variation among the genotypes studied. Higher PCV value than GCV revealed that variation is not only due to the genotypes but also due to the influence of environment and therefore selection will be misleading. These results are in accordance with the findings of Rajanna (2010), Bazi (2011), Kulkarni *et al.* (2011), Elango *et al.* (2012) and Asha *et al.* (2013a).

Moderate heritability (40.00) coupled with low genetic advance as per cent of mean (3.65) was observed for fibre elongation indicating that this trait is controlling by non-additive gene action and further improvement of this character would be possible through heterosis breeding rather than simple selection. Similar results were also reported by Kulkarni *et al.* (2011), Elango *et al.* (2012) and Asha *et al.* (2013a).

4.5.15 Seed cotton yield Plant⁻¹ (g)

The range of variation was from 88.90 (TCB 37) to 253.36 g (H 1442 × GSB 41) with a mean of 172.27 g. The estimates of PCV and GCV (28.43 and 21.74) were high indicating more variation among the genotypes studied and difference between them is large revealing the influence of environment. Similar results were also reported by Kaushik and Kapoor (2006), Kishore *et al.* (2011), Asha *et al.* (2013a), Farooq *et al.* (2014), Ahsan *et al.* (2015) and Khan *et al.* (2015).

High heritability (58.50) coupled with high genetic advance as per cent of mean (34.24) was observed for this trait making selection effective due to additive gene action. Similar findings were also reported by Elango *et al.* (2012), Haritha *et al.* (2012), Asha *et al.* (2013a), Paramjit and Buttar (2013), Vinodhana *et al.* (2013), Farooq *et al.* (2014), Ahsan *et al.* (2015) and Khan *et al.* (2015).

4.5.16 Lint yield Plant⁻¹ (g)

The mean variation ranged from 25.26 (SUVIN) to 83.71 g (H 1442 × GSB 41) with an average of 51.01 g. The PCV and GCV estimates (30.91 and 24.47) were high indicating more variation among the genotypes evaluated and difference between them is large indicating the influence of environment. These results are in conformity with the findings of Patnaik *et al.* (2004), Rajanna (2010) and Erande *et al.* (2014).

High heritability (62.70) and high genetic advance as per cent of mean (39.91) were recorded for this trait making selection effective due to the preponderance of additive gene action. These findings are in conformity with the results of Mahantesh (2009), Rajanna (2010), Elango *et al.* (2012) and Erande *et al.* (2014).

The perusal of results revealed that wide variability was observed for number of monopodia plant⁻¹, number of bolls plant⁻¹, seed cotton yield plant⁻¹ and lint yield plant⁻¹ which indicates their amenability towards directional selection. The traits viz., plant height, number of sympodia plant⁻¹, boll weight and micronaire value recorded moderate variability, while the other traits exhibited low variability.

High heritability coupled with high genetic advance as per cent of mean was observed in case of micronaire value, seed cotton yield plant⁻¹ and lint yield plant⁻¹ which suggests the role of additive gene action in the inheritance of these traits and directional selection could be profitably exploited. High heritability and moderate genetic advance as per cent of mean was observed for boll weight, 2.5% span length and bundle strength revealing the involvement of both additive and non-additive gene actions in the inheritance of these traits. Further, improvement of these traits would be possible through breeding procedures like biparental mating, diallel selective mating system or cyclic hybridization.

Thus, moderate heritability and moderate genetic advance as per cent of mean were recorded in case of plant height, ginning out-turn, lint index and seed index while days to 50% flowering, uniformity ratio and fibre elongation exhibited moderate heritability coupled with low genetic advance as per cent of mean. These results are clearly showing the operation of non-additive gene action and can be exploited through heterosis breeding or population improvement programmes.

4.6 CHARACTER ASSOCIATION

Seed cotton yield is a polygenically controlled complex character resulting from multiplicative interaction of yield components. The cumulative effects of such characters determine the dependent variable yield. These characters play an important role in modifying the system of yield as a whole in magnitude as well as in direction. Further, direct selection for seed cotton yield is not effective as it is a complex quantitative character and much influenced by the environment. The change in one character brings about a series of changes in other characters, since they are interrelated. Unfavourable associations between the desired attributes under selection may limit genetic advance. Hence, the study of correlation between yield and yield components are of considerable importance in selection programmes.

The phenotypic and genotypic correlation coefficients between seed cotton yield and its component characters and among themselves were worked out over three locations (pooled) and were furnished in the Table 4.21. The results are discussed character wise here under.

4.6.1 Days to 50% Flowering

Days to 50% flowering showed positive significant association with seed index (0.1921**) and recorded significant negative association with plant height (-0.0919*) at genotypic level only. The significant positive association with 2.5% span length (0.3362** and 0.2380**), bundle strength (0.3613** and 0.2373**) and fibre elongation (0.3037** and 0.1570**) indicates that increase in one character will lead to increase in second and *vice versa* and significant negative association with number of sympodia plant⁻¹ (-0.2368** and -0.1375**), number of bolls plant⁻¹ (-0.2298** and -0.1031**), boll weight (-0.6085** and -0.4391**), ginning out turn % (-0.2403** and -0.1260**), uniformity ratio (-0.3074** and -0.1775**), micronaire value (-0.1310** and -0.0977**), seed cotton yield plant⁻¹ (-0.4835** and -0.2890**) and lint yield (-0.5206** and -0.3124**) where increase in one variable cause decrease in another variable and *vice versa* at both genotypic and phenotypic levels. These results are in conformity with the earlier reports of Reddy (2001), Muraleedhar (2005), Neelima *et al.* (2005), Pratap *et al.* (2007), Vijayalaxmi *et al.* (2008), Venkateswaralu *et al.* (2010a), Rajanna *et al.* (2011), Rajamani *et al.* (2013) and Kumar *et al.* (2014).

4.6.2 Plant Height

At genotypic level only this trait showed significant positive association with fibre elongation (0.1387**). Whereas, it exhibited significant positive association with number of monopodia plant⁻¹ (0.6043** and 0.2988**), number of sympodia plant⁻¹ (0.8647** and 0.6930**), number of bolls plant⁻¹ (0.8233** and 0.6842**), lint index (0.5191** and 0.3075**), seed index (0.7469** and 0.4667**), 2.5% span length (0.6727** and 0.4518**), bundle strength (0.6495** and 0.4425**), seed cotton yield plant⁻¹ (0.6917** and 0.5815**) and lint yield plant⁻¹ (0.5600** and 0.4929**) and negative significant association with boll weight (-0.1332** and -0.0851*), ginning out-turn (-0.2650** and -0.2138**), uniformity ratio (-0.5528** and -0.2877**) and micronaire value (-0.7752** and -0.5493**) at both genotypic and phenotypic levels. The positive association of seed cotton yield plant⁻¹ with plant height at both genotypic and phenotypic levels suggests that the breeder should prefer long stature genotypes rather than short stature genotypes for increased seed cotton yield. The magnitude and direction of association was similar to the previous findings by Rajanna *et al.* (2011), Chitti *et al.* (2014), Erande *et al.* (2014), Farooq *et al.* (2014) and Kumar *et al.* (2014).

4.6.3 Number of Monopodia Plant⁻¹

This trait exhibited significant negative association with boll weight (-0.1082**) at genotypic level and with micronaire value (-0.3602**) at phenotypic level, respectively. Number of monopodia plant⁻¹ recorded significant positive association with number of sympodia plant⁻¹ (0.5872** and 0.3064**), number of bolls plant⁻¹ (0.5827** and 0.3393**), lint index (0.1939** and 0.1996**), seed index (0.5851** and 0.3784**), 2.5% span length (0.5770** and 0.3486**), bundle strength (0.5155** and 0.3139**), seed cotton yield plant⁻¹ (0.4712** and 0.2957**) and lint yield plant⁻¹ (0.3278** and 0.2249**) indicating possibility for simultaneous improvement of these traits and significant negative association with ginning out-turn (-0.3864** and -0.1805**) and uniformity ratio (-0.4527** and -0.1577**) at both genotypic and phenotypic levels.

The selection for high seed cotton yield plant⁻¹ based on number of monopodia plant⁻¹ is beneficial as their association is significantly positive at both genotypic and phenotypic levels. Rajanna (2010), Mohan (2011), Hafiz *et al.* (2013), Paramjit and Buttar (2013), Chitti *et al.* (2014), Erande *et al.* (2014), Kumar *et al.* (2014) and Ranjan *et al.* (2014) also reported similar correlations for these traits.

4.6.4 Number of Sympodia Plant⁻¹

This trait showed significant positive association with fibre elongation (0.1271**) at genotypic level only. Whereas, it exhibited significant positive association with number of bolls plant⁻¹ (0.8672** and 0.6713**), lint index (0.4847** and 0.3232**), seed index (0.6457** and 0.4553**), 2.5% span length (0.5903** and 0.3940**), bundle strength (0.5841** and 0.3913**), seed cotton yield plant⁻¹ (0.7804** and 0.6027**) and lint yield plant⁻¹ (0.6699** and 0.5270**) indicating possibility for simultaneous improvement of these traits and significant negative association with ginning out-turn (-0.2038** and -0.1783**), uniformity ratio (-0.4414** and -0.2254**) and micronaire value (-0.6462** and -0.4663**) at both genotypic and phenotypic levels, respectively.

The selection for high seed cotton yield plant⁻¹ based on number of sympodia plant⁻¹ is beneficial as their association is significantly positive at both genotypic and phenotypic levels. Similar trends were also evident from the studies of Rajanna *et al.* (2011), Vinodhana *et al.* (2013), Chitti *et al.* (2014), Erande *et al.* (2014) and Khan *et al.* (2015).

4.6.5 Number of Bolls Plant⁻¹

Number of bolls plant⁻¹ recorded significant positive association with lint index (0.4447** and 0.2578**), seed index (0.5363** and 0.3137**), 2.5% span length (0.5019** and 0.3194**), bundle strength (0.5474** and 0.3547**), fibre elongation (0.2266** and 0.1001**), seed cotton yield plant⁻¹ (0.8693** and 0.8539**) and lint yield plant⁻¹ (0.7564** and 0.7735) and significant negative association with boll weight (-0.0814* and -0.0830*), ginning out-turn (-0.1332** and -0.1000**), uniformity ratio (-0.3566** and -0.1768**) and micronaire value (-0.5906** and -0.4020**) at both genotypic and phenotypic levels indicating selection for high seed cotton yield plant⁻¹ based on number of bolls plant⁻¹ is beneficial. Similar correlation reports were earlier observed by Vijayalaxmi *et al.* (2008) Rajanna *et al.* (2011), Hafiz *et al.* (2013), Vinodhana *et al.* (2013), Chitti *et al.* (2014), Farooq *et al.* (2014) and Kumar *et al.* (2014).

4.6.6 Boll Weight

At genotypic level only this trait showed significant negation association with fibre elongation (-0.1702**). While it exhibited significant positive association with lint index (0.1307** and 0.1012**), ginning out-turn (0.4652** and 0.2348**), uniformity ratio (0.5040** and 0.2927**), micronaire value (0.4036** and 0.2670**), seed cotton yield plant⁻¹ (0.4115** and 0.4136**) and lint yield (0.5147** and 0.4541**) and significant negative association with seed index (-0.3710** and -0.1321**), 2.5 % span length (-0.5355** and -0.3753**) and bundle strength (-0.5332** and -0.3431**) at both genotypic and phenotypic levels. The meaningful association of seed cotton yield plant⁻¹ with boll weight can be exploited in selection programmes leading towards the improvement of cotton varieties. These results were in agreement with the reports of Vinodhana *et al.* (2013), Chitti *et al.* (2014), Erande *et al.* (2014), Kumar *et al.* (2014) and Khan *et al.* (2015).

4.6.7 Lint index

At both genotypic and phenotypic levels, this character showed significant positive association with seed index (0.3738** and 0.4075**), ginning out-turn (0.5016** and 0.4747**), 2.5 % span length (0.3289** and 0.2503**), bundle strength (0.3678** and 0.2416**), fibre elongation (0.3103** and 0.1643**), seed cotton yield plant⁻¹ (0.5070** and 0.3146**) and lint yield plant⁻¹ (0.6133** and 0.4366**).

indicating selection based on lint index would be beneficial and significant negative association with uniformity ratio (-0.2228** and -0.1019**) and micronaire value (-0.2629** and -0.1926**), respectively. This is clearly revealing selection for high seed cotton yield plant⁻¹ based on lint index is beneficial. Similar type of results were also reported by Sambamurthy *et al.* (2006), Rajanna *et al.* (2011), Rajamani *et al.* (2013), Chitti *et al.* (2014) and Kumar *et al.* (2014).

4.6.8 Seed index

This trait showed highly significant positive association with 2.5% span length (0.8153** and 0.5629**), bundle strength (0.7713** and 0.5186**) and seed cotton yield plant⁻¹ (0.3129** and 0.2382**) indicating close association of these characters with seed index and recorded significant negative association with ginning out-turn (-0.6123** and -0.5977**), uniformity ratio (-0.6799** and -0.3162**) and micronaire value (-0.8114** and -0.5299**) at both genotypic and phenotypic levels. The selection for high seed cotton yield plant⁻¹ based on seed index is beneficial as their association is significantly positive at both genotypic and phenotypic levels. These results were in agreement with the reports of Rajanna *et al.* (2011), Rajamani *et al.* (2013), Kumar *et al.* (2014) and Ranjan *et al.* (2014).

4.6.9 Ginning out-turn

At genotypic level this trait showed significant positive association with seed cotton yield plant⁻¹ (0.1330**) but non-significant positive (0.0341) association at phenotypic level indicating strong association between these two characters genetically, but the phenotypic value is lessened by significant interaction of environment. At both genotypic and phenotypic levels this trait exhibited significant positive association with uniformity ratio (0.4598** and 0.2373**), micronaire value (0.5370** and 0.3529**), fibre elongation (0.2143** and 0.1072**) and lint yield plant⁻¹ (0.4082** and 0.3238**) respectively, revealing simultaneous selection for these traits is rewarding. These findings are in accordance with the results of Muthu *et al.* (2004), Rajanna *et al.* (2011), Patel *et al.* (2013b), Erande *et al.* (2014) and Kumar *et al.* (2014).

4.6.10 2.5% span length

2.5% span length recorded significant positive association with lint yield plant⁻¹ (0.0843*) at genotypic level only. This character exhibited significant positive association with seed cotton yield plant⁻¹ (0.2269** and 0.1476**), bundle strength

(0.9371** and 0.8456**) and fibre elongation (0.1633** and 0.1105**) indicating simultaneous selection for these traits is beneficial and significant negative association with uniformity ratio (-0.8612** and -0.5609**) and micronaire value (-0.8126** and -0.6567**), respectively at both genotypic and phenotypic levels. These findings are in agreement with results of Rajanna *et al.* (2011), Rajamani *et al.* (2013), Vinodhana *et al.* (2013), Erande *et al.* (2014) and Kumar *et al.* (2014).

4.6.11 Uniformity ratio

At both genotypic and phenotypic levels, uniformity ratio showed significant positive association with micronaire value (0.7726** and 0.5172**) and fibre elongation (0.1747** and 0.1815**) and significant negative association with bundle strength (-0.6856** and -0.3935**). Uniformity ratio exhibited significant negative association at genotypic level (-0.0878*) and non-significant association at phenotypic level (-0.0333) with seed cotton yield plant⁻¹ indicating that simultaneous selection of these traits is not possible. Similar results were earlier reported by Sakthi *et al.* (2007), Rajamani *et al.* (2013), Erande *et al.* (2014) and Kumar *et al.* (2014).

4.6.12 Micronaire value

This character showed significant positive association with fibre elongation (0.0820* and 0.1037**) and significant negative association with bundle strength (-0.7591** and -0.5980**), seed cotton yield plant⁻¹ (-0.3394** and -0.2447**) and lint yield plant⁻¹ (-0.1599** and -0.1304**) at both genotypic and phenotypic levels. Its association with seed cotton yield plant⁻¹ indicates that simultaneous selection of these traits is not possible. These results are in accordance with the results of Rao *et al.* (2009a), Rajanna (2010), Erande *et al.* (2014) and Kumar *et al.* (2014).

4.6.13 Bundle strength

At both genotypic and phenotypic levels, this trait recorded significant positive association with fibre elongation (0.3879** and 0.3185**), seed cotton yield plant⁻¹ (0.2781** and 0.2005**) and lint yield plant⁻¹ (0.1503** and 0.1058**) revealing simultaneous improvement of these traits is possible. Similar trends were also evident from the studies of Dedaniya and Pethani (1994), Vijayalaxmi *et al.* (2008), Rajanna *et al.* (2011) and Kumar *et al.* (2014).

4.6.14 Fibre elongation

Fibre elongation exhibited significant positive association with seed cotton yield plant⁻¹ (0.1664** and 0.0959**) and lint yield plant⁻¹ (0.2101** and 0.1211**) at both genotypic and phenotypic levels. Selection for high seed cotton yield plant⁻¹ is reliable based on fibre elongation as their association is significantly positive at both genotypic and phenotypic levels. These results were in broad agreement with the findings of Rao *et al.* (2009a).

4.6.15 Lint yield plant⁻¹

This trait showed highly significant positive association with seed cotton yield plant⁻¹ (0.9566** and 0.9488**) at both genotypic and phenotypic levels indicating simultaneous selection for these traits is beneficial. These results were in conformity with the reports of Pratap *et al.* (2007), Vijayalaxmi *et al.* (2008), Rajanna *et al.* (2011), Lakshmi *et al.* (2012) and Erande *et al.* (2014).

Thus, character association studies indicated plant height, number of monopodia plant⁻¹, number of sympodia plant⁻¹, number of bolls plant⁻¹, boll weight, lint index, seed index, ginning out-turn, 2.5% span length, bundle strength, fibre elongation and lint yield plant⁻¹ exhibited significant positive association with seed cotton yield plant⁻¹. Hence, these traits may be given due importance in selection programmes for the improvement of seed cotton yield.

4.7 PATH COEFFICIENT ANALYSIS

The observed correlation between yield and a particular yield component character is the net result of the direct effect of that component and indirect effects through other yield attributes. The total correlation coefficient between yield and its component characters may sometimes be misleading, as it may be an over or under estimate of its association with other characters. Hence, direct selection by correlated response may not prove fruitful. When many characters are affecting a given trait, it is necessary to separate the correlation into direct and indirect effects of cause as devised by Wright (1921) and utilized by Dewey and Lu (1959) in selection programmes. If the correlation coefficients between causal factor and yield are equal to its direct effect, then the correlation explains the true relationship and direct selection of this trait will be effective. If the correlation coefficient is positive and its direct effect is negative or negligible, then

the indirect effects seem to be the cause of correlations. Under such situations, the other factors have to be considered simultaneously. Sometimes correlations 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).

The direct and indirect effects of different yield contributing and quality traits on seed cotton yield plant⁻¹ were estimated over three locations (pooled) through path analysis at phenotypic and genotypic levels and are presented in Tables 4.22 and 4.23, respectively. The phenotypic and genotypic path diagrams are given in Fig. 4.9 and 4.10, respectively.

4.7.1 Days to 50% Flowering

The direct contribution of this character on seed cotton yield plant⁻¹ was low and positive (0.0106) at phenotypic level. The indirect effects *via* plant height (0.0001), number of monopodia plant⁻¹ (0.0001), number of sympodia plant⁻¹ (0.0024), lint index (0.0051), seed index (0.0073), ginning out-turn (0.0112), micronaire value (0.0002) and bundle strength (0.0058) were low and positive. Number of bolls plant⁻¹ (-0.0299), boll weight (-0.0695), 2.5% span length (-0.0029), uniformity ratio (-0.0008) and fibre elongation (-0.0002) showed low and negative indirect effects whereas indirect effect *via* lint yield plant⁻¹ was high and negative (-0.2284).

At genotypic level, direct contribution of this trait on seed cotton yield plant⁻¹ was low and positive (0.0178). The indirect effects *via* number of monopodia plant⁻¹ (0.0004), number of sympodia plant⁻¹ (0.0068), lint index (0.0067), seed index (0.0209), 2.5% span length (0.0190), bundle strength (0.0043) and fibre elongation (0.0002) were low and positive. While, the indirect effects *via* plant height (-0.0021), number of bolls plant⁻¹ (-0.1227), boll weight (-0.1812), ginning out turn (-0.0009), uniformity ratio (-0.0082), micronaire value (-0.0021) and lint yield plant⁻¹ (-0.2424) were negative.

This character had negative significant correlation with seed cotton yield plant⁻¹ (-0.4835** and -0.2890**) at both genotypic and phenotypic levels and recorded low and positive direct effect. This indicates days to 50% flowering had little positive effect on yield as its own but its effect on seed cotton yield plant⁻¹ may be through its component characters. These results are in conformity with the findings of Rajanna *et al.* (2011), Patel *et al.* (2013b), Rajamani *et al.* (2013) and Ranjan *et al.* (2014).

4.7.2 Plant Height (cm)

The direct contribution of this character on seed cotton yield plant⁻¹ was negative and low (-0.0020) at phenotypic level. The indirect effects through number of bolls plant⁻¹ (0.1984), seed index (0.0586), ginning out-turn (0.0189), uniformity ratio (0.0013) and micronaire value (0.0009) were positive whereas, lint yield plant⁻¹ showed high positive indirect effect (0.3603). Days to 50% flowering (-0.0004), number of monopodia plant⁻¹ (-0.0013), number of sympodia plant⁻¹ (-0.0118), boll weight (-0.0135), lint index (-0.0305), 2.5% span length (-0.0056) and fibre elongation (-0.0001) showed low and negative indirect effects.

At genotypic level, the direct effect of this trait on seed cotton yield plant⁻¹ was low and positive (0.0227). The indirect effects via number of bolls plant⁻¹ (0.4394), seed index (0.0814), 2.5% span length (0.0380), bundle strength (0.0077), fibre elongation (0.0001) and lint yield plant⁻¹ (0.2608) were positive and through days to 50% flowering (-0.0016), number of monopodia plant⁻¹ (-0.0104), number of sympodia plant⁻¹ (-0.0248), boll weight (-0.0397), lint index (-0.0540), ginning out-turn (-0.0010), uniformity ratio (-0.0147) and micronaire value (-0.0122) were low and negative.

This trait recorded significant positive correlation with seed cotton yield plant⁻¹ (0.6917** and 0.5815**) at both genotypic and phenotypic levels. Significant positive association and low direct effects indicate that greater emphasis in selection should be placed on positive indirect effects for improvement in seed cotton yield plant⁻¹. This was supported by earlier works of Rajamani *et al.* (2013), Vinodhana *et al.* (2013), Chitti *et al.* (2014) and Kumar *et al.* (2014).

4.7.3 Number of Monopodia Plant⁻¹

Direct effect of this trait on seed cotton yield plant⁻¹ was negative and low (-0.0045) at phenotypic level and its indirect effects through number of bolls plant⁻¹ (0.0984), seed index (0.0475), ginning out-turn (0.0160), micronaire value (0.0006), bundle strength (0.0077) and lint yield plant⁻¹ (0.1644) were positive. Days to 50% flowering (-0.0001), plant height (-0.0006), number of sympodia plant⁻¹ (-0.0052), boll weight (-0.0035), lint index (-0.0198), 2.5 % span length (-0.0043) and uniformity ratio (-0.0007) showed low and negative indirect effects.

At genotypic level, the direct effect of this trait on seed cotton yield plant⁻¹ was negative and low (-0.0173). The indirect effects through plant height (0.0137), number of bolls plant⁻¹ (0.3110), seed index (0.0638), 2.5% span length (0.0326), bundle strength (0.0061) and lint yield plant⁻¹ (0.1526) were positive. While low and negative effects were observed through days to 50% flowering (-0.0004), number of sympodia plant⁻¹ (-0.0169), boll weight (-0.0322), lint index (-0.0202), ginning out-turn (-0.0015), uniformity ratio (-0.0120) and micronaire value (-0.0083).

This trait possessed significant positive correlation (0.4712** and 0.2957**) at both genotypic and phenotypic levels. Significant positive association and negative low direct effect indicates that indirect effects seem to be the cause of positive correlation. In such a situation, the indirect causal factors are to be considered for simultaneous selection. These results were also supported by the earlier works of Rajamani *et al.* (2013), Erande *et al.* (2014), Farooq *et al.* (2014) and Kumar *et al.* (2014).

4.7.4 Number of Sympodia Plant⁻¹

At phenotypic level, number of sympodia plant⁻¹ recorded negative and low (-0.0171) direct effect on seed cotton yield plant⁻¹. The indirect effects of this trait *via* number of bolls plant⁻¹ (0.1946), seed index (0.0571), ginning out-turn (0.0158), micronaire value (0.0008) and bundle strength (0.0096) were low and positive. Positive and high indirect effect was exhibited through lint yield plant⁻¹ (0.3852). Days to 50% flowering (-0.0015), plant height (-0.0014), number of sympodia plant⁻¹ (-0.0014), boll weight (-0.0011), lint index (-0.0321), 2.5% span length (-0.0048) and uniformity ratio (-0.0010) showed low and negative indirect effects.

At genotypic level, the direct influence of this character on seed cotton yield plant⁻¹ was low and negative (-0.0287). Plant height (0.0196), seed index (0.0704), 2.5% span length (0.0334), bundle strength (0.0069) and fibre elongation (0.0001) showed low and positive indirect effects. Positive and high indirect effects were recorded through number of bolls plant⁻¹ (0.4629) and lint yield plant⁻¹ (0.3120). The indirect effects of this trait *via* days to 50 % flowering (-0.0042), number of monopodia plant⁻¹ (-0.0101), boll weight (-0.0087), lint index (-0.0504), ginning out-turn (-0.0008), uniformity ratio (-0.0117) and micronaire value (-0.0102) were low and negative.

This trait showed significant positive correlations (0.7804** and 0.6027**) with seed cotton yield plant⁻¹ and negative direct effects at both genotypic and phenotypic levels. This indicates that indirect effects seem to be the cause of positive correlation. In

such a situation, the indirect causal factors are to be considered for simultaneous selection. Similar trends were also evident from the studies of Tuteja *et al.* (2006), Venkateswarlu *et al.* (2010a) and Farooq *et al.* (2014).

4.7.5 Number of Bolls Plant⁻¹

The direct effect exhibited by number of bolls plant⁻¹ on seed cotton yield plant⁻¹ was high and positive (0.2899) at phenotypic level. However, the indirect effects of this trait *via* seed index (0.0394), ginning out-turn (0.0089), micronaire value (0.0006) and bundle strength (0.0087) were low and positive. Lint yield plant⁻¹ (0.5654) exhibited positive and high indirect effect. Days to 50% flowering (-0.0011), plant height (-0.0014), number of monopodia plant⁻¹ (-0.0015), number of sympodia plant⁻¹ (-0.0115), boll weight (-0.0131), lint index (-0.0256), 2.5% span length (-0.0039), uniformity ratio (-0.0008) and fibre elongation (-0.0001) showed low and negative indirect effects.

The direct effect exhibited by number of bolls plant⁻¹ on seed cotton yield plant⁻¹ was high and positive (0.5337) at genotypic level. Plant height (0.0187), seed index (0.0585), 2.5% span length (0.0284), bundle strength (0.0065) and fibre elongation (0.0001) showed low and positive indirect effects. Lint yield plant⁻¹ (0.3523) exhibited positive and high indirect effects while, days to 50% flowering (-0.0041), number of monopodia plant⁻¹ (-0.0101), boll weight (-0.0242), lint index (-0.0462), ginning out - turn (-0.0005), uniformity ratio (-0.0095) and micronaire value (-0.0093) recorded low and negative indirect effects.

This trait had high significant positive correlations (0.8693** and 0.8539**) with seed cotton yield plant⁻¹ at both genotypic and phenotypic levels. High direct effects and positive correlations with seed cotton yield plant⁻¹ suggest number of bolls plant⁻¹ as one of the major contributors towards seed cotton yield plant⁻¹. These results are in agreement with the findings of Patel *et al.* (2013b), Vinodhana *et al.* (2013), Chitti *et al.* (2014), Erande *et al.* (2014), Kumar *et al.* (2014) and Ranjan *et al.* (2014).

4.7.6 Boll Weight (g)

The trait, boll weight revealed a positive (0.1582) direct effect on seed cotton yield plant⁻¹ at phenotypic level. The indirect effects of this trait through plant height (0.0002), number of monopodia plant⁻¹ (0.0001), number of sympodia plant⁻¹ (0.0001), 2.5% span length (0.0046), uniformity ratio (0.0013) and fibre elongation (0.0001) were

low and positive. High positive indirect effect was recorded by lint yield plant⁻¹ (0.3320). Days to 50% flowering (-0.0047), number of bolls plant⁻¹ (-0.0241), lint index (-0.0100), seed index (-0.0166), ginning out-turn (-0.0208), micronaire value (-0.0004) and bundle strength (-0.0084) showed low negative indirect effects.

At genotypic level, the direct influence of this trait on seed cotton yield plant⁻¹ was positive and high (0.2977). The indirect effects through number of monopodia plant⁻¹ (0.0019), number of sympodia plant⁻¹ (0.0008), ginning out-turn (0.0018), uniformity ratio (0.0134) and micronaire value (0.0064) were low and positive whereas, lint yield plant⁻¹ (0.2397) showed positive and high indirect effects. Low and negative indirect effects were exhibited through days to 50% flowering (-0.0108), plant height (-0.0030), number of bolls plant⁻¹ (-0.0434), lint index (-0.0136), seed index (-0.0404), 2.5% span length (-0.0303), bundle strength (-0.0063) and fibre elongation (-0.0001).

This trait expressed significant positive correlations (0.4136** and 0.4115**) with seed cotton yield plant⁻¹ at both genotypic and phenotypic levels. High direct effects and significant positive associations suggest that direct selection for seed cotton yield plant⁻¹ through this trait will be rewarding. Similar trends were also evident from the studies of Rajamani *et al.* (2013), Vinodhana *et al.* (2013), Erande *et al.* (2014), Farooq *et al.* (2014) and Ranjan *et al.* (2014).

4.7.7 Lint index (g)

The direct contribution of this character on seed cotton yield plant⁻¹ was low and negative (-0.0993) at phenotypic level. However, the indirect effects of this trait *via* number of bolls plant⁻¹ (0.0748), boll weight (0.0160), seed index (0.0511), micronaire value (0.0003) and bundle strength (0.0059) were low and positive whereas, lint yield plant⁻¹ (0.3192) exhibited high positive indirect effect. Days to 50% flowering (-0.0006), plant height (-0.0006), number of monopodia plant⁻¹ (-0.0009), number of sympodia plant⁻¹ (-0.0055), ginning out-turn (-0.0421), 2.5% span length (-0.0031), uniformity ratio (-0.0004) and fibre elongation (-0.0002) showed low and negative effects.

This character showed negative and low (-0.1040) direct effect on seed cotton yield plant⁻¹ at genotypic level. The indirect effects *via* plant height (0.0118), boll weight (0.0389), seed index (0.0408), ginning out-turn (0.0019), 2.5% span length (0.0186), bundle strength (0.0044) and fibre elongation (0.0002) were low and positive while number of bolls plant⁻¹ (0.2374) and lint yield plant⁻¹ (0.2856) recorded high and positive

indirect effects. Days to 50 % flowering (-0.0011), number of monopodia plant⁻¹ (-0.0033), number of sympodia plant⁻¹ (-0.0139), uniformity ratio (-0.0059) and micronaire value (-0.0041) exhibited low and negative indirect effects.

This character exhibited positive correlations (0.5070** and 0.3146**) with seed cotton yield plant⁻¹ at both genotypic and phenotypic levels. Significant positive association and negative direct effects indicates that indirect effects seem to be the cause of positive correlation. In such a situation, the indirect causal factors are to be considered for simultaneous selection. These results are in agreement with the findings of Pratap *et al.* (2007), Venkateswarlu *et al.* (2010a) and Farooq *et al.* (2014).

4.7.8 Seed index (g)

At phenotypic level, the direct contribution of this trait to seed cotton yield plant⁻¹ was low and positive (0.1255). The indirect effects of this trait through days to 50% flowering (0.0006), number of bolls plant⁻¹ (0.0909), ginning out-turn (0.0530), micronaire value (0.0009), bundle strength (0.0127) and lint yield plant⁻¹ (0.0348) were low and positive. Plant height (-0.0009), number of monopodia plant⁻¹ (-0.0017), number of sympodia plant⁻¹ (-0.0078), boll weight (-0.0209), lint index (-0.0405), 2.5% span length (-0.0069) and uniformity ratio (-0.0014) showed low and negative indirect effects.

The trait expressed positive (0.1090) direct effect on seed cotton yield plant⁻¹ at genotypic level. The indirect effects of this character through days to 50% flowering (0.0034), plant height (0.0169), 2.5% span length (0.0461), bundle strength (0.0092) and lint yield plant⁻¹ (0.0532) were low and positive. Number of bolls plant⁻¹ (0.2863) exhibited high positive indirect effect. Whereas, the traits number of monopodia plant⁻¹ (-0.0101), number of sympodia plant⁻¹ (-0.0185), boll weight (-0.1105), lint index (-0.0389), ginning out-turn (-0.0024), uniformity ratio (-0.0810) and micronaire value (-0.0128) showed negative and low indirect effects.

However, this trait recorded significant positive correlations (0.3129** and 0.2382**) and positive direct effects at both genotypic and phenotypic levels. Significant positive association and positive direct effect indicates that selection for this trait will be rewarding for improvement of seed cotton yield plant⁻¹. Similar trends were also evident from the studies of Rajanna *et al.* (2011), Rajamani *et al.* (2013), Kumar *et al.* (2014) and Ranjan *et al.* (2014).

4.7.9 Ginning out-turn (%)

The direct contribution of this character on seed cotton yield plant⁻¹ was low and negative (-0.0886) at phenotypic level. The indirect effects of this trait through plant height (0.0004), number of monopodia plant⁻¹ (0.0008), number of sympodia plant⁻¹ (0.0030), boll weight (0.0371), 2.5% span length (0.0042) and uniformity ratio (0.0010) were low and positive among the traits studied lint yield plant⁻¹ (0.2367) exhibited high positive indirect effect. Days to 50% flowering (-0.0013), number of bolls plant⁻¹ (-0.0290), lint index (-0.0471), seed index (-0.0750), micronaire value (-0.0006), bundle strength (-0.0075) and fibre elongation (-0.0001) showed low and negative indirect effects.

The direct influence of this character was low and positive (0.0038) on seed cotton yield plant⁻¹ at genotypic level. The indirect effects through number of monopodia plant⁻¹ (0.0067), number of sympodia plant⁻¹ (0.0059), boll weight (0.1385), uniformity ratio (0.0122), micronaire value (0.0085), fibre elongation (0.0001) and lint yield plant⁻¹ (0.1901) were positive. While, days to 50% flowering (-0.0043), plant height (-0.0060), number of bolls plant⁻¹ (-0.0711), lint index (-0.0521), seed index (-0.0668), 2.5% span length (-0.0275) and bundle strength (-0.0049) showed low and negative indirect effects.

This character showed significant positive (0.1330**) and non-significant positive (0.0341) correlations at genotypic and phenotypic level. Significant positive association and low direct effects at genotypic level indicating indirect causal factors were to be considered for simultaneous selection. These findings are in agreement with the results of Venkateswarlu *et al.* (2010a), Rajamani *et al.* (2013), Vinodhana *et al.* (2013), Chitti *et al.* (2014), Farooq *et al.* (2014) and Kumar *et al.* (2014).

4.7.10 2.5% span length (mm)

At phenotypic level, the direct contribution of this character on seed cotton yield plant⁻¹ was low and negative (-0.0123). This trait showed low and positive effects through days to 50% flowering (0.0025), number of bolls plant⁻¹ (0.0926), seed index (0.0706), ginning out-turn (0.0304), micronaire value (0.0011), bundle strength (0.0207) and lint yield plant⁻¹ (0.0380). Plant height (-0.0009), number of monopodia plant⁻¹ (-0.0016), number of sympodia plant⁻¹ (-0.0067), boll weight (-0.0594), lint index (-0.0249), uniformity ratio (-0.0025) and fibre elongation (-0.0001) were showed low and negative indirect effects.

The direct contribution of this character on seed cotton yield plant⁻¹ was low and positive (0.0565) at genotypic level. The indirect effects of this trait *via* days to 50% flowering (0.0060), plant height (0.0152), bundle strength (0.0111), fibre elongation (0.0001) and lint yield plant⁻¹ (0.0392) were low and positive. Number of bolls plant⁻¹ (0.2679) showed high positive indirect effects. Number of monopodia plant⁻¹ (-0.0100), number of monopodia plant⁻¹ (-0.0170), boll weight (-0.1594), lint index (-0.0342), ginning out-turn (-0.0019), uniformity ratio (-0.0229) and micronaire value (-0.0128) exhibited low and negative indirect effects.

This trait recorded significant positive correlations (0.2269** and 0.1476**) and positive low and negative low direct effects at genotypic and phenotypic levels, respectively with seed cotton yield plant⁻¹. This revealing indirect effects seems to be the cause of positive association. Hence, indirect causal factors are to be considered for simultaneous selection. Similar trends were also evident from the studies of Venkateswarlu *et al.* (2010a), Farooq *et al.* (2013) and Vinodhana *et al.* (2013).

4.7.11 Uniformity ratio

The direct contribution of this character on seed cotton yield plant⁻¹ was low and positive (0.0044). The indirect effects of this trait *via* plant height (0.0006), number of monopodia plant⁻¹ (0.0007), number of sympodia plant⁻¹ (0.0039), boll weight (0.0463), 2.5% span length (0.0069) and lint yield plant⁻¹ (0.0184) were low and positive. Days to 50% flowering (-0.0019), number of bolls plant⁻¹ (-0.0512), seed index (-0.0397), ginning out-turn (-0.0210), micronaire value (-0.0008), bundle strength (-0.0096) and fibre elongation (-0.0002) showed low and negative indirect effects.

This character showed low and positive (0.0265) direct effect on seed cotton yield plant⁻¹ at genotypic level. Number of monopodia plant⁻¹ (0.0078), number of sympodia plant⁻¹ (0.0127), boll weight (0.1501), lint index (0.0232), ginning out-turn (0.0018), micronaire value (0.0122), fibre elongation (0.0001) and lint yield plant⁻¹ (0.0171) showed low and positive indirect effects. Days to 50% flowering (-0.0055), plant height (-0.0125), number of bolls plant⁻¹ (-0.1903), seed index (-0.0741), 2.5% span length (-0.0487) and bundle strength (-0.0081) exhibited low and negative indirect effects.

This trait possessed significant negative correlation (-0.0878*) at genotypic level and non-significant negative correlation (-0.0333) at phenotypic level. The direct influence of this character on seed cotton yield was positive and low (0.0265 and 0.0044)

at both the levels. The positive low direct effects of this trait were outweighed by high negative indirect effects by causal factors thus gave negative correlation with seed cotton yield plant⁻¹. These results are in agreement with the findings of Srinivasulu *et al.* (2010a), Rajanna *et al.* (2011), Erande *et al.* (2014) and Kumar *et al.* (2014).

4.7.12 Micronaire value (10⁻⁶g/inch)

At phenotypic level, the direct contribution of this trait on seed cotton yield plant⁻¹ was low and negative (-0.0016). The indirect effects of this trait through plant height (0.0011), number of monopodia plant⁻¹ (0.0016), number of sympodiaplant⁻¹ (0.0080), boll weight (0.0422), lint index (0.0191), 2.5% span length (0.0081) and uniformity ratio (0.0023) were low and positive. Days to 50% flowering (-0.0010), number of bolls plant⁻¹ (-0.1165), seed index (-0.0665), ginning out-turn (-0.0313), bundle strength (-0.0146), fibre elongation (-0.0001) and lint yield plant⁻¹ (-0.0953) showed low and negative indirect effects.

At genotypic level, the direct contribution of this character on seed cotton yield plant⁻¹ was low and positive (0.0157). The indirect effects through number of monopodia plant⁻¹ (0.0091), number of sympodiaplant⁻¹ (0.0186), boll weight (0.1202), lint index (0.0273), ginning out-turn (0.0021) and uniformity ratio (0.0205) were low and positive. Days to 50 % flowering (-0.0023), plant height (-0.0176), seed index (-0.0885), 2.5 % span length (-0.0459), bundle strength (-0.0090) and lint yield plant⁻¹ (-0.0745) showed low and negative indirect effects whereas, number of bolls plant⁻¹ (-0.3152) exhibited high negative indirect effects.

This trait exhibited significant negative correlations (-0.3394** and -0.1447**) with seed cotton yield plant⁻¹ at both genotypic and phenotypic levels. Low direct effects and significant negative association indicated that selection for this trait would not be realized in increased seed cotton yield plant⁻¹. Similar trends were also evident from the studies of Venkateswarlu *et al.* (2010a), Vinodhana *et al.* (2013) and Kumar *et al.* (2014).

4.7.13 Bundle strength (g/tex)

The direct contribution of this character towards seed cotton yield plant⁻¹ was low and positive (0.0244). At phenotypic level, indirect effects of this trait *via* days to 50% flowering (0.0025), number of bolls plant⁻¹ (0.1028), seed index (0.0651), ginning

out-turn (0.0270), micronaire value (0.0010) and lint yield plant⁻¹ (0.0774) were positive. Plant height (-0.0009), number of monopodia plant⁻¹ (-0.0014), number of sympodiaplant⁻¹ (-0.0067), boll weight (-0.0543), lint index (-0.0240), 2.5% span length (-0.0104), uniformity ratio (-0.0017) and fibre elongation (-0.0004) showed low negative indirect effects.

At genotypic level the direct contribution of this character on seed cotton yield plant⁻¹ was low and positive (0.0119). Indirect effects *via* days to 50 % flowering (0.0064), plant height (0.0147), number of bolls plant⁻¹ (0.2922), seed index (0.0841), 2.5% span length (0.0530), fibre elongation (0.0002) and lint yield plant⁻¹ (0.0700) were positive while, number of monopodia plant⁻¹ (-0.0089), number of sympodia plant⁻¹ (-0.0168), boll weight (-0.1588), lint index (-0.0382), ginning out-turn (-0.0016), uniformity ratio (-0.0182) and micronaire value (-0.0119) showed low negative indirect effects.

This trait recorded significant positive correlations with seed cotton yield plant⁻¹ (0.2781** and 0.2005**) at both genotypic and phenotypic levels. Significant positive association and low direct effects indicated that greater emphasis in selection should be placed on positive indirect effects for improvement in seed cotton yield plant⁻¹. These findings were in agreement with the results of Sambamurthy *et al.* (2006), Sakthi *et al.* (2007) and Rajanna *et al.* (2011).

4.7.14 Fibre elongation (%)

The direct contribution of this character on seed cotton yield plant⁻¹ was low and negative (-0.0012). At phenotypic level, indirect effects of this trait *via* days to 50% flowering (0.0017), number of bolls plant⁻¹ (0.0290), seed index (0.0048), uniformity ratio (0.0008), bundle strength (0.0078) and lint yield plant⁻¹ (0.0885) were low and negative. Plant height (-0.0001), number of monopodia plant⁻¹ (-0.0002), number of sympodiaplant⁻¹ (-0.0006), boll weight (-0.0072), lint index (-0.0163), ginning out-turn (-0.0095), 2.5% span length (-0.0014) and micronaire value (-0.0002) exhibited low negative indirect effects.

At genotypic level, direct contribution of this character towards seed cotton yield plant⁻¹ was low and positive (0.0006). Indirect effects *via* days to 50% flowering (0.0054), plant height (0.0031), number of bollsplant⁻¹ (0.1210), seed index (0.0056),

ginning out-turn (0.0008), 2.5% span length (0.0092), uniformity ratio (0.0046), micronaire value (0.0013), bundle strength (0.0046) and lint yield plant⁻¹ (0.0978) were low and positive. Number of monopodia plant⁻¹ (-0.0011), number of sympodiaplant⁻¹ (-0.0036), boll weight (-0.0507) and lint index (-0.0323) showed low negative indirect effects.

This trait exhibited significant positive correlations (0.1664** and 0.0959**) at both genotypic and phenotypic levels and positive low direct effect at genotypic level suggest that selection of this trait along with other causal factors which have high indirect effects on seed cotton yield through fibre elongation will be rewarding. This was in agreement with the previous works of Vijayalaxmi *et al.* (2008), Anandan (2009), Srinivasulu (2009) and Mahantesh *et al.* (2010).

4.7.15 Lint yield Plant⁻¹ (g)

At phenotypic level, the direct contribution of this character on seed cotton yield plant⁻¹ was high and positive (0.7310). The indirect effects of this trait through boll weight (0.0718), ginning out -turn (0.0060), uniformity ratio (0.0001), micronaire value (0.0002) and bundle strength (0.0026) were low and positive. Among the traits studied number of bolls plant⁻¹ (0.2242) exhibited high positive indirect effects. Days to 50% flowering (-0.0033), plant height (-0.0010), number of monopodia plant⁻¹ (-0.0010), number of sympodiaplant⁻¹ (-0.0090), lint index (-0.0434), ginning out-turn (-0.0287), 2.5% span length (-0.0006) and fibre elongation (-0.0001) showed low negative indirect effects.

The direct contribution of this character on seed cotton plant⁻¹ was high and positive (0.4657) at genotypic level. The indirect effects *via* plant height (0.0127), boll weight (0.1532), seed index (0.0125), ginning out-turn (0.0016), 2.5% span length (0.0048, uniformity ratio (0.0010), bundle strength (0.0018) and fibre elongation (0.0001) were low and positive whereas, number of bolls plant⁻¹ (0.4038) exhibited high and positive indirect effect. Days to 50% flowering (-0.0093), number of monopodia plant⁻¹ (-0.0057), number of sympodiaplant⁻¹ (-0.0192), lint index (-0.0638) and micronaire value (-0.0025) showed low negative indirect effects.

This character showed significant positive association with seed cotton yield plant⁻¹ (0.9566** and 0.9488**) at both genotypic and phenotypic levels. High direct effects and pronounced correlations suggest that direct selection for seed cotton yield plant⁻¹ through this trait will be rewarding. These results are in agreement with the findings of Dedaniya and Pethani (1994), Tomar and Singh (1996), Pratap *et al.* (2007), Vijayalaxmi *et al.* (2008) and Rajanna *et al.* (2011).

The path analysis indicated that plant height, number of bolls plant⁻¹, boll weight, lint index, ginning out-turn, 2.5% span length, bundle strength, fibre elongation and lint yield plant⁻¹ showed direct positive effects and significant correlation with seed cotton yield plant⁻¹. In plant breeding, it is very difficult to have complete knowledge of all component traits of yield. The residual effect permits precise explanation about the pattern of interaction of other possible components of yield. In other words, residual effect measures the role of the possible independent variables which were not included in the study on the dependent variable. In the present study, the residual effect observed was low both at phenotypic (0.1036) and genotypic (0.0206) levels, so the characters included in the study clearly explained the direct and indirect effects on the dependent variable. The present study also revealed that due weightage should be laid on selection process with more number of bolls plant⁻¹ and boll weight and there should be economic balance among these traits to get higher seed cotton yield plant⁻¹.

4.8 COMBINING ABILITY ANALYSIS

The knowledge of genetic structure and mode of inheritance of quantitative and qualitative traits helps the breeders to employ suitable breeding method for improvement of these traits. Combining ability analysis is an important tool for selection of the desirable parents together with the information regarding nature and magnitude of gene action controlling quantitative and qualitative traits. The information on gene action and combining ability over locations (pooled) helps in identifying the best combiners which may be hybridized to produce superior stable heterotic cross combinations or to produce transgressive or recombinant segregants in F₂ and subsequent generations. Exploitation of heterosis is primarily dependant on the screening and selection of the lines in the available germplasm that could produce better combinations of important characters.

The entire genetic variability observed in the analysis for each trait was partitioned into its components *i.e.*, general and specific combining ability (Sprague and Tatum, 1942). General combining ability (*gca*) is used to designate the average

performance of a line in hybrid combinations while specific combining ability (*sca*) define those cases in which certain combinations do relatively better or worse than expected on the basis of the average performance of the lines involved. The general combining ability (*gca*) effects were due to the additive type of gene action whereas, specific combining ability (*sca*) effects are due to the genes which are non-additive *i.e.*, either dominant or epistatic in nature (Sprague and Tatum, 1942). The relative importance of general and specific combining ability can be assessed by estimating the components of variance and expressed in the ratio of $\sigma^2_{gca}/\sigma^2_{sca}$ (Singh and Chaudhary, 1977). The closer the ratio to unity, greater is the magnitude of additive gene action and *vice versa*. The purpose of this study was to determine the *gca* and *sca* effects for seed cotton yield plant⁻¹, yield contributing and fibre quality traits so as to choose appropriate parents and hybrids for the genetic enhancement.

In the present field experiment, 72 inter-specific cross combinations were made in a line × tester fashion utilizing 12 lines and 6 testers. The 72 F₁'s along with 18 parents (12 lines + 6 testers) were evaluated over three locations during *kharif*, 2014-15 to study the combining ability and gene action.

Line × Tester Pooled Analysis for Combining Ability

The pooled analysis of variance for combining ability over three locations recorded significant differences for all the characters studied (Table 4.24). The differences among the parents, parents vs crosses and crosses were observed to be significant for all the characters studied. Partitioning of crosses into lines, testers and line × tester revealed that the variance due to lines was significant for all the characters whereas, for testers all the characters were found to be significant except for days to 50% flowering, number of monopodia plant⁻¹, number of bolls plant⁻¹, seed index, micronaire value and bundle strength. The interaction due to lines × testers were significant for all the traits evaluated.

Interaction effect of locations × parents vs crosses, locations × crosses were significant for all the characters, except for uniformity ratio in locations × parents vs crosses interaction. Further, locations × line effect interaction showed significant differences for days to 50% flowering, plant height, number of monopodia plant⁻¹, number of sympodia plant⁻¹, number of bolls plant⁻¹, micronaire value, seed cotton yield

plant⁻¹ and lint yield plant⁻¹. While, locations × tester effect interaction exhibited non-significant for all the characters except for number of monopodia plant⁻¹ and 2.5% span length. Interaction effects of locations × line × testers were significant for all the characters studied.

Combining Ability Effects

General combining ability effects of parents and specific combining ability effects of crosses over locations (pooled) were estimated and presented in Tables 4.25 to 4.28. The results are discussed character wise here under.

Combining Ability Variances and Gene Action

The estimate of *gca* and *sca* variances in pooled analysis is presented in the Table 4.29. General combining ability is generally associated with additive gene action, while specific combining ability is due to dominance and epistasis. In the present study *sca* variances were higher than *gca* variances in pooled analysis for days to 50% flowering, plant height, number of monopodia plant⁻¹, number of sympodia plant⁻¹, lint index, ginning out-turn, micronaire value, bundle strength, fibre elongation and lint yield plant⁻¹ indicating the predominance of non-additive gene action for these characters and boll weight was controlled by both additive and non-additive gene actions whereas, additive gene action controls the remaining traits.

4.8.1 Days to 50% Flowering

General combining ability effects for days to 50% flowering in pooled analysis varied from -2.88 (L 762) to 2.12 (BS 37) in lines and from -1.09 (DB 16) to 1.15 (TCB 37) in testers. The lines, L 762 (-2.88**), H 1442 (-1.90*) and NDLH 1938 (-0.64*) and the testers DB 16 (-1.09*) and GSB 41 (-0.45*) recorded significant *gca* effects in desired direction for this trait. These results suggest that these parents were good general combiners with favourable genes for earliness over locations.

In pooled analysis, estimates of specific combining ability effects for this trait ranged from -5.72 (H 1442 × GSB 41) to 5.70 (L 1058 × DB 16). Out of 72 cross combinations evaluated, seventeen hybrids recorded significant negative *sca* effects. The top five crosses among them were, H 1442 × GSB 41 (-5.72**), TSH 0250 × GSB 40 (-4.27**), MCU 5 × TCB 37 (-3.11**), NDLH 1938 × DB 11 (-2.42**) and L 1058 × GSB 40 (-2.42**).

The estimated component of variance due to *sca* (2.557**) was higher than the *gca* (0.523*) in pooled analysis. The ratio of *gca* variance to *sca* variance was low (0.204) indicating the presence of non-additive gene action. Biparental mating or diallel selective mating or heterosis breeding may be employed for the improvement of this trait. Similar results were also reported by Patil *et al.* (2011), Amir *et al.* (2012), Vineela *et al.* (2012), Yanal *et al.* (2013), Simon *et al.* (2013) and Deosarkar *et al.* (2014).

When compared over their *per se* performance and *sca* effects the crosses, H 1442 × GSB 41(High × High), TSH 0250 × GSB 40 (Low × Low) and NDLH 1938 × DB 11 (High × Low) were identified as best specific cross combinations for this trait. The cross combinations involving high × high general combiners revealed additive and additive × additive genetic component of variance where the characters could be easily improved through simple selection procedures in recombination breeding. The crosses between two low combiners producing crosses with significant *sca* effects was mainly due to nicking ability/genetic diversity of their parents and high × low *gca* general combiners resulted in superior cross combinations which may be due to complementary gene action and also revealed the importance of both additive and non-additive gene action.

4.8.2 Plant Height (cm)

The *gca* effects ranged from -8.56 (MCU 5) to 9.32 (NDLH 1938) in lines and from -6.12 (SUVIN) to 5.96 (GSB 40) in testers for plant height across the locations. Significant positive *gca* effects desirable for this trait was recorded by the lines, NDLH 1938 (9.32**), MR 786 (7.35**) and ADB 542 (3.32*) and the tester GSB 40 (5.96**). These parents can be utilized in basic breeding programmes for improvement of this trait.

The estimates of *sca* effects for plant height varied from -20.14 (NDLH 1938 × DB 11) to 19.74 (ADB 532 × DB 16). Significant positive *sca* effects in desirable direction was exhibited by ten cross combinations and the top five cross combinations were, ADB 532 × DB 16 (19.74**), H 1442 × DB 11 (16.57**), TSH 0250 × GSB 40 (10.79**), L 1058 × SUVIN (10.37**) and NDLH 1938 × TCB 37 (9.36*).

In pooled analysis the variance due to *gca* (14.810*) was lesser than the *sca* variance (20.200*) indicating the presence of non-additive gene action and it can be exploited by biparental mating or diallel selective mating or heterosis breeding. These results are in conformity with the reports of Mohammad *et al.* (2010), Patil *et al.* (2011), Patel *et al.* (2012), Vineela *et al.* (2012), Simon *et al.* (2013), Yanal *et al.* (2013) and Deosarkar *et al.* (2014).

The superior cross combinations identified based on their *per se* performance and *sca* effects were, H 1442 × DB 11 (Low × Low), TSH 0250 × GSB 40 (Low × High) and NDLH 1938 × TCB 37 (High × Low). The crosses between two low combiners producing crosses with significant *sca* effect indicating the presence of non-additive inter-allelic interaction. Low × high and high × low *gca* effects resulted in superior cross combinations which may be due to complementary gene action and also revealed the importance of both additive and non-additive gene actions.

4.8.3 Number of Monopodia Plant⁻¹

A range of -0.31 (NDLH 1938) to 0.51 (BS 37) *gca* effects was observed for lines. Whereas, testers recorded a range from -0.09 (DB 16) to 0.07 (GSB 40 and SUVIN). Among the lines, BS 37 (0.51**), WGCV 48 (0.36**), ADB 532 (0.18**), ADB 542 (0.10**) and L 1058 (0.07*) while, in testers GSB 40 (0.07**), SUVIN (0.07**) and GSB 41 (0.04*) showed significant positive *gca* effects over locations. These parents may serve as useful source for improvement of this trait in hybridization programmes.

Lowest and highest *sca* effects recorded in pooled analysis were -0.80 (MCU 5 × GSB 41) and 0.74 (TSH 0250 × GSB 40). Among the 72 hybrids, twenty three crosses exhibited significant positive *sca* effects. The top five performing crosses were, TSH 0250 × GSB 40 (0.74**), MCU 5 × TCB 37 (0.59**), MCU 5 × GSB 40 (0.58**), ADB 532 × GSB 41 (0.55**) and L 762 × GSB 41 (0.48**).

The variance due to *gca* (-0.005) was very low and negative than variance due to *sca* (0.041) and both were non-significant. The ratio of *gca* variance to *sca* variance (-0.121) was low and negative indicating this trait may be controlling by non-additive additive gene action. Biparental mating or diallel selective mating or heterosis breeding may be employed for the improvement of this trait. These results are supported by the results obtained by Patil *et al.* (2011), Vineela *et al.* (2012), Yanal *et al.* (2013), Tuteja and Banga (2013), Patel *et al.* (2014) and Rajamani *et al.* (2014).

The crosses, ADB 532 × GSB 41 (High × High), TSH 0250 × GSB 40 (Low × High) and MCU 5 × GSB 40 (Low × High) were identified as best specific combiners as per their *per se* performance and *sca* effects. The cross combinations involving high × high general combiners revealed additive and additive × additive genetic component of variance where the characters could be easily improved through simple selection procedures in recombination breeding and the crosses with low × high combiners resulted in superior combinations which may be due to complementary gene action.

4.8.4 Number of Sympodia Plant⁻¹

In pooled analysis *gca* effects for number of sympodia plant⁻¹ varied from -1.91 (MCU 5) to 1.72 (MR 786) in lines and from -1.24 (TCB 37) to 0.95 (DB 16) in testers. The lines, MR 786 (1.72**), SCS 793 (1.06**), H 1442 (0.91**) and ND LH 1938 (0.40*) and the testers DB 16 (0.95**), GSB 41 (0.69**) and GSB 40 (0.33*) exhibited significant and positive *gca* effects for this trait.

Sca effects for this trait ranged from -2.91 (WGCV 48 × GSB 41) to 5.60 (MR 786 × GSB 41). Out of 72 cross combinations studied, fifteen hybrids showed significant positive *sca* effects. The crosses, MR 786 × GSB 41 (5.60**), ADB 542 × DB 16 (3.55**), SCS 793 × SUVIN (3.22**), H 1442 × DB 16 (2.03**) and TSH 0250 × GSB 40 (1.94**) were top five specific cross combinations for this trait.

In the present investigation number of sympodia plant⁻¹ seems to be mostly under the control of non-additive gene action in pooled analysis as the *sca* variance (1.111*) was higher than the *gca* variance (0.385*). Further improvement of this trait can be possible through biparental mating or diallel selective mating or heterosis breeding. Similar results were reported by Kumar *et al.* (2010), Patil *et al.* (2011), Vineela *et al.* (2012), Tuteja and Banga (2013), Yanal *et al.* (2013), Patel *et al.* (2014) and Rajamani *et al.* (2014).

The best specific cross combinations identified based on their *per se* performance and *sca* effects were MR 786 × GSB 41 (High × High), ADB 542 × DB 16 (Low × High) and H 1442 × DB 16 (High × High). The cross combinations involving high × high general combiner revealed additive and additive × additive genetic component of variance where the characters could be easily improved through simple selection procedures in recombination breeding and the crosses with low × high combiners resulted in superior combinations which may be due to complementary gene action.

4.8.5 Number of Bolls Plant⁻¹

Among the lines *gca* effects ranged from -14.61 (MCU 5) to 6.54 (H 1442) and among the testers, *gca* effects varied from -2.95 (TCB 37) to GSB 41 (2.71**). The lines, H 1442 (6.54**), NDLH 1938 (6.43**), L 762 (4.41**), SCS 793 (3.68**), BS 37 (2.68**), MR 786 (1.60**) and ADB 542 (1.16*) and the testers GSB 41 (2.71**), DB 16 (2.46**) and DB 11 (1.42**) recorded significant positive *gca* effects in pooled analysis.

The range of *sca* effects was from -13.96 (TSH 0250 × TCB 37) to 14.26 (BS 37 × SUVIN) and significant positive *sca* effects were noticed in 24 cross combinations. The hybrids, BS 37 × SUVIN (14.26**), TSH 0250 × GSB 40 (9.14**), WGCV 48 × DB 11 (8.23**), ADB 542 × DB 16 (7.25**) and BS 37 × GSB 41 (6.86**) were found superior.

Estimated component of *gca* variance (7.721) was higher than the *sca* (1.740) and both were non-significant for this character. The ratio of *gca* variance to *sca* variance was high (4.437) revealing that additive gene action may be the cause of inheritance of number of bolls plant⁻¹. This character can be improved by hybridization followed by simple selection through pedigree method. These results are in accordance with the results of Ambhore *et al.* (2012), Tariq and Uzair (2012), Kumar *et al.* (2013) and Simon *et al.* (2013).

The crosses, BS 37 × SUVIN (High × Low), BS 37 × GSB 41 (High × High) and ADB 542 × DB 16 (High × High) were identified as best specific cross combinations based on their *sca* effects and *per se* performance. The crosses with high × low combiners resulted in superior combinations which may be due to complementary gene action and cross combinations involving high × high general combiners revealed additive and additive × additive genetic component of variance where the characters could be easily improved through simple selection procedures in recombination breeding.

4.8.6 Boll Weight (g)

Estimates of *gca* effects in pooled analysis ranged from -0.33 (MCU 5) to 0.23 (MR 786) among lines and from -0.27 (SUVIN) to 0.20 (GSB 40) among testers. *gca* effects were positive and significant for the lines, MR 786 (0.23**), ADB 532 (0.21**), NDLH 1938 (0.14**), ADB 542 (0.13**), H 1442 (0.12**) and BS 37 (0.08**) and in the testers GSB 40 (0.20**), DB 16 (0.16**) and DB 11 (0.03*).

The *sca* effects varied from -0.53 (L 762 × GSB 41) to 0.86 (TSH 0250 × GSB 40). Among 72 cross combinations evaluated, twenty four crosses recorded significant positive *sca* effects. The top five specific cross combinations were, TSH 0250 × GSB 40 (0.86**), L 762 × TCB 37 (0.57**), H 1442 × GSB 41 (0.54**), ADB 542 × DB 11 (0.32**) and L 762 × SUVIN (0.24**).

Boll weight seems to be under the control of both additive and non-additive gene actions in pooled analysis as variance due to *gca* (0.024*) was nearly equal to *sca* variance (0.025*). Further it was confirmed by the ratio of *gca* variance to *sca* variance which was nearer to unity (0.96). For improvement of number bolls plant⁻¹ breeding programmes like population improvement as well as heterosis breeding can be employed for exploitation of both the gene actions. These results are in conformity with the findings of Gamal *et al.* (2009), Bbebe *et al.* (2010), Rajamani *et al.* (2012), Baloch *et al.* (2014) and Patel and Jadon (2014).

Based on *per se* performance and *sca* effects the crosses viz., TSH 0250 × GSB 40 (Low × High), H 1442 × GSB 41 (High × Low) and ADB 542 × DB 11 (High × High) were noticed as superior hybrids for boll weight. The crosses involving low × high and high × low general combiners resulted in superior combinations which may be due to complementary gene action and the cross combinations involving high × high general combiners revealed additive and additive × additive genetic component of variance where the characters could be easily improved through simple selection procedures in recombination breeding.

4.8.7 Lint index (g)

Range of *gca* effects over locations for lint index was from -0.45 (BS 37) to 0.50 (L 1058) among lines and from -0.26 (SUVIN) to 0.38 (DB 16) among testers. Out of 12 lines, L 1058 (0.50**), MR 786 (0.29**), L 762 (0.24**), ADB 532 (0.15**) and H 1442 (0.10**) recorded significant positive *gca* effects. Whereas, in the testers DB 16 (0.38**), GSB 41 (0.12**) and GSB 40 (0.06**) exhibited significant *gca* effects in desired direction for this character.

The *sca* effects for lint index varied from -0.65 (MR 786 × DB 11) to 0.92 (TSH 0250 × GSB 40). Out of seventy two hybrids evaluated, twenty seven cross combinations exhibited significant positive *sca* effects and the hybrids, TSH 0250 × GSB 40 (0.92**), WGCV 48 × SUVIN (0.61**), SCS 793 × DB 11 (0.50**), L 762 × SUVIN (0.47**) and BS 37 × GSB 40 (0.44**) were observed as superior for this trait.

Estimated component of variance due to general combining ability (0.049*) was lower than due to specific combining ability (0.058*). The ratio of *gca* variance to *sca* variance (0.844) indicates that this trait was under control of non-additive gene action. Biparental mating or diallel selective mating or heterosis breeding may be employed for the improvement of this trait. Similar results were also reported by Mahantesh *et al.* (2010), Yanal *et al.* (2013), Patel *et al.* (2014) and Rajamani *et al.* (2014).

Based on *per se* performance and *sca* effects, the crosses, TSH 0250 × GSB 40 (Low × High), L 762 × SUVIN (High × Low) and WGCV 48 × SUVIN (Low × Low) were detected as promising specific cross combinations. The crosses with low × high and high × low combiners resulted in superior combinations which may be due to complementary gene action and the crosses between two low combiners producing crosses with significant *sca* effect due to nicking ability/genetic diversity of their parents.

4.8.8 Seed index (g)

General combining ability effects for seed index in pooled analysis varied from -0.79 (L 762) to 0.89 (ADB 532) in lines and in testers it ranged from -0.38 (GSB 41) to 0.28 (GSB 40). The lines, ADB 532 (0.89**), MCU 5 (0.50**), L 1058 (0.28**), MR 786 (0.22**) and SCS 793 (0.21**) and the testers GSB 40 (0.28**) and TCB 37 (0.15**) possessed significant positive *gca* effects for this character.

The cross combination, BS 37 × SUVIN (-1.52) recorded lowest *sca* effect whereas, the highest was exhibited by MR 786 × TCB 37 (1.18). Nineteen hybrids showed significant *sca* effects in positive direction and the top five crosses among them were, MR 786 × TCB 37 (1.18**), MCU 5 × DB 16 (0.97**), TSH 0250 × DB 11 (0.85**), BS 37 × TCB 37 (0.80**) and ADB 542 × GSB 41 (0.78**).

This character may be under the control of additive gene action as the variance due to *gca* (0.058) was higher than the *sca* (-0.122) and both were non-significant. This trait can be improved through hybridization followed by simple selection *i.e.*, pedigree method. These results are in accordance with the results of Kalpande *et al.* (2008), Wandhare *et al.* (2010), Kumar *et al.* (2013) and Usharani *et al.* (2014).

The crosses, MR 786 × TCB 37 (High × High), MCU 5 × DB 16 (High × Low) and BS 37 × TCB 37 (Low × High) were registered as good specific cross combinations as per their *per se* performance and *sca* effects. The cross combinations involving

high $\times$ high general combiners revealed additive and additive $\times$ additive genetic component of variance where the characters could be easily improved through simple selection procedures in recombination breeding. The crosses involving low $\times$ high and high $\times$ low *gca* effects resulted in superior combinations which may be due to complementary gene action.

4.8.9 Ginning out-turn (%)

In pooled analysis *gca* effects for lines ranged from -2.15 (MCU 5) to L 762 (2.22) whereas, for testers it was from -1.05 (SUVIN) to 1.35 (DB 16). Significant positive *gca* effects was recorded by L 762 (2.22**), L 1058 (1.45**), H 1442 (1.21**), MR 786 (0.73**), NDLH 1938 (0.65**) and ADB 542 (0.58**) in lines and DB 16 (1.35**) and GSB 41 (1.08**) in testers.

Among the crosses *sca* effects varied from -3.20 (TSH 0250 $\times$ SUVIN) to 5.17 (TSH 0250 $\times$ GSB 40). Out of 72 cross combinations evaluated, twenty one hybrids exhibited significant positive *sca* effects. The crosses, TSH 0250 $\times$ GSB 40 (5.17**), BS 37 $\times$ GSB 40 (2.56**), NDLH 1938 $\times$ DB 11 (2.42**), MR 786 $\times$ GSB 41 (2.29**), MR 786 $\times$ SUVIN (2.13**) and ADB 542 $\times$ DB 16 (2.13**) showed high *sca* effects in desirable direction for this character.

The component of variance due to *sca* (1.615**) was greater than *gca* (1.000**) indicating the predominance of non-additive gene action and can be exploited by biparental mating or diallel selective mating or heterosis breeding. Similar results were also reported by Patel *et al.* (2012), Yanal *et al.* (2013), Deosarkar *et al.* (2014) and Patel *et al.* (2014).

The superior specific cross combinations identified based on their *per se* performance and *sca* effects were, TSH 0250 $\times$ GSB 40 (Low $\times$ Low), MR 786 $\times$ GSB 41 (High $\times$ High) and ADB 542 $\times$ DB 16 (High $\times$ High). Superiority of low $\times$ low cross combination was mainly due to nicking ability/genetic diversity of their parents. The cross combinations involving high $\times$ high general combiners revealed additive and additive $\times$ additive genetic component of variance where the characters could be easily improved through simple selection procedures in recombination breeding.

4.8.10 2.5% span length (mm)

The *gca* effects for 2.5 % span length in pooled analysis varied from -1.54 (MR 786) to 1.56 (MCU 5) in lines and from -0.74 (DB 11) to 0.68 (TCB 37) in testers. The lines, MCU 5 (1.56**), BS 37 (0.90**), L 1058 (0.76**), ADB 532 (0.48**) and TSH 0250 (0.42**) and among the testers, TCB 37 (0.68**) and SUVIN (0.59**) exhibited significant positive *gca* effects in desired direction for this trait.

The *sca* effects exhibited variation from -1.50 (TSH 0250 × GSB 41) to 2.08 (H 1442 × DB 16) and significant positive *sca* effects was registered in 14 cross combinations. The top five cross combinations were, H 1442 × DB 16 (2.08**), TSH 0250 × GSB 40 (1.38**), SCS 793 × GSB 40 (1.25**), ADB 542 × SUVIN (0.99**), MR 786 × GSB 41 (0.99**) and L 1058 × DB 11 (0.92**).

The variance due to *gca* (0.399**) was higher than *sca* (0.331**). The ratio of *gca* variance to *sca* variance (1.205) indicated the importance of additive gene action in governing the inheritance of this trait. Hybridization followed by simple selection through pedigree method can be employed for improvement of this character. These results are in accordance with the results of Karademir *et al.* (2009), Ambhore *et al.* (2012), Amir *et al.* (2012), Kumar *et al.* (2013) and Mohammad *et al.* (2013).

Based on *per se* performance and *sca* effects the hybrids viz., TSH 0250 × GSB 40 (High × Low), H 1442 × DB 16 (Low × Low) and ADB 542 × SUVIN (Low × High) were detected as superior specific cross combinations. Low × high and high × low *gca* effects resulted in superior cross combinations which may be due to complementary gene action and also revealed the importance of both additive and non-additive gene actions. The superior cross combination between two low combiners mainly due to nicking ability/genetic diversity of their parents.

4.8.11 Uniformity ratio

Among the lines *gca* effects ranged from -0.79 (TSH 0250) to MR 786 (0.93) and among the testers it was from -0.62 (SUVIN) to 0.53 (DB 11). Out of 12 lines three lines viz., MR 786 (0.93**), SCS 793 (0.61**) and NDLH 1938 (0.52**) and three testers viz., DB 11 (0.53**), GSB 40 (0.36**) and GSB 41 (0.25*) exhibited significant positive *gca* effects.

For uniformity ratio *sca* effects exhibited a range from -1.16 (MR 786 × SUVIN) to 1.26 (MR 786 × TCB 37). Six hybrids viz., MR 786 × TCB 37 (1.26**), WGCV 48 × DB 11 (1.20**), BS 37 × GSB 40 (1.16**), L 762 × DB 16 (0.93*), L 1058 × SUVIN (0.85*) and MCU 5 × GSB 40 (0.80*) recorded significant positive *sca* effects.

In pooled analysis this character may be under the control of additive gene action as the variance due to *gca* (0.205) was higher than the *sca* (0.054) and both were non-significant. This character can be improved through hybridization followed by simple selection *i.e.*, pedigree method. Similar results were also reported by Mohammad *et al.* (2009), Deshmukh *et al.* (2010), Wandhare *et al.* (2010), Ambhore *et al.* (2012) and Nimbalkar *et al.* (2014).

The crosses, MR 786 × TCB 37 (High × Low), WGCV 48 × DB 11 (Low × High) and BS 37 × GSB 40 (Low × High) identified as good specific cross combinations based on positive *sca* effects and *per se* performance. The superior cross combinations between low × high and high × low *gca* effects resulted mainly due to complementary gene action and also revealed the importance of both additive and non-additive gene actions.

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

In pooled analysis over locations *gca* effects for lines varied from -0.16 (MCU 5) to 0.15 (H 1442) whereas, in testers it was from -0.06 (DB 11 and SUVIN) to 0.08 (DB 16). Estimates of *gca* effects were positive and significant for lines, H 1442 (0.15**), ADB 542 (0.14**), WGCV 48 (0.12**), L 762 (0.12**) and NDLH 1938 (0.11**) and for testers, DB 16 (0.08**), GSB 40 (0.03**) and GSB 41 (0.03**).

The *sca* effects ranged from -0.28 (NDLH 1938 × TCB 37 and H 1442 × DB 16) to 0.33 (ADB 542 × DB 16) and significant *sca* effects were recorded in 15 crosses. Highest *sca* effect was recorded by ADB 542 × DB 16 (0.33**) followed by H 1442 × GSB 41 (0.28**), TSH 0250 × GSB 40 (0.25**), NDLH 1938 × DB 11 (0.23**) and NDLH 1938 × DB 16 (0.22**).

The general combining ability variance (0.004**) was lower than specific combining ability variance (0.010**) showing the importance of non-additive gene action governing the inheritance of this character. Further, it was revealed by the ratio of *gca* variance to *sca* variance (0.400). Biparental mating or diallel selective mating or

heterosis breeding may be employed for the improvement of this trait. Similar results were also reported by Amir *et al.* (2012), Vineela *et al.* (2012), Kumar *et al.* (2013), Tuteja and Banga (2013), Deosarkar *et al.* (2014) and Rajamani *et al.* (2014).

The superior cross combinations found based on *per se* performance and *sca* effects were, ADB 542 × DB 16 (High × High), H 1442 × GSB 41 (High × High) and NDLH 1938 × DB 16 (High × High). The cross combinations involving high × high general combiners revealed additive and additive × additive genetic component of variance where the characters could be easily improved through simple selection procedures in recombination breeding.

4.8.13 Bundle strength (g/tex)

Estimates of *gca* effects over locations in pooled analysis for this trait varied from -1.15 (MR 786) to 0.82 (ADB 532) in lines and from -0.40 (DB 11) to 0.14 (DB 16) in testers. Significant and positive *gca* effects exhibited by ADB 532 (0.82**), MCU 5 (0.42**), BS 37 (0.34**) and SCS 793 (0.34**) in lines whereas, the testers DB 16 (0.14) GSB 40 (0.12), SUVIN (0.12) and TCB 37 (0.11) exhibited non-significant and positive *gca* effects.

The crosses, BS 37 × SUVIN (-1.86) and MCU 5 × GSB 40 (2.61) registered lowest and highest *sca* effects, respectively. Out of 72 cross combinations studied, fourteen hybrids possessed significant positive *sca* effects. Crosses viz., MCU 5 × GSB 40 (2.61**), H 1442 × DB 16 (2.36**), BS 37 × GSB 40 (1.78**), SCS 793 × DB 11 (1.46**) and L 1058 × SUVIN (1.23**) were the top five superior cross combinations.

The variance due to *sca* (0.564**) was high and significant than the *gca* (0.025) which was low and non-significant revealing the predominant role of non-additive gene action in controlling this character. Biparental mating or diallel selective mating or heterosis breeding may be employed for the improvement of this trait. These results are also confirmed by the findings of Karademir *et al.* (2009), Mahantesh *et al.* (2010), Vineela *et al.* (2012), Tuteja and Banga (2013) and Deosarkar *et al.* (2014).

Based on *per se* performance and positive *sca* effects the crosses, MCU 5 × GSB 40 (High × Low), H 1442 × DB 16 (Low × Low) and BS 37 × GSB 40 (High × Low) were detected as best specific cross combinations for this character. The crosses with high × low combiners resulted in superior combinations which may be due to

complementary gene action and the crosses between two low combiners producing superior cross combinations indicating the nicking ability/genetic diversity of their parents.

4.8.14 Fibre elongation (%)

The *gca* effects for lines in pooled analysis ranged from -0.14 (TSH 0250) to 0.08 (NDLH 1938) and from -0.07 (TCB 37) to 0.09 (DB 16) in testers. Among the lines, NDLH 1938 (0.08**), ADB 542 (0.06**), BS 37 (0.05*) and L 762 (0.05*) whereas, in testers, DB 16 (0.09**) and GSB 41(0.03*) possessed significant positive *gca* effects

Estimates of *sca* effects varied from -0.23 (MR 786 × DB 11) to 0.20 (MR 786 × GSB 41). Thirteen crosses recorded significant *sca* effects and the top five specific cross combinations were, MR 786 × GSB 41 (0.20**), BS 37 × GSB 40 (0.19**), MR 786 × TCB 37 (0.18**), TSH 0250 × DB 16 (0.16**) and NDLH 1938 × DB 16 (0.14**).

The component of variance due to specific combining ability (0.008*) was greater than the general combining ability (0.002**). The ratio of *gca* variance to *sca* variance (0.300) exhibiting the operation of non-additive gene action and it can be exploited by bi-parental mating or diallel selective mating or heterosis breeding. Similar results were also reported by Preetha and Raveendran (2008), Basal *et al.* (2009), Mahantesh *et al.* (2010), Vineela *et al.* (2012) and Deosarkar *et al.* (2014).

The crosses, BS 37 × GSB 40 (High × Low), MR 786 × GSB 41 (Low × High) and TSH 0250 × DB 16 (Low × High) were identified as best specific cross combinations based on their *per se* performance and *sca* effects. The crosses involving high × low and low × high *gca* effects resulted in superior combinations which may be due to complementary gene action.

4.8.15 Seed cotton yield Plant⁻¹ (g)

The *gca* effects among the lines ranged from -55.60 (MCU 5) to 25.40 (H 1442) and from -22.73 (SUVIN) to 16.62 (DB 16) in testers. Significant and positive *gca* effects were desirable for this trait and were noticed in the lines, H 1442 (25.40**), NDLH 1938 (25.23**), MR 786 (16.75**), ADB 542 (11.21**), BS 37 (10.51**), L 762 (7.56**) and ADB 532 (4.22*) and the testers viz., DB 16 (16.62**), GSB 41 (8.90**), GSB 40 (7.58**) and DB 11 (4.83**).

Among the cross combinations, *sca* effects varied from -43.25 (L 762 × GSB 41) to 76.56 (TSH 0250 × GSB 40) and significant positive *sca* effects were shown by 22 cross combinations. The hybrids, TSH 0250 × GSB 40 (76.56**), L 762 × TCB 37 (49.58**), H 1442 × GSB 41 (34.97**), BS 37 × SUVIN (28.63**) and ADB 542 × DB 16 (28.56**) were identified as superior crosses.

The estimated component of general combining ability variance (242.903**) was higher than the specific combining ability variance (178.669*) revealing the predominance of additive gene action in controlling this trait. The ratio of *gca* variance to *sca* variance (1.359) showed the same. Further improvement of this trait can be possible through hybridization followed by simple selection *i.e.*, pedigree method. These results are in accordance with the results of Bbebe *et al.* (2010), Amir *et al.* (2012), Mohammad *et al.* (2013), Simon *et al.* (2013), Patel *et al.* (2014) and Usharani *et al.* (2014).

The crosses, H 1442 × GSB 41 (High × High), TSH 0250 × GSB 40 (Low × High) and ADB 542 × DB 16 (High × High) were identified as best specific cross combinations as per their *per se* performance and *sca* effects. The cross combinations involving high × high general combiners leading to superior performance revealed additive and additive × additive genetic component of variance where the characters could be easily improved through simple selection procedures in recombination breeding and the crosses with low × high combiners resulted in superior combinations which may be due to complementary gene action.

4.8.16 Lint yield Plant⁻¹ (g)

Range of *gca* effects for lint yield plant⁻¹ varied from -19.40 (MCU 5) to 9.87 (H 1442) in lines and from -8.50 (SUVIN) to 7.26 (DB 16) in testers. Out of twelve lines, H 1442 (9.87**), NDLH 1938 (8.97**), MR 786 (6.08**), L 762 (5.69**) and ADB 542 (4.16**) and three testers *viz.*, DB 16 (7.26**), GSB 41 (4.58**) and GSB 40 (2.12**) exhibited significant and positive *gca* effects in desirable direction for this character.

Specific combining ability effects ranged from -14.25 (L 762 × GSB 41) to 33.18 (TSH 0250 × GSB 40) and significant positive *sca* effects were exhibited by 21 cross combinations. The top five superior cross combinations identified were, TSH 0250 × GSB 40 (33.18**), L 762 × TCB 37 (17.38**), H 1442 × GSB 41 (15.37**), ADB 542 × DB 16 (14.28**) and BS 37 × SUVIN (10.73**).

The variance due to specific combining ability (47.246**) was greater than the general combining ability (34.949**). The ratio of *gca* variance to *sca* variance (0.739) revealed the importance of non-additive gene action in the inheritance of this character. Biparental mating or diallel selective mating or heterosis breeding can be employed for the improvement of this trait. These results are in agreement with the findings of Sheraz *et al.* (2011), Imran *et al.* (2012), Patel *et al.* (2012) and Vineela *et al.* (2012).

Based on *per se* performance and *sca* effects H 1442 × GSB 41 (High × High), TSH 0250 × GSB 40 (Low × High) and ADB 542 × DB 16 (High × High) were identified as best specific cross combinations. The cross combinations involving high × high general combiners revealed additive and additive × additive genetic component of variance which could be easily improved through simple selection procedures in recombination breeding. Low × high *gca* effects resulted in superior cross combinations which may be due to complementary gene action and revealed the importance of both additive and non-additive gene actions.

A perusal of *gca* effects from pooled analysis revealed that out of 18 parents (12 lines + 6 testers) tested none of the parent recorded significant *gca* effects for all the characters in desirable direction. Among the lines studied, the line NDH 1938 recorded significant *gca* effects in desirable direction for days to 50% flowering, plant height, number of sympodia plant⁻¹, number of bolls plant⁻¹, boll weight, ginning out-turn, micronaire, uniformity ratio, fibre elongation, seed cotton yield plant⁻¹ and lint yield plant⁻¹ and H 1442 recorded significant *gca* effects in desirable direction for days to 50% flowering, number of sympodia plant⁻¹, number of bolls plant⁻¹, boll weight, lint index, ginning out-turn, micronaire value, seed cotton yield plant⁻¹ and lint yield plant⁻¹. The line, ADB 542, recorded significant positive *gca* effects for plant height, number of monopodia plant⁻¹, number of bolls plant⁻¹, boll weight, ginning out-turn, micronaire value, fibre elongation, seed cotton yield plant⁻¹ and lint yield plant⁻¹. While, ADB 532 showed significant positive *gca* effects for number of monopodia plant⁻¹, boll weight, lint index, seed index, 2.5% span length, bundle strength and seed cotton yield plant⁻¹ and WGCV 48 exhibited significant positive *gca* effects for number of monopodia plant⁻¹ and micronaire value. Whereas, the line, MR 786, recorded significant positive *gca* effects for plant height, number of sympodia plant⁻¹, number of bolls plant⁻¹, boll weight, lint index, seed index, ginning out-turn, uniformity ratio, seed cotton yield plant⁻¹ and lint yield plant⁻¹ and TSH 0250 showed significant positive *gca* effects only for one character *i.e.*, 2.5% span length.

The line, BS 37 exhibited significant *gca* effects for number of monopodia plant⁻¹, number of bolls plant⁻¹, boll weight, 2.5% span length, bundle strength, elongation and seed cotton yield plant⁻¹ and SCS 793 recorded significant positive *gca* effects for number of sympodia plant⁻¹, number of bolls plant⁻¹, seed index, bundle strength and uniformity ratio. Whereas, MCU 5 recorded significant positive *gca* effects for seed index, 2.5% span length and bundle strength and L 1058 exhibited significant positive *gca* effects for number of monopodia plant⁻¹, lint index, seed index, ginning out-turn and 2.5% span length. While, L 762 showed significant *gca* effects in desirable direction for days to 50% flowering, number of bolls plant⁻¹, lint index, ginning out-turn, micronaire value, fibre elongation, seed cotton yield plant⁻¹ and lint yield plant⁻¹.

Among the testers, GSB 40 exhibited significant *gca* effects for plant height, number of monopodia plant⁻¹, number of sympodia plant⁻¹, boll weight, lint index, seed index, micronaire value, uniformity ratio, seed cotton yield plant⁻¹ and lint yield plant⁻¹ and DB 16 recorded significant *gca* effects in desirable direction for days to 50% flowering, number of sympodia plant⁻¹, number of bolls plant⁻¹, boll weight, lint index, ginning out-turn, micronaire value, fibre elongation, seed cotton yield plant⁻¹ and lint yield plant⁻¹. The tester, DB 11 showed significant positive *gca* effects for number of bolls plant⁻¹, boll weight, uniformity ratio and seed cotton yield plant⁻¹ and GSB 41 exhibited significant *gca* effects in desirable direction for days to 50% flowering, number of monopodia plant⁻¹, number of sympodia plant⁻¹, number of bolls plant⁻¹, lint index, ginning out-turn, micronaire value, uniformity ratio, fibre elongation, seed cotton yield plant⁻¹ and lint yield plant⁻¹. While, TCB 37 recorded significant positive *gca* effects for seed index and 2.5 % span length and SUVIN exhibited significant positive *gca* effects only for two characters viz., number of monopodia plant⁻¹ and 2.5% span length (Table 4.30).

The crosses between two low combiners producing crosses with significant *sca* effect revealed the role of non-additive inter-allelic interaction. This may be due to high nicking ability/genetic diversity of parents involved. This component may be exploited through heterosis breeding. The crosses between high $\times$ low or low $\times$ high combiners resulted in superior cross combinations due to complementary gene action which has arisen out of both additive and non-additive gene action. These crosses may likely to throw superior transgressive segregants for desirable traits. These components may be exploited by adopting breeding procedures like cyclic hybridization, biparental mating and diallel selective mating system. The cross

combinations involving high $\times$ high general combiners producing crosses with significant *sca* effect revealed the role of additive and additive $\times$ additive genetic component of variance which could be easily improved through simple selection procedures.

The crosses, H 1442 $\times$ GSB 41, TSH 0250 $\times$ GSB 40 and ADB 542 $\times$ DB 16, showed high *per se* performance and positive *sca* effects for seed cotton yield plant⁻¹ and also recorded significant *sca* effects for yield contributing and fibre quality traits like, number of sympodia plant⁻¹ (TSH 0250 $\times$ GSB 40, ADB 542 $\times$ DB 16), number of bolls plant⁻¹ (TSH 0250 $\times$ GSB 40, ADB 542 $\times$ DB 16), boll weight (H 1442 $\times$ GSB 41, TSH 0250 $\times$ GSB 40 and ADB 542 $\times$ DB 16), ginning out-turn (H 1442 $\times$ GSB 41, TSH 0250 $\times$ GSB 40 and ADB 542 $\times$ DB 16) and 2.5% span length (TSH 0250 $\times$ GSB 40).

4.9 HETEROSIS

Study on the magnitude of heterosis in F₁s helps to assess the ability of the test genotypes to transmit the desirable characters to the F₁s upon hybridization. This facilitates in identification of genotypes that exhibit high amount of exploitable heterosis. In the present investigation, 72 inter-specific cotton hybrids obtained by crossing twelve *hirsutum* genotypes with six *barbadense* genotypes in line $\times$ tester fashion. Heterosis of F₁s over mid parent (average heterosis), better parent (heterobeltiosis) and standard checks (standard heterosis) estimated for seed cotton yield, yield components and quality traits over three locations (pooled) and presented in Tables 4.31 to 4.36 and described character-wise here under.

4.9.1 Days to 50% Flowering

Days to 50% flowering in pooled analysis recorded significant positive average heterosis in 53 hybrids, ranging from -17.25 (L 762 $\times$ DB 16) to 5.25 (L 1058 $\times$ DB 16). All the hybrids exhibited significant negative heterobeltiosis and ranging from -21.35 (H 1442 $\times$ GSB 41) to -2.62 (L 1058 $\times$ DB 16). The negative standard heterosis was observed in two hybrids which was ranged from -7.22 (H 1442 $\times$ GSB 41) to 16.85 (L 1058 $\times$ DB 16) over DCH 32 and it was from -7.73 (H 1442 $\times$ GSB 41) to 16.21 (L 1058 $\times$ DB 16) over Mahalakshmi.

High significant negative standard heterosis over both the checks was recorded by H 1442 $\times$ GSB 41(55.67) and L 762 $\times$ DB 16 (58.11) and superiority of these hybrids was further confirmed by their *per se* performance and high *sca* effects. These results are

in agreement with the reports of Dukre *et al.* (2007), Deosarkar *et al.* (2009a) and Amalabalu *et al.* (2012) for heterosis over mid parent and are in agreement with the reports of Deosarkar *et al.* (2009a), Haleem *et al.* (2010) and Amalabalu *et al.* (2012) for heterobeltiosis and Deosarkar *et al.* (2009a) and Amalabalu *et al.* (2012) for heterosis over standard check.

4.9.2 Plant Height (cm)

Average heterosis ranged from 17.70 (H 1442 × DB 16) to 47.72 (ADB 542 × TCB 37), heterobeltiosis from 6.66 (H 1442 × DB 16) to 40.55 (NDLH 1938 × TCB 37) and standard heterosis over DCH 32 and Mahalakshmi ranged from -6.56 (ADB 532 × TCB 37) to 21.36 (NDLH 1938 × GSB 40) and from -16.31 (ADB 532 × TCB 37) to 8.70 (NDLH 1938 × GSB 40), respectively. All the hybrids recorded significant positive heterosis over mid parent. Seventy one hybrids exhibited heterobeltiosis in desirable direction whereas, forty two hybrids over DCH 32 and seventeen hybrids over Mahalakshmi showed significant positive heterosis.

Based on overall performance (*per se*, *sca* effects and standard heterosis) the top three specific combiners identified for this trait were, NDLH 1938 × GSB 40 (194.54), NDLH 1938 × GSB 41 (190.59) and H 1442 × DB 11 (189.85). These results are in agreement with the reports of Dukre *et al.* (2007), Jesus *et al.* (2007), Deosarkar *et al.* (2009a), Amalabalu *et al.* (2012), Patel *et al.* (2012) and Punitha *et al.* (2012) for heterosis over mid parent; Patel *et al.* (2005), Jesus *et al.* (2007), Deosarkar *et al.* (2009a), Wankhade *et al.* (2009), Amalabalu *et al.* (2012), Patel *et al.* (2012) and Punitha *et al.* (2012) for heterobeltiosis and Deosarkar *et al.* (2009a), Wankhade *et al.* (2009), Amalabalu *et al.* (2012), Patel *et al.* (2012), Kumar *et al.* (2013) and Nirania *et al.* (2014) for heterosis over standard check.

4.9.3 Number of Monopodia Plant⁻¹

Number of monopodia plant⁻¹ in pooled analysis recorded significant positive average heterosis in 66 hybrids, ranging from -2.91 (H 1442 × DB 16) to 164.73 (MCU 5 × TCB 37). The significant positive heterosis over better parent was registered in 59 hybrids, with a range of -18.27 (TSH 0250 × DB 11) to 144.23 (MCU 5 × TCB 37). Standard heterosis over DCH 32 and Mahalakshmi ranged from -15.19 (TSH 0250 × TCB 37) to 87.94 (ADB 532 × GSB 41) and -47.26 (TSH 0250 × TCB 37) to 16.86 (ADB 532 × GSB 41), respectively. Sixty two and eight hybrids showed significant positive heterosis over DCH 32 and Mahalakshmi, respectively.

The best heterotic hybrids identified based on *per se* and *sca* effects were, ADB 532 × GSB 41(3.20) followed by BS 37 × GSB 40 (3.18) and WGCV 48 × TCB 37 (3.03). These results are in agreement with the reports of Reddy (2001) and Deosarkar *et al.* (2009a) for heterosis over mid parent; for heterobeltiosis, with the results of Reddy (2001) and Deosarkar *et al.* (2009a); Kumar *et al.* (2013), Nirania *et al.* (2014) and Tuteja (2014) for heterosis over standard check.

4.9.4 Number of Sympodia Plant⁻¹

Heterosis over mid parent ranged from 18.63 (ADB 532 × GSB 41) to 94.95 (MR 786 × GSB 41) and over better parent it ranged from 16.80 (ADB 532 × GSB 41) to 80.34 (MR 786 × GSB 41). Heterosis over standard checks DCH 32 and Mahalakshmi ranged from -12.52 (MCU 5 × TCB 37) to 36.96 (MR 786 × GSB 41) and -21.46 (MCU 5 × TCB 37) to 22.97 (MR 786 × GSB 41), respectively. Significant positive average heterosis and heterobeltiosis was observed in all the hybrids. Among seventy two hybrids studied, twenty one and four hybrids exhibited significant positive values over DCH 32 and Mahalakshmi, respectively.

Based on *per se* performance, *sca* effects and standard heterosis the hybrids viz., MR 786 × GSB 41(31.43), ADB 542 × DB 16 (28.02) and H 1442 × DB 16 (27.29) were found to be superior. These findings are on par with the reports of Potdukhe (2002), Dukre *et al.* (2007), Deosarkar *et al.* (2009a), Haleem *et al.* (2010), Amalabalu *et al.* (2012) and Punitha *et al.* (2012) for heterosis over mid parent; whereas, Deosarkar *et al.* (2009a), Wankhade *et al.* (2009), Haleem *et al.* (2010), Amalabalu *et al.* (2012), Nidagundi *et al.*(2012) and Punitha *et al.* (2012) for heterobeltiosis; Deosarkar *et al.* (2009a), Wankhade *et al.* (2009), Amalabalu *et al.* (2012), Nirania *et al.* (2014) and Tuteja (2014) for heterosis over standard check.

4.9.5 Number of Bolls Plant⁻¹

Relative heterosis for this character varied from 11.01 (SCS 793 × GSB 40) to 83.89 (NDLH 1938 × TCB 37), heterobeltiosis ranged from -5.91 (MCU 5 × GSB 40) to 77.73 (BS 37 × SUVIN) and standard heterosis over DCH 32 and Mahalakshmi ranged from -27.95 (TSH 0250 × TCB 37) to 30.09 (BS 37 × SUVIN) and -38.84 (TSH 0250 × TCB 37) to 10.43 (BS 37 × SUVIN), respectively. All the hybrids recorded significant positive heterosis over mid parent. Out of 72 hybrids studied, sixty seven hybrids over better parent, forty one hybrids over DCH 32 and six hybrids over Mahalakshmi showed positive significant heterosis.

The potential hybrids identified as per *per se* performance, *sca* effects and standard heterosis were, BS 37 × SUVIN (79.98), H 1442 × DB 16 (78.91) and BS 37 × GSB 41(77.89). Similar results for number of bolls plant⁻¹ were earlier reported by Deosarkar *et al.* (2009a), Haleem *et al.* (2010), Amalabalu *et al.* (2012), Patel *et al.* (2012) and Punitha *et al.* (2012) for heterosis over mid parent; Deosarkar *et al.* (2009a), Wankhade *et al.* (2009), Amalabalu *et al.* (2012) and Patil *et al.* (2014) for heterosis over better parent; Deosarkar *et al.* (2009a), Amalabalu *et al.* (2012), Kumar *et al.* (2013), Nirania *et al.* (2014) and Tuteja (2014) for heterosis over standard check.

4.9.6 Boll Weight (g)

Boll weight in pooled analysis recorded significant positive heterosis over mid parent in twenty six hybrids which was ranged from -18.08 (MCU 5 × DB 11) to 26.67 (TSH 0250 × GSB 40). Heterobeltiosis ranged from -33.96 (MCU 5 × SUVIN) to 8.88 (TSH 0250 × GSB 40) and only one hybrid (TSH 0250 × GSB 40) exhibited significant positive heterobeltiosis. Standard heterosis over DCH 32 and Mahalakshmi ranged from -23.36 (SCS 793 × TCB 37) to 23.29 (TSH 0250 × GSB 40) and -30.60 (SCS 793 × TCB 37) to 11.63 (TSH 0250 × GSB 40), respectively. Standard heterosis in desirable direction was observed in seventeen hybrids over DCH 32 and two hybrids over Mahalakshmi.

Based on overall performance (*per se* performance, *sca* effects and standard heterosis) the best specific cross combinations identified were, TSH 0250 × GSB 40 (4.21), H 1442 × GSB 41(3.97) and ADB 532 × GSB 40 (3.84). These results are in conformity with the reports of Deosarkar *et al.* (2009a), Haleem *et al.* (2010), Amalabalu *et al.* (2012), Patel *et al.* (2012) and Seoudy *et al.* (2014) for heterosis over mid parent; Wankhade *et al.* (2009), Amalabalu *et al.* (2012), Nidagundi *et al.* (2012), Punitha *et al.* (2012) and Seoudy *et al.* (2014) over better parent; Wankhade *et al.* (2009), Amalabalu *et al.* (2012), Patel *et al.* (2012), Kumar *et al.* (2013) and Nirania *et al.* (2014) over standard check.

4.9.7 Lint index (g)

Mid parent heterosis ranged from -13.27 (MCU 5 × GSB 40) to 29.99 (L 762 × SUVIN), heterobeltiosis from -20.98 (MCU 5 × GSB 40) to 27.41 (L 762 × SUVIN) and over standard checks DCH 32 and Mahalakshmi varied from -19.80 (TSH 0250 × SUVIN) to 19.82 (L 1058 × DB 16) and -30.60 (TSH 0250 × SUVIN) to 3.70 (L 1058 ×

DB 16), respectively. Significant positive average heterosis was found in forty seven hybrids, heterobeltiosis in twenty eight hybrids while standard heterosis over DCH 32 was found in thirty two hybrids and over Mahalakshmi in one hybrid (L 1058 $\times$ DB 16).

The best performing hybrids identified based on *per se* performance, *sca* effects and standard heterosis were ADB 532 $\times$ DB 16 (6.02) and TSH 0250 $\times$ GSB 40 (5.93). These results are in conformity with the reports of Amalabalu *et al.* (2012), Punitha *et al.* (2012) and Seoudy *et al.* (2014) for heterosis over mid parent; Wankhade *et al.* (2009), Amalabalu *et al.* (2012), Nidagundi *et al.* (2012), Punitha *et al.* (2012) and Seoudy *et al.* (2014) for heterosis over better parent and Amalabalu *et al.* (2012) and Kumar *et al.* (2013) for heterosis over standard check.

4.9.8 Seed index (g)

In pooled analysis all the hybrids recorded significant positive average heterosis and it ranged from 6.01 (L 762 $\times$ GSB 41) to 41.62 (MR 786 $\times$ TCB 37). The significant positive heterobeltiosis was observed in 56 hybrids with a range of -2.98 (TSH 0250 $\times$ GSB 40) to 36.83 (MR 786 $\times$ TCB 37). The significant positive heterosis was detected in fifty nine hybrids over DCH 32 and it varied from -3.59 (BS 37 $\times$ SUVIN) to 24.59 (ADB 532 $\times$ GSB 40), one hybrid (ADB 532 $\times$ GSB 40) over Mahalakshmi and it ranged from -19.73 (BS 37 $\times$ SUVIN) to 3.73 (ADB 532 $\times$ GSB 40).

Based on *per se* performance, positive *sca* effects and standard heterosis superior cross combinations identified were, ADB 532 $\times$ GSB 40 (14.34), ADB 532 $\times$ DB 16 (14.22) and MR 786 $\times$ TCB 37 (14.19). Similar type of results were earlier reported by Pole *et al.* (2008), Amalabalu *et al.* (2012), Punitha *et al.* (2012) and Seoudy *et al.* (2014) for heterosis over mid parent; Deosarkar *et al.* (2009a), Amalabalu *et al.* (2012), Punitha *et al.* (2012) and Seoudy *et al.* (2014) for heterosis over better parent; Amalabalu *et al.* (2012), Kumar *et al.* (2013), Nirania *et al.* (2014) and Tuteja (2014) for heterosis over standard check.

4.9.9 Ginning out-turn (%)

Relative heterosis for this trait varied from -26.77 (BS 37 $\times$ TCB 37) to 7.22 (L 762 $\times$ SUVIN), heterobeltiosis varied from -28.00 (BS 37 $\times$ TCB 37) to 3.49 (MR 786 $\times$ GSB 41) and only one hybrid (MR 786 $\times$ GSB 41) exhibited positive significant heterobeltiosis. The heterosis over DCH 32 and Mahalakshmi ranged from -22.21 (BS

37 × TCB 37) to 9.43 (TSH 0250 × GSB 40) and -20.45 (BS 37 × TCB 37) to 11.92 (TSH 0250 × GSB 40), respectively. Among 72 hybrids studied, seven hybrids for average heterosis, nine hybrids over DCH 32 and twelve hybrids over Mahalakshmi exhibited significant positive heterosis.

Best specific cross combinations detected based on overall performance for this trait were, TSH 0250 × GSB 40 (33.49), L 1058 × DB 16 (33.24) and MR 786 × GSB 41(33.13). These results are in conformity with the reports of Deosarkar *et al.* (2009a), Amalabalu *et al.* (2012) and Patel *et al.* (2012).

4.9.10 2.5 % span length (mm)

All the hybrids exhibited significant positive mid parent heterosis for this character ranging from 5.45 (NDLH 1938 × GSB 41) to 22.89 (H 1442 × DB 16). The significant positive heterobeltiosis was recorded in twenty four hybrids with a range of -6.52 (L 762 × TCB 37) to 11.66 (MCU 5 × GSB 40). The significant standard heterosis was recorded in 36 hybrids over DCH 32 and it varied from -3.45 (MR 786 × GSB 40) to 12.30 (MCU 5 × SUVIN). Heterosis over Mahalakshmi ranged from -5.12 (MR 786 × GSB 40) to 10.36 (MCU 5 × SUVIN) and was recorded positive values in twenty six hybrids.

Based on *per se* performance, *sca* effects and standard heterosis the hybrids viz., MCU 5 × SUVIN (37.97), MCU 5 × GSB 40 (37.29) and L 1058 × SUVIN (37.02) were identified as superior specific cross combinations. Karademir *et al.* (2009), Rajamani *et al.* (2009), Amalabalu *et al.* (2012), Patil *et al.* (2012) and Punitha *et al.* (2012) for heterosis over mid parent; Syed and Sajid (2008), Wankhade *et al.* (2009), Amalabalu *et al.* (2012) and Deshmukh *et al.* (2014) for heterosis over better parent and Amalabalu *et al.* (2012), Patil *et al.* (2012) and Tuteja (2014) for heterosis over standard check reported positive heterosis.

4.9.11 Uniformity ratio

Heterosis over mid parent varied from -6.78 (ADB 532 × DB 16) to 0.24 (MCU 5 × GSB 40). Heterobeltiosis ranged from -10.38 (MR 786 × SUVIN) to -0.53 (BS 37 × GSB 40). None of the hybrid showed significant positive heterosis over both mid and better parents. Heterosis over DCH 32 and Mahalakshmi varied from -3.56 (MCU 5 × DB 16) to 4.41 (MR 786 × TCB 37) and -6.37 (MCU 5 × DB 16) to 1.36 (MR 786 ×

TCB 37), respectively. None of the hybrid exhibited significant positive heterosis over Mahalakshmi whereas, nine hybrids recorded significant heterosis over DCH 32 in desirable direction for this trait.

Potential hybrids detected based on overall performance for uniformity ratio were, MR 786 × TCB 37 (47.50), WGCV 48 × DB 11 (47.42) and BS 37 × GSB 40 (47.22). These findings are in conformity with the results of Reddy (2001), Rajamani *et al.* (2009) and Patil *et al.* (2012).

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

Heterosis over mid parent varied from -34.03 (MR 786 × SUVIN) to -2.09 (NDLH 1938 × DB 16) whereas, heterobeltiosis varied from -38.29 (L 762 × SUVIN) to -11.21 (NDLH 1938 × DB 16). Heterosis over standard checks, DCH 32 and Mahalakshmi ranged from -0.26 (TSH 0250 × GSB 41) to 34.06 (ADB 542 × DB 16) and -17.46 (TSH 0250 × GSB 41) to 10.94 (ADB 542 × DB 16), respectively. None of the hybrid recorded significant positive relative heterosis and heterobeltiosis for this trait. Sixty six hybrids over DCH 32 and three hybrids over Mahalakshmi possessed significant positive heterosis.

The top three superior specific cross combinations were viz., ADB 542 × DB 16 (3.40), H 1442 × GSB 41 (3.32) and NDLH 1938 × DB 16 (3.26) as per their overall performance. These findings are in accordance with the results of Dukre *et al.* (2007), Karademir *et al.* (2009), Rajamani *et al.* (2009) and Patil *et al.* (2012) over mid parent; Jesus *et al.* (2007), Rajamani *et al.* (2009) and Deshmukh *et al.* (2014) over better parent; whereas, positive heterosis over standard check was reported by Rajamani *et al.* (2009) and Patil *et al.* (2012).

4.9.13 Bundle strength (g/tex)

Pooled analysis for heterosis over locations revealed that 71 hybrids recorded significant average heterosis and it ranged from -1.10 (BS 37 × SUVIN) to 25.89 (H 1442 × DB 16). The significant heterobeltiosis was recorded in nine hybrids with a range of -12.65 (MR 786 × SUVIN) to 13.80 (MCU 5 × GSB 40). The significant positive heterosis registered in 49 hybrids over DCH 32 and it ranged from -2.65 (MR 786 × DB 11) to 17.50 (MCU 5 × GSB 40) and 25 hybrids over Mahalakshmi and it ranged from -5.71 (MR 786 × DB 11) to 13.80 (MCU 5 × GSB 40).

The hybrids, MCU 5 × GSB 40 (30.17), H 1442 × DB 16 (29.66) and BS 37 × GSB 40 (29.26) were identified as best specific cross combinations as per their *per se* performance, *sca* effects and standard heterosis. These findings are in agreement with the results of heterosis over mid parent reported by Rajamani *et al.* (2009), Patil *et al.* (2012) and Punitha *et al.* (2012); over better parent by Karademir *et al.* (2009), Rajamani *et al.* (2009), Punitha *et al.* (2012) and Deshmukh *et al.* (2014) whereas, heterosis over standard check was reported by Wankhade *et al.* (2009), Patil *et al.* (2012), Tuteja *et al.* (2013) and Tuteja (2014).

4.9.14 Fibre elongation (%)

Relative heterosis for this trait varied from -9.38 (MR 786 × DB 11) to 2.69 (NDLH 1938 × DB 16) while, heterobeltiosis ranged from -11.50 (MR 786 × DB 11) to 0.02 (MR 786 × GSB 41). Heterosis over DCH 32 and Mahalakshmi varied from -1.82 (TSH 0250 × SUVIN) to 13.26 (NDLH 1938 × DB 16) and -7.54 (TSH 0250 × SUVIN) to 6.66 (NDLH 1938 × DB 16), respectively. One hybrid (NDLH 1938 × DB 16) over mid parent and none of the hybrid over better parent exhibited significant positive values. Sixty four hybrids over DCH 32 and nine hybrids over Mahalakshmi recorded significant heterosis in desirable direction.

The potential hybrids identified based on overall performance for fibre elongation % were NDLH 1938 × DB 16 (5.25), BS 37 × GSB 40 (5.19) and MR 786 × GSB 41 (5.15). These findings are in conformity with the results of heterosis over mid parent reported by Karademir *et al.* (2009) and Patil *et al.* (2012); over better parent was reported by Patil *et al.* (2012) and Deshmukh *et al.* (2014), while, heterosis over standard check was reported by Patil *et al.* (2012).

4.9.15 Seed cotton yield Plant⁻¹ (g)

Seed cotton yield plant⁻¹ in pooled analysis recorded significant positive average heterosis in 67 hybrids and it ranged from -2.11 (MCU 5 × DB 11) to 106.74 (H 1442 × GSB 41). Significant positive heterobeltiosis was registered in sixty two hybrids with a range of -21.95 (SCS 793 × TCB 37) to 96.40 (TSH 0250 × GSB 40). Heterosis over DCH 32 and Mahalakshmi ranged from -38.33 (TSH 0250 × TCB 37) to 45.61 (H 1442 × GSB 41) and -46.14 (TSH 0250 × TCB 37) to 27.18 (H 1442 × GSB 41), respectively. Thirty four hybrids over DCH 32 and thirteen hybrids over Mahalakshmi showed significant positive heterosis.

Based on *per se* performance, *sca* effects and standard heterosis superior specific cross combinations identified were, H 1442 × GSB 41(253.36), H 1442 × DB 16 (251.38) and TSH 0250 × GSB 40 (248.02). Similar results for significant positive heterosis over mid parent were reported by Syed and Sajid (2008), Karademir *et al.* (2009), Haleem *et al.* (2010), Punitha *et al.* (2012) and Seoudy *et al.* (2014); over better parent was reported by Rajamani *et al.* (2009), Amalabalu *et al.* (2012), Nidagundi *et al.* (2012), Punitha *et al.* (2012) and Deshmukh *et al.* (2014) whereas, heterosis over standard check was reported by Wankhade *et al.* (2009), Amalabalu *et al.* (2012), Patel *et al.* (2012), Kumar *et al.* (2013), Tuteja *et al.* (2013), Nirania *et al.* (2014) and Tuteja (2014).

4.9.16 Lint yield Plant⁻¹ (g)

Average heterosis for this character varied from -20.39 (TSH 0250 × TCB 37) to 112.76 (TSH 0250 × GSB 40) and heterobeltiosis ranged from -32.88 (TSH 0250 × TCB 37) to 101.38 (ADB 542 × DB 16). Heterosis over DCH 32 and Mahalakshmi ranged from -47.27 (TSH 0250 × TCB 37) to 57.03 (H 1442 × GSB 41) and -52.87 (TSH 0250 × TCB 37) to 40.36 (H 1442 × GSB 41), respectively. Significant positive average heterosis was observed in sixty two hybrids whereas, forty nine hybrids recorded significant positive heterobeltiosis. Twenty five hybrids over DCH 32 and eleven hybrids over Mahalakshmi exhibited significant positive heterosis in desirable direction.

The hybrids, H 1442 × GSB 41 (83.71), TSH 0250 × GSB 40 (83.08) and ADB 542 × DB 16 (79.60) were identified as best specific cross combinations for lint yield plant⁻¹ based on their *per se* performance, *sca* effects and standard heterosis. Similar findings were earlier reported by Paulo *et al.* (2007), Pole *et al.* (2008), Karademir *et al.* (2009), Haleem *et al.* (2010) and Seoudy *et al.* (2014) for heterosis over mid parent; whereas, Pole *et al.* (2008), Haleem *et al.* (2010), Nidagundi *et al.* (2012), Patil *et al.* (2014) and Seoudy *et al.* (2014) for heterobeltiosis and Tuteja *et al.* (2005) and Patil *et al.* (2014) over standard check.

Promising hybrids based on *per se* performance, *sca* effects and standard heterosis

Based on overall performance (*per se* performance, significant *sca* effects and standard heterosis) for seed cotton yield plant⁻¹ in pooled analysis the hybrids, H 1442 × GSB 41, H 1442 × DB 16 and TSH 0250 × GSB 40 recorded high *per se* performance

(253.36, 251.38 and 248.02), significant *sca* effects (34.97, 25.28 and 76.56) and standard heterosis over DCH 32 and Mahalakshmi (45.61% & 27.18%, 44.47% & 26.18%, 42.54 % & 24.50%). Besides seed cotton yield plant⁻¹ the hybrids exhibited good *per se* performance, significant *sca* effects and standard heterosis for other important yield contributing characters viz., number of sympodia plant⁻¹, number of boll plant⁻¹, boll weight and ginning out-turn and fibre quality traits like 2.5% span length and micronaire value. The best heterotic cross combinations identified based on overall performance for different characters are presented in the Table 4.37.

4.10 STABILITY ANALYSIS

The presently cultivated inter-specific hybrids (*Gossypium hirsutum* L. × *Gossypium barbadense* L.) though are having high seed cotton yield plant⁻¹ along with good fibre quality they are unpredictable in their performance even under less varied conditions of cultivation. Lack of inter-specific hybrids suitable for specific location accounts for the decline in the area and productivity of extra-long staple cotton, apart from the yield losses due to biotic and abiotic stresses. This needs the attention of the plant breeders to evolve superior inter-specific hybrids that would sustain well in different environmental conditions. Hence, in the present study the generated inter-specific hybrids were evaluated for their stability for seed cotton yield plant⁻¹ and yield contributing traits using Eberhart and Russell (1966) and Additive Main effects and Multiplicative Interaction (AMMI) (Gauch, 1988) models.

Bartlett's test

Bartlett's test was performed to study the homogeneity of error variances. Bartlett's test statistic was non-significant for all the characters studied. As the coefficients of variations were very low, the data were pooled over environments for different characters.

4.10.1 Eberhart and Russell's Stability model

Finlay and Wilkinson (1963) considered the linear regression (b_i) as a measure of stability, but later, Eberhart and Russell (1966) emphasized the need of both b_i and s^2d_i in judging the stability of a genotype. According to Eberhart and Russell (1966) a stable genotype is one which shows (i) a high mean, (ii) a regression coefficient equal to unity ($b_i=1$) and (iii) a least mean square deviation from regression (s^2d_i). A genotype

with high mean performance with near to unity regression and least deviation from regression could perform well under average environmental conditions. If a genotype exhibited high mean with greater than unity regression, it was considered to be stable for favourable environmental conditions. However, if a genotype possessed high mean with less than unity regression, the genotype is considered to be suitable for poor environmental conditions. In the present study stability analysis was carried out as per Eberhart and Russell's (1966) model for hybrids over locations.

Environmental Indices

Environmental index reveals the suitability of an environment for a particular trait (Table 4.38). Based on the positive values of environmental index, Bapatla location was found to be most suitable location for number of monopodia plant⁻¹ (0.02), boll weight (0.047), 2.5% span length (0.05), bundle strength (0.05) and uniformity ratio (0.11). J M Puram was found to be the most suitable location for all the traits except for days to 50% flowering, number of bolls plant⁻¹, ginning out-turn and lint yield plant⁻¹. While, Lam Farm was the most suitable location for days to 50% flowering (2.31), plant height (13.83), number of sympodia plant⁻¹ (0.55), number of bolls plant⁻¹ (9.60), ginning out-turn (1.88), seed cotton yield plant⁻¹ (13.41) and lint yield plant⁻¹ (7.68).

The data obtained from three locations was subjected to statistical analysis as per Eberhart and Russell model and the analysis of variance for stability is presented in the Table 4.39. Stability analysis of variance revealed mean sum of squares due to genotypes were significant for all the characters except for number of monopodia plant⁻¹ and seed index indicating presence of sufficient variability among the genotypes. The environments showed significant differences for all the characters. The genotype × environment interaction component showed non-significance for all the traits except for micronaire value.

Significance of environment (linear) component for all the characters confirms the observations of widely differing environments, in the analysis of variance. The environment + (genotype × environment) component was significant for all the traits except for number of monopodia plant⁻¹, boll weight and uniformity ratio. The genotype × environment (linear) interaction component exhibited significance for number of bolls plant⁻¹, 2.5% span length, micronaire, bundle strength, uniformity ratio, seed cotton yield

plant⁻¹ and lint yield plant⁻¹ and non-significance for remaining all the characters. Pooled deviation component was significant for all the traits except for uniformity ratio indicating the importance of non-linear component in the genotype-environment interaction. Similar reports were given by Saini *et al.* (2008), Satish *et al.* (2009b), Patil and Patel (2010), Basanagouda *et al.* (2011), Taranjit *et al.* (2012), Dewdar (2013), Kavithamani *et al.* (2013), Patel *et al.* (2013a), Verma *et al.* (2013) and Reddy and Sarma (2014). The data pertaining to stability parameters are presented in Tables 4.40 to 4.47 and discussed character-wise here under.

4.10.1.1 Days to 50% flowering

The number of days to 50% flowering ranged from 55.67 (H 1442 × GSB 41) to 70.11 days (L 1058 × DB 16) with a general mean of 63.72 days. Two hybrids viz., MR 786 × DB 16 ($b_i=0.94$) and L 762 × TCB 37 ($b_i=0.98$) had low mean than grand mean with regression co-efficient around unity ($b_i=1$) and non-significant deviation from regression. Hence, these hybrids were considered to possess the average stability for early flowering at different locations. Regression coefficient less than one ($b_i<1$) with low mean than general mean and non-significant deviation from regression were observed in NDLH 1938 × DB 11 ($b_i=0.18$), NDLH 1938 × GSB 41 ($b_i=-0.19$), H 1442 × DB 16 ($b_i=0.07^*$), H 1442 × DB 11 ($b_i=0.88$), H 1442 × GSB 41 ($b_i=-0.06$), ADB 542 × DB 16 ($b_i=0.30^*$), ADB 532 × DB 11 ($b_i=0.45^*$), WGCV 48 × DB 16 ($b_i=-0.19$), WGCV 48 × DB 11 ($b_i=0.14$), MR 786 × GSB 41 ($b_i=0.14$), TSH 0250 × GSB 40 ($b_i=0.25$), TSH 0250 × DB 16 ($b_i=0.35$), SCS 793 × DB 11 ($b_i=0.85$), SCS 793 × GSB 41 ($b_i=0.48$), L 762 × DB 11 ($b_i=0.88$) and L 762 × SUVIN ($b_i=-0.18$). These hybrids perform well in unfavourable environments with early flowering. Whereas, hybrids viz., NDLH 1938 × SUVIN ($b_i=1.32$) and WGCV 48 × GSB 40 ($b_i=1.32$) recorded b_i values greater than one, low mean than grand mean and non-significant deviation from regression and these were predicted to perform well in favourable environments for early flowering.

4.10.1.2 Plant height (cm)

For plant height, mean values ranged from 149.78 (ADB 532 × TCB 37) to 194.54 cm (NDLH 1938 × GSB 40) with an overall mean of 171.60 cm. The regression coefficient (b_i) values ranged from -0.83 (MCU 5 × TCB 37) to 2.11 (L 1058 × GSB 41). The hybrids viz., NDLH 1938 × DB 16 ($b_i=0.97$), BS 37 × DB 16 ($b_i=0.98$), SCS 793 × DB 16 ($b_i=1.01$) and L 762 × SUVIN ($b_i=1.04$) had recorded mean plant height higher than grand mean with nearly unit regression coefficient (b_i) and non-significant deviation from regression (s^2d_i) and were found to be stable for plant height over locations.

The hybrids viz., NDLH 1938 × SUVIN ($b_i = -0.16$), H 1442 × GSB 41 ($b_i = 0.29$), ADB 542 × GSB 40 ($b_i = -0.18$), ADB 542 × DB 16 ($b_i = 0.40$), ADB 542 × TCB 37 ($b_i = 0.87$), WGCV 48 × DB 16 ($b_i = 0.75$), MR 786 × DB 11 ($b_i = 0.54$), MR 786 × GSB 41 ($b_i = 0.20$), TSH 0250 × GSB 40 ($b_i = 0.05$), BS 37 × SUVIN ($b_i = 0.45$) and L 1058 × SUVIN ($b_i = 0.48$) had higher mean than general mean with $b_i < 1$ and were suitable for poor environments. Whereas, the hybrids viz., NDLH 1938 × GSB 40 ($b_i = 1.23$), NDLH 1938 × GSB 41 ($b_i = 1.13^*$), ADB 542 × DB 11 ($b_i = 1.78$), ADB 532 × GSB 40 ($b_i = 1.21$), ADB 532 × DB 11 ($b_i = 1.35$), MR 786 × GSB 40 ($b_i = 1.17$), MR 786 × DB 16 ($b_i = 1.53$), MR 786 × TCB 37 ($b_i = 1.64$), SCS 793 × DB 11 ($b_i = 1.47$), SCS 793 × GSB 41 ($b_i = 1.27$), L 1058 × GSB 40 ($b_i = 1.64$), L 1058 × DB 11 ($b_i = 1.56$), L 1058 × TCB 37 ($b_i = 1.29$), L 762 × GSB 40 ($b_i = 1.42$) and L 762 × GSB 41 ($b_i = 1.26$) had b_i values greater than one with higher than grand mean and non-significant deviation from regression and were considered to perform well under favourable conditions.

4.10.1.3 Number of monopodia plant⁻¹

Mean values for number of monopodia plant⁻¹ ranged from 1.45 (TSH 0250 × TCB 37) to 3.20 (ADB 532 × GSB 41) with an overall mean of 2.43. None of the hybrid observed with average stability for number of monopodia plant⁻¹ over locations. The hybrids viz., ADB 542 × DB 16 ($b_i = -0.21$), BS 37 × DB 11 ($b_i = -1.03$) and BS 37 × GSB 41 ($b_i = -0.19$) had more mean than general mean with regression values (b_i) < 1 and these hybrids were considered to be suitable for unfavourable environments.

Whereas, the hybrids H 1442 × DB 11 ($b_i = 1.51$), ADB 542 × DB 11 ($b_i = 3.18$), ADB 532 × GSB 41 ($b_i = 5.19$), BS 37 × SUVIN ($b_i = 2.13$), MCU 5 × TCB 37 ($b_i = 1.87$) and L 762 × SUVIN (1.70) possessed above average mean values, showed b_i values greater than one with predictable performance in favourable environments.

4.10.1.4 Number of sympodia plant⁻¹

Mean values for number of sympodia plant⁻¹ ranged from 20.07 (MCU 5 × TCB 37) to 31.43 (MR 786 × GSB 41) with an overall mean of 23.40. The regression coefficient (b_i) values ranged from -0.05 (H 1442 × DB 16) to 1.73 (NDLH 1938 × GSB 41 and ADB 542 × GSB 41). The hybrids viz., NDLH 1938 × SUVIN ($b_i = 0.97$) and L 1058 × DB 11 ($b_i = 1.05$) had recorded mean number of sympodia plant⁻¹ higher than grand mean with regression coefficient around unity ($b_i = 1$) and non-significant deviation from regression (s^2d_i) and were found to be stable for number of sympodia plant⁻¹ over locations.

The hybrids viz., H 1442 $\times$ DB 16 ($b_i=-0.05^*$), H 1442 $\times$ GSB 41 ($b_i=0.07^*$), ADB 542 $\times$ DB 16 ($b_i=0.08$), MR 786 $\times$ GSB 41 ($b_i=0.01$) and SCS 793 $\times$ DB 11 ($b_i=0.89$) had more mean than general mean with $b_i < 1$ and were found to have predictable performance in poor environments. Whereas, the hybrids, NDLH 1938 $\times$ DB 16 ($b_i=1.15$), MR 786 $\times$ GSB 40 ($b_i=1.23$), MR 786 $\times$ TCB 37 ($b_i=1.34$), MR 786 $\times$ SUVIN ($b_i=1.16$), SCS 793 $\times$ GSB 40 ($b_i=1.53$), L 1058 $\times$ GSB 41 ($b_i=1.49$), L 1058 $\times$ SUVIN ($b_i=1.13$) and L 762 $\times$ GSB 40 (1.26) had b_i values greater than one with higher mean than grand mean and non-significant deviation from regression and were considered to be perform well under favourable conditions. Stable hybrids for number of sympodia plant⁻¹ were also reported by Satish *et al.* (2009b) and Nidagundi *et al.* (2012).

4.10.1.5 Number of bolls plant⁻¹

For number of bolls plant⁻¹, the regression coefficient (b_i) values ranged from -1.36 (BS 37 $\times$ SUVIN) to 3.52 (BS 37 $\times$ GSB 40) and mean values varied from 44.29 (TSH 0250 $\times$ TCB 37) to 79.98 (BS 37 $\times$ SUVIN) with an overall mean of 65.63.

The hybrids, H 1442 $\times$ DB 11 ($b_i=0.90$) and L 762 $\times$ TCB 37 ($b_i=0.94$) had recorded mean number of bolls plant⁻¹ higher than grand mean with around unit regression coefficient (b_i) and non-significant deviation from regression (s^2d_i) and were found to be stable for number of bolls plant⁻¹ over locations.

The hybrids viz., H 1442 $\times$ DB 16 ($b_i=0.03$), H 1442 $\times$ GSB 41 ($b_i=0.28$), H 1442 $\times$ SUVIN (0.19**), ADB 542 $\times$ DB 16 ($b_i=-0.06^*$), WGCV 48 $\times$ DB 16 (-0.04*), MR 786 $\times$ GSB 41 ($b_i=0.05^*$), TSH 0250 $\times$ GSB 40 (0.20*), BS 37 $\times$ DB 16 ($b_i=0.22$) and SCS 793 $\times$ DB 16 ($b_i=-0.19^*$) recorded mean above grand mean with regression values less than unity and non-significant s^2d_i and these hybrids were suitable to unfavourable environments.

Whereas, the hybrids, NDLH 1938 $\times$ GSB 40 ($b_i=1.40$), NDLH 1938 $\times$ GSB 41 (1.32), WGCV 48 $\times$ DB 11 ($b_i=1.58$), MR 786 $\times$ DB 11 ($b_i=1.22$), MR 786 $\times$ TCB 37 ($b_i=2.10$) and L 762 $\times$ DB 11 ($b_i=1.84$) had recorded mean above grand mean with regression values greater than unity and non-significant s^2d_i and these hybrids were found to be suitable for favourable environments. Patil and Patel (2010), Basanagouda *et al.* (2011), Nidagundi *et al.* (2012), Dewdar (2013), Kavithamani *et al.* (2013), Verma *et al.* (2013) and Reddy and Sarma (2014) also identified stable hybrids for number of bolls plant⁻¹.

4.10.1.6 Boll weight (g)

The range of mean values for boll weight was 2.62 (SCS 793 × TCB 37) to 4.21 g (TSH 0250 × GSB 40) with an overall mean of 3.30 g. The regression coefficient (b_i) values ranged from -1.47 (L 1058 × GSB 41) to 3.26 (L 762 × TCB 37).

None of the hybrid observed with average stability for boll weight over locations. The hybrids, NDLH 1938 × DB 16 ($b_i=0.86$), H 1442 × DB 16 ($b_i=0.24$), H 1442 × GSB 41 ($b_i=0.44$), ADB 542 × DB 16 ($b_i=0.07$), ADB 542 × DB 11 ($b_i=0.36$), MR 786 × GSB 41 ($b_i=0.21^{**}$), TSH 0250 × GSB 40 ($b_i=-0.27$), MCU 5 × DB 16 ($b_i=-0.36$) and L 1058 × DB 11 ($b_i=-0.92^{*}$) had more mean than general mean with $b_i < 1$ and were predictable under poor environments.

Whereas, the hybrids, H 1442 × GSB 40 ($b_i=1.67$), MR 786 × DB 11 ($b_i=1.63$), MR 786 × TCB 37 ($b_i=1.34$) and BS 37 × DB 16 ($b_i=2.22$) had b_i values greater than one with higher mean than grand mean and non-significant deviation from regression and were considered to be perform well under favourable conditions. Earlier findings of Patil and Patel (2010), Basanagouda *et al.* (2011), Nidagundi *et al.* (2012), Dewdar (2013), Kavithamani *et al.* (2013), Verma *et al.* (2013) and Reddy and Sarma (2014) also recorded stable hybrids for this trait over environments.

4.10.1.7 Lint index (g)

Mean values for lint index was ranged from 4.07 (TSH 0250 × SUVIN) to 6.07 g (L 1058 × DB 16) with an overall mean of 5.12 g. None of the hybrid had shown stability for lint index over locations.

The hybrids viz., NDLH 1938 × GSB 41 ($b_i=-0.79$), H 1442 × DB 16 ($b_i=0.33$), H 1442 × GSB 41 ($b_i=0.29$), H 1442 × TCB 37 ($b_i=0.47$), ADB 542 × DB 16 ($b_i=-0.27^{*}$), ADB 542 × GSB 41 ($b_i=0.22^{**}$), ADB 532 × GSB 40 ($b_i=-0.97$), WGCV 48 × SUVIN ($b_i=-0.17$), MR 786 × DB 16 ($b_i=0.37$), BS 37 × GSB 40 ($b_i=0.67$), SCS 793 × DB 11 ($b_i=-0.36^{*}$), L 762 × DB 16 ($b_i=0.32$), L 762 × GSB 41 ($b_i=0.73^{*}$) and L 762 × SUVIN ($b_i=0.39$) had higher mean than general mean with $b_i < 1$ and were predictable performance in poor environments.

Whereas, the hybrids, NDLH 1938 × DB 16 ($b_i=1.38$), MR 786 × GSB 40 ($b_i=2.71^{*}$), MR 786 × TCB 37 ($b_i=1.24$) and L 762 × DB 11 ($b_i=1.37$) had b_i values greater than one with mean higher than grand mean and non-significant deviation from

regression and were considered to perform well under favourable conditions. For this trait stable hybrids were also reported by Nidagundi *et al.* (2012), Taranjit *et al.* (2012), Dewdar (2013) and Verma *et al.* (2013).

4.10.1.8 Seed index (g)

Seed index had shown mean values ranged from 11.09 (BS 37 × SUVIN) to 14.34 g (ADB 532 × GSB 40) with an overall mean of 12.64 g. The regression coefficient (b_i) values ranged from -0.07 (ADB 542 × DB 16) to 2.05 (SCS 793 × GSB 40). The hybrids, WGCV 48 × TCB 37 ($b_i=0.93$) and MR 786 × DB 11 ($b_i=0.90$) had recorded mean seed index higher than grand mean with nearly unit regression coefficient (b_i) and non-significant deviation from regression (s^2d_i) and had found to be stable for seed index over locations.

The hybrids, ADB 532 × GSB 40 ($b_i=0.87$), ADB 532 × DB 16 ($b_i=0.82$) and BS 37 × DB 16 ($b_i=0.70$) had more mean than general mean with $b_i < 1$ and were predictable under poor environments. Whereas, the hybrids, H 1442 × GSB 40 ($b_i=1.99$), ADB 542 × DB 11 ($b_i=1.92^*$), ADB 532 × SUVIN ($b_i=1.46$), MCU 5 × TCB 37 ($b_i=1.49$), MCU 5 × SUVIN ($b_i=1.63^*$) and L 1058 × SUVIN ($b_i=1.61$) had b_i values greater than one with higher mean than grand mean and non-significant deviation from regression and were considered to be perform well under favourable conditions. Stable hybrids for seed index also reported by Patil and Patel (2010), Nidagundi *et al.* (2012), Taranjit *et al.* (2012) and Verma *et al.* (2013) in cotton.

4.10.1.9 Ginning out-turn (%)

Mean values for ginning out-turn ranged from 23.80 (BS 37 × TCB 37) to 33.49 per cent (TSH 0250 × GSB 40) with an overall mean of 29.03 per cent. The regression coefficient (b_i) values ranged from -0.66 (MCU 5 × GSB 40) to 2.66 (SCS 793 × GSB 40). The hybrid, NDLH 1938 × GSB 41 ($b_i=0.97$) had recorded mean ginning out-turn higher than grand mean with regression coefficient (b_i) nearer to unity and non-significant deviation from regression (s^2d_i) and were found to be stable for ginning out turn over locations.

The hybrids viz., NDLH 1938 × GSB 40 ($b_i=-0.33$), H 1442 × DB 16 ($b_i=-0.05$), H 1442 × GSB 41 ($b_i=0.15$), H 1442 × TCB 37 ($b_i=0.58$), ADB 542 × DB 16 ($b_i=0.06$), ADB 532 × GSB 41 ($b_i=0.52^*$), MR 786 × GSB 41 ($b_i=-0.10^*$), TSH 0250 × GSB 40

($b_i=-0.05$), L 1058 $\times$ GSB 40 ($b_i=0.31$), L 1058 $\times$ DB 16 ($b_i=0.75$), L 1058 $\times$ GSB 41 ($b_i=0.58^*$), L 762 $\times$ DB 11 (0.23^*) and L 762 $\times$ GSB 41 ($b_i=0.68$) had more mean than general mean with $b_i < 1$ and were predictable to perform well in poor environments.

Whereas, the hybrids, NDLH 1938 $\times$ DB 11 ($b_i=1.51$), WGCV 48 $\times$ DB 11 ($b_i=2.35$), SCS 793 $\times$ DB 16 ($b_i=1.43$) and L 762 $\times$ TCB 37 ($b_i=1.49$) had b_i values greater than one with higher mean than grand mean and non-significant deviation from regression and were considered to be perform well under favourable conditions. Patil and Patel (2010), Nidagundi *et al.* (2012), Taranjit *et al.* (2012), Kavithamani *et al.* (2013), Verma *et al.* (2013) and Reddy and Sarma (2014) also reported stable hybrids for ginning out-turn.

4.10.1.10 2.5% span length (mm)

Mean values for 2.5% span length ranged from 32.64 (MR 786 $\times$ GSB 40) to 37.97 mm (MCU 5 $\times$ SUVIN) with an overall mean of 34.91 mm. The regression coefficient (b_i) values ranged from -0.29 (BS 37 $\times$ TCB 37) to 2.37 (L 1058 $\times$ SUVIN). The hybrids, SCS 793 $\times$ GSB 40 ($b_i=0.98$) and ADB 532 $\times$ SUVIN ($b_i=1.00$) had recorded mean 2.5% span length higher than grand mean with unit regression coefficient (b_i) and non-significant deviation from regression (s^2d_i) and were found to be stable for 2.5% span length over locations.

Whereas, the hybrids viz., H 1442 $\times$ DB 16 ($b_i=0.07$), ADB 542 $\times$ DB 16 ($b_i=0.04^*$), ADB 532 $\times$ DB 16 ($b_i=0.63$), ADB 532 $\times$ GSB 41 ($b_i=0.64$), ADB 532 $\times$ TCB 37 ($b_i=0.31$), TSH 0250 $\times$ GSB 40 ($b_i=0.09$), BS 37 $\times$ GSB 40 ($b_i=0.23$), BS 37 $\times$ DB 16 ($b_i=0.79$), BS 37 $\times$ GSB 41 ($b_i=0.39$), MCU 5 $\times$ GSB 41 ($b_i=0.68$), L 1058 $\times$ DB 11 ($b_i=0.75$) and L 1058 $\times$ TCB 37 ($b_i=0.88$) had more mean than general mean with $b_i < 1$ and were predictable to perform well in poor environments.

Regression values (b_i) greater than one recorded by H 1442 $\times$ SUVIN ($b_i=1.57$), ADB 542 $\times$ TCB 37 ($b_i=1.23$), ADB 542 $\times$ SUVIN ($b_i=1.21$), WGCV 48 $\times$ GSB 40 ($b_i=1.33$), WGCV 48 $\times$ TCB 37 ($b_i=1.61$), TSH 0250 $\times$ DB 16 ($b_i=1.64^*$), TSH 0250 $\times$ SUVIN ($b_i=1.99$), BS 37 $\times$ DB 11 ($b_i=1.64$), BS 37 $\times$ SUVIN ($b_i=1.87$), SCS 793 $\times$ TCB 37 ($b_i=1.63$), MCU 5 $\times$ DB 16 ($b_i=1.29$), L 1058 $\times$ GSB 41 ($b_i=1.27$) and L 1058 $\times$ SUVIN ($b_i=2.37$) with mean greater than grand mean and non-significant deviation from regression. These were considered to be performed well in favourable environments. For this trait stable hybrids were also reported by Taranjit *et al.* (2012) and Verma *et al.* (2013).

4.10.1.11 Uniformity ratio

Mean values for uniformity ratio ranged from 43.87 (MCU 5 × DB 16) to 47.50 (MR 786 × TCB 37) with an overall mean of 45.72. The regression coefficient (b_i) values ranged from -9.54 (SCS 793 × TCB 37) to 11.55 (ADB 542 × SUVIN). None of the hybrid recorded average stability for uniformity ratio over locations. The hybrids, H 1442 × DB 16 ($b_i=-0.33$), H 1442 × TCB 37 ($b_i=-0.54$), ADB 542 × DB 11 ($b_i=-0.15$), ADB 532 × DB 11 ($b_i=-0.60$), MR 786 × GSB 40 ($b_i=0.01$), BS 37 × GSB 41 ($b_i=0.36$), SCS 793 × GSB 40 ($b_i=0.42$) and L 1058 × DB 11 ($b_i=0.31$) had recorded regression coefficient (b_i) less than unity. Whereas, NDLH 1938 × GSB 41 ($b_i=-1.69$), ADB 542 × DB 16 ($b_i=-3.44$), ADB 542 × TCB 37 ($b_i=-3.86$), ADB 532 × GSB 40 ($b_i=-7.45$), WGCV 48 × SUVIN ($b_i=-2.79$), MR 786 × DB 18 ($b_i=-2.22$), MR 786 × DB 11 ($b_i=-5.01$), MR 786 × TCB 37 ($b_i=-4.03$), BS 37 × GSB 40 ($b_i=-6.53^*$), SCS 793 × DB 16 ($b_i=-2.08$) and SCS 793 × TCB 37 ($b_i=-9.54$) had recorded higher than grand mean with more than unity negative regression coefficient (b_i) and non-significant deviation from regression (s^2d_i) and were found to be suitable for unfavourable environments.

Regression values greater than one was registered by the hybrids viz., NDLH 1938 × GSB 40 ($b_i=7.79^*$), NDLH 1938 × DB 16 ($b_i=4.39^{**}$), NDLH 1938 × DB 11 ($b_i=2.00$), NDLH 1938 × TCB 37 ($b_i=1.31$), H 1442 × GSB 40 ($b_i=5.57$), H 1442 × DB 11 ($b_i=6.29$), ADB 542 × GSB 40 ($b_i=7.36$), ADB 542 × GSB 41 ($b_i=3.39$), ADB 532 × GSB 41 ($b_i=7.35$), WGCV 48 × GSB 41 ($b_i=2.26$), MR 786 × GSB 41 ($b_i=6.08$), TSH 0250 × DB 11 ($b_i=1.78$), SCS 793 × GSB 41 ($b_i=2.84$), MCU 5 × GSB 40 ($b_i=6.05$) and L 762 × GSB 40 (3.72) had recorded mean higher than grand mean and non-significant deviation from regression and were considered to be perform well under favourable conditions.

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

Mean values for micronaire value ranged from 2.53 (TSH 0250 × GSB 41) to 3.40 10^{-6} g/inch (ADB 542 × DB 16) with an overall mean of 2.85 10^{-6} g/inch. The regression coefficient values (b_i) ranged from -0.09 (TSH 0250 × SUVIN) to 2.01 (H 1442 × SUVIN). The hybrids viz., ADB 532 × TCB 37 ($b_i=1.00$) and L 1058 × GSB 41 ($b_i=1.09$) had recorded mean micronaire value higher than grand mean with regression coefficient (b_i) nearly one and non-significant deviation from regression (s^2d_i) and was found to be stable for micronaire value over locations. Whereas, the hybrids, ADB 542 × GSB 41 ($b_i=0.53^*$) and L 762 × TCB 37 ($b_i=0.65$) had more mean than general mean with $b_i < 1$ and expected to be perform well in poor environments.

The hybrids, NDLH 1938 × GSB 40 ($b_i=1.59$), NDLH 1938 × DB 11 ($b_i=1.80$), H 1442 × GSB 40 ($b_i=1.93$), H 1442 × TCB 37 ($b_i=1.56$), WGCV 48 × DB 11 ($b_i=1.91^*$), WGCV 48 × TCB 37 ($b_i=1.52$), MR 786 × DB 16 ($b_i=1.23$), MR 786 × GSB 41 ($b_i=1.57^*$), MR 786 × TCB 37 ($b_i=1.58$), BS 37 × SUVIN ($b_i=1.11$), L 762 × GSB 40 ($b_i=1.36$) and L 762 × GSB 41 ($b_i=1.11$) had b_i values greater than one with higher mean than grand mean and non-significant deviation from regression and were considered to be perform well under favourable conditions. Stable hybrids for micronaire value were also reported by Verma *et al.* (2013).

4.10.1.13 Bundle strength (g/tex)

Bundle strength registered the mean values ranged from 24.99 (MR 786 × DB 11) to 30.17 g/tex (MCU 5 × GSB 40) with an overall mean of 27.02 g/tex. The regression coefficient (b_i) values ranged from -0.12 (BS 37 × GSB 40) to 2.26 (MCU 5 × DB 11). The hybrids viz., ADB 542 × SUVIN ($b_i=0.97$), ADB 532 × GSB 41 ($b_i=1.01$), WGCV 48 × DB 16 ($b_i=1.07$), TSH 0250 × DB 16 ($b_i=1.09$) and SCS 793 × GSB 40 (0.95^{**}) had recorded higher grand mean with regression coefficient nearly one and non-significant deviation from regression (s^2d_i) and were found to be stable for bundle strength over locations.

Whereas, the hybrids, H1442 × DB 16 ($b_i=0.30$), ADB 542 × GSB 41 ($b_i=0.11$), ADB 532 × GSB 40 ($b_i=0.14$), ADB 532 × DB 16 ($b_i=0.58$), ADB 532 × TCB 37 ($b_i=0.68$), WGCV 48 × GSB 40 ($b_i=0.88$), WGCV 48 × TCB 37 ($b_i=0.85$), MR 786 × TCB 37 ($b_i=0.54$), TSH 0250 × GSB 40 ($b_i=-0.01^*$), BS 37 × GSB 40 ($b_i=-0.12^*$), BS 37 × GSB 41 ($b_i=0.50$), BS 37 × TCB 37 ($b_i=0.82$), SCS 793 × SUVIN (0.22^{**}) and L 1058 × TCB 37 ($b_i=0.34$) had recorded higher mean than grand mean with regression coefficient less than one and non-significant deviation from regression indicating predictable performance in poor environments. The hybrids, NDLH 1938 × GSB 40 ($b_i=1.24$), NDLH 1938 × DB 16 ($b_i=1.52$), WGCV 48 × SUVIN ($b_i=1.45$), TSH 0250 × TCB 37 ($b_i=1.43$), BS 37 × DB 11 ($b_i=1.44$), SCS 793 × TCB 37 ($b_i=1.22$), L 1058 × GSB 41 ($b_i=1.12$) and L 762 × SUVIN ($b_i=1.29$) had b_i values greater than one with higher mean than grand mean and non-significant deviation from regression and were considered to be perform well under favourable conditions. For this trait stable hybrids were also reported by Taranjit *et al.* (2012) and Verma *et al.* (2013) in their studies in cotton.

4.10.1.14 Fibre elongation (%)

The regression coefficient (b_i) for fibre elongation varied from -0.51 (BS 37 × GSB 40) to 2.08 (H 1442 × DB 16) and mean values ranged from 4.55 (TSH 0250 × SUVIN) to 5.25 (NDLH 1938 × DB 16) with an overall mean of 4.93. The hybrids, NDLH 1938 × GSB 41 ($b_i=0.97$), H 1442 × GSB 41 ($b_i=1.03$), ADB 542 × GSB 41 ($b_i=0.96$) and MR 786 × TCB 37 ($b_i=1.09$) had recorded mean fibre elongation higher than grand mean with regression coefficient (b_i) nearly one and non-significant deviation from regression (s^2d_i) and was found to be stable for fibre elongation over locations.

The hybrids viz., NDLH 1938 × DB 16 ($b_i=0.89^*$), ADB 542 × DB 16 ($b_i=0.20^*$), ADB 542 × SUVIN ($b_i=0.51^*$), ADB 532 × DB 11 ($b_i=0.62$), WGCV 48 × DB 16 ($b_i=0.67$), BS 37 × GSB 40 ($b_i=-0.51$), BS 37 × GSB 41 ($b_i=0.84$), SCS 793 × GSB 40 ($b_i=0.64$), SCS 793 × DB 16 ($b_i=0.84$), SCS 793 × DB 11 ($b_i=0.44^*$), SCS 793 × GSB 41 ($b_i=-0.22$) and L 1058 × DB 11 ($b_i=0.50$) had more mean than general mean with $b_i < 1$ and were suitable for poor environments. Whereas, the hybrids, NDLH 1938 × GSB 40 ($b_i=1.36$), NDLH 1938 × DB 11 ($b_i=1.80$), NDLH 1938 × SUVIN ($b_i=1.36$), H 1442 × GSB 40 ($b_i=1.18$), H 1442 × DB 16 ($b_i=2.08$), H 1442 × DB 11 ($b_i=1.81^*$), H 1442 × SUVIN ($b_i=1.46$), ADB 542 × GSB 40 ($b_i=1.43$), ADB 532 × DB 16 ($b_i=1.61$), WGCV 48 × DB 11 ($b_i=1.73$), MR 786 × DB 16 ($b_i=1.41$), MR 786 × GSB 41 ($b_i=1.38$), BS 37 × TCB 37 ($b_i=1.12$), L 1058 × SUVIN ($b_i=1.47$), L 762 × DB 11 ($b_i=1.90$) and L 762 × GSB 41 ($b_i=1.43$) had b_i values greater than one with higher mean than grand mean and non-significant deviation from regression and were considered to be perform well under favourable conditions.

4.10.1.15 Seed cotton yield plant⁻¹ (g)

Seed cotton yield plant⁻¹ had mean values ranged from 107.31 (TSH 0250 × TCB 37) to 253.36 g (H 1442 × GSB 41) with an overall mean of 184.10 g. The regression coefficient (b_i) values ranged from -3.08 (BS 37 × SUVIN) to 4.75 (L 1058 × GSB 41). Deviation from regression was ranged from -70.15 (ADB 542 × GSB 40) to 7848.48 (ADB 532 × GSB 40). The hybrid, ADB 542 × GSB 41 ($b_i=1.10$), was considered to be stable for seed cotton yield plant⁻¹ over locations as it recorded mean higher than grand mean with regression coefficient equal to one and non-significant deviation from regression.

The hybrids viz., NDLH 1938 $\times$ TCB 37 ($b_i=0.14$), H 1442 $\times$ DB 16 ($b_i=0.12$), H 1442 $\times$ GSB 41 ($b_i=0.19$), ADB 542 $\times$ GSB 40 ($b_i=-0.52^*$), ADB 542 $\times$ DB 16 ($b_i=0.13$), WGCV 48 $\times$ DB 16 ($b_i=0.84$), MR 786 $\times$ GSB 41 ($b_i=0.04$) and TSH 0250 $\times$ GSB 40 ($b_i=0.59$) had more mean than general mean with $b_i < 1$ and will better suited to poor environments. Whereas, the hybrids, NDLH 1938 $\times$ GSB 40 ($b_i=1.92$), NDLH 1938 $\times$ GSB 41 ($b_i=1.23$), WGCV 48 $\times$ DB 11 ($b_i=2.23$), MR 786 $\times$ TCB 37 ($b_i=2.21$), L 762 $\times$ DB 16 ($b_i=2.05$) and L 762 $\times$ DB 11 ($b_i=1.82$) had b_i values greater than one with higher than grand mean and non-significant deviation from regression and were considered to perform well under favourable conditions. Stable hybrids for seed cotton yield plant⁻¹ were also reported by Patil and Patel (2010), Basanagouda *et al.* (2011), Nidagundi *et al.* (2012), Taranjit *et al.* (2012), Dewdar (2013), Kavithamani *et al.* (2013), Patel *et al.* (2013a), Verma *et al.* (2013) and Reddy and Sarma (2014).

4.10.1.16 Lint yield plant⁻¹ (g)

For lint yield plant⁻¹, mean values ranged from 28.11 (TSH 0250 $\times$ TCB 37) to 83.71g (H 1442 $\times$ GSB 41) with an overall mean of 53.90 g. The regression coefficient (b_i) values ranged from -2.64 (BS 37 $\times$ SUVIN) to 4.18 (L 1058 $\times$ GSB 41). The hybrids, NDLH 1938 $\times$ GSB 41 ($b_i=0.94$) and ADB 542 $\times$ GSB 41 ($b_i=0.99$) had recorded mean lint yield plant⁻¹ higher than grand mean with unit regression coefficient (b_i) and non-significant deviation from regression (s^2d_i) and were found to be stable for lint yield plant⁻¹ over locations. The hybrids, H 1442 $\times$ DB 16 ($b_i=0.05$), H 1442 $\times$ DB 11 ($b_i=0.05$), H 1442 $\times$ GSB 41 ($b_i=0.44^*$), H 1442 $\times$ SUVIN ($b_i=-0.66$), ADB 542 $\times$ GSB 40 ($b_i=0.19$), ADB 542 $\times$ DB 16 ($b_i=0.07$), WGCV 48 $\times$ DB 16 ($b_i=0.87$), MR 786 $\times$ GSB 41 ($b_i=0.02^*$), MR 786 $\times$ SUVIN ($b_i=0.84$), TSH 0250 $\times$ GSB 40 ($b_i=0.66$) and SCS 793 $\times$ DB 16 ($b_i=0.08^*$) had more mean than general mean with $b_i < 1$ with non-significant deviation from regression (s^2d_i). Hence, these hybrids are suitable for unfavourable environments.

Whereas, the hybrids, WGCV 48 $\times$ DB 11 ($b_i=2.31^*$), MR 786 $\times$ GSB 40 ($b_i=1.14$), MR 786 $\times$ TCB 37 ($b_i=1.88^*$), L 1058 $\times$ DB 16 ($b_i=3.85^*$), L 1058 $\times$ GSB 41 ($b_i=4.18^*$) and L 762 $\times$ SUVIN ($b_i=2.88$) had b_i values greater than one with higher than grand mean and non-significant deviation from regression were considered to perform well under favourable conditions. Patil and Patel (2010), Nidagundi *et al.* (2012), Taranjit *et al.* (2012), Dewdar (2013), Kavithamani *et al.* (2013) and Patel *et al.* (2013a) also identified stable hybrids for lint yield plant⁻¹ over locations.

4.10.2 Additive Main Effects and Multiplicative Interaction Model (AMMI) Analysis

The AMMI model is a hybrid model involving both additive and multiplicative components of two way data structure. The AMMI model separates the additive variance and then applies principal component analysis to the interaction portion to extract a new set of co-ordinate axes which explain in more detail the interaction pattern, after fitting the genotype and environment main effects in the model. The amount of pattern, the portion of genotype $\times$ environment interaction variation representing real responses to genotypes and environments and the random variation affecting genotype $\times$ environment interaction effects are determined. The members of the AMMI analysis are identified according to the number of PCA axes. The IPCA scores of a genotype in the analysis are an indication of the stability of a genotype over environments.

AMMI analysis provides a graphical representation (biplot) to summarize information on the main effects and interactions of both genotypes and environments simultaneously. The model computes the principal component scores for genotypes and environments that represent the genotype $\times$ interaction. The biplot display of PCA scores plotted against each other provides visual inspection and interpretation of the genotype $\times$ environment interaction components. AMMI analysis permits estimation of interaction effect of a genotype in each location and it helps to identify genotypes best suited for specific locations. According to AMMI model, the genotypes which are characterized by mean greater than the grand mean and the PCA scores nearly zero are considered as generally adaptable to all environments. However, the genotypes with high mean performance and with large value of IPCA scores are considered having specific adaptability to the environments (Sharma *et al.*, 1998). In the present study, the interaction of 72 hybrids over three locations was best predicted by first interaction principal component.

The combined analysis of variance (ANOVA) of hybrids over three locations pertaining to AMMI model for seed cotton yield and its contributing traits along with the quality traits is presented in the Table 4.48 and AMMI I biplot figures are presented in Fig. 4.11 to 4.26.

4.10.2.1 Days to 50% flowering

AMMI analysis of variance showed that the genotypes and environments main effects were significant, indicating the existence of wide range of variation between the genotypes and between the environments. The genotype, environment and genotype $\times$ environment interaction accounted for 43.93%, 25.05% and 31.00% of the total variance. IPCA I was significant with 63.47% of the total $G \times E$ interaction sum of squares.

According to AMMI I biplot (Fig. 4.11), the hybrids, H 1442 $\times$ DB 16 (8), H 1442 $\times$ GSB 41 (10), ADB 542 $\times$ DB 16 (14), ADB 532 $\times$ DB 11 (21), TSH 0250 $\times$ GSB 40 (37) and L 762 $\times$ TCB 37 (71) had below general mean (63.72) with zero ICPC score and were identified as stable hybrids over locations for early flowering. The hybrids, H 1442 $\times$ GSB 40 (7), BS 37 $\times$ DB 11 (45), BS 37 $\times$ TCB 37 (47) and SCS 793 $\times$ SUVIN (54) had slightly higher mean than grand mean with IPCA score nearly zero. Bapatla location had mean equal to grand mean but exhibiting high interaction effects indicating suitability for specially adapted hybrids. Whereas, J M Puram location recorded low mean with negative interaction effects indicating favourable conditions for poor environment adapted hybrids for early flowering.

4.10.2.2 Plant height (cm)

The genotypes and environments were significant for this trait. IPCA I was significant and explained 57.74% of the total $G \times E$ interaction sum of squares. The contribution of genotype, environment and environment $\times$ genotype interaction were 27.41%, 43.29% and 29.29%, respectively, of the total variation.

From the biplot interaction (Fig. 4.12), the hybrids, NDLH 1938 $\times$ TCB 37 (5), H 1442 $\times$ DB 11 (9), ADB 542 $\times$ TCB 37 (17), BS 37 $\times$ DB 16 (44), SCS 793 $\times$ DB 16 (50) and L 762 $\times$ SUVIN (72) were stable with IPCA score zero and higher mean than grand mean (171.60 cm). The hybrids, H 1442 $\times$ SUVIN (12), WGCV 48 $\times$ DB 11 (27), WGCV 48 $\times$ TCB 37 (29) and BS 37 $\times$ DB 16 (44) had recorded IPCA score nearer to zero with low mean. For plant height Lam Farm had high mean with high interaction effects and showed suitability for specially adapted genotypes. IPCA score of J M Puram location was nearly zero with high mean indicating stable performance of all the hybrids at this location.

4.10.2.3 Number of monopodia plant⁻¹

For number of monopodia plant⁻¹ only environment component was significant and contributed 9.52% of total variance. Genotype and G × E interaction accounted for 36.10% and 54.37% of total variance. ICPA I was significant and explained 55.68% of G × E interaction sum of squares.

In the biplot presentation (Fig. 4.13) H 1442 × DB 11 (9), ADB 542 × GSB 41 (16), ADB 542 × SUVIN (18), WGCV 48 × SUVIN (30), TSH 0250 × GSB 40 (37), BS 37 × DB 16 (44), BS 37 × TCB 37 (47), BS 37 × SUVIN (48), SCS 793 × SUVIN (54) and MCU 5 × GSB 40 (55) had above general mean (2.43) with ICPA score zero and were stable for this trait. The genotypes, H 1442 × GSB 41 (10), MR 786 × GSB 41 (34), L 1058 × DB 11 (63) and L 762 × TCB 37 (71) showed low mean with IPCA score nearly zero. J M Puram location had high mean with high interaction effects exhibiting suitability for specially adapted genotypes.

4.10.2.4 Number of sympodia plant⁻¹

AMMI analysis for number of sympodia plant⁻¹ showed that genotypes and environments were significant. The genotypes, environment and genotype × environment interaction accounted for 17.65%, 64.20% and 18.15% of the total variation. A large sum of squares for environments indicated that the environments were diverse, with large differences among environmental means causing most of the variation in number of sympodia plant⁻¹. The ANOVA indicated that ICPA I axis was significant and explained 64.63% of the total G × E interaction sum of squares.

According to AMMI I biplot (Fig. 4.14), hybrids NDLH 1938 × SUVIN (6), H 1442 × GSB 40 (7), ADB 532 × DB 16 (20) and MR 786 × DB 11 (33) were identified to be stable across the environments since they had high mean than grand mean (23.40) and IPCA score nearer to zero. ADB 532 × TCB 37 (23), MCU 5 × GSB 40 (55), MCU 5 × DB 16 (56), L 1058 × TCB 37 (65) and L 762 × DB 16 (68) were nearer to ICPA axis and recorded low mean. J M Puram and Lam Farm locations showed favourable conditions for specially adapted hybrids for this character.

4.10.2.5 Number of bolls plant⁻¹

Variation due to the environments was significant and expressed 26.95% of total variation, whereas, genotypes and G × E interaction were 31.50% and 41.54%. ICPA I score was significant and expressed 69.16% in total G × E interaction sum of squares.

In the biplot presentation (Fig. 4.15) the hybrids, NDLH 1938 × DB 11 (3), NDLH 1938 × GSB 41 (4), H 1442 × DB 11 (9), ADB 532 × DB 11 (21), TSH 0250 × GSB 41 (40) and L 762 × TCB 37 (71) were stable with more than grand mean (65.63) and IPCA score nearly zero. The hybrids, ADB 542 × SUVIN (18), ADB 532 × DB 16 (20), MR 786 × SUVIN (36), TSH 0250 × SUVIN (42), MCU 5 × GSB 40 (55), MCU 5 × DB 16 (56) and L 1058 × SUVIN (66) recorded low mean with ICPA score near to zero. For the trait number of bolls plant⁻¹ Lam Farm location had good conditions for specially adapted hybrids.

4.10.2.6 Boll weight (g)

Out of the total variation, variation due to genotypes and environments were significant and contributed 51.26% and 15.10%. G × E interaction showed 33.63% of non-significant variation in total variation. IPCA I was significant and contributed 61.74% of the total G × E interaction sum of squares.

From the biplot interaction (Fig. 4.16), the hybrids, NDLH 1938 × GSB 40 (1), NDLH 1938 × DB 16 (2), NDLH 1938 × GSB 41 (4), H 1442 × DB 16 (8), H 1442 × GSB 41 (10), ADB 542 × DB 16 (14), ADB 542 × DB 11 (15), ADB 532 × GSB 40 (19), ADB 532 × DB 16 (20), ADB 532 × DB 11 (21), ADB 532 × GSB 41 (22), MR 786 × DB 11 (33), MR 786 × GSB 41 (34), MR 786 × TCB 37 (35), MR 786 × SUVIN (36), BS 37 × DB 16 (44), BS 37 × GSB 41 (46), MCU 5 × DB 16 (56), L 1058 × DB 11 (63) and L 1058 × GSB 41 (64) were stable with ICPA score zero and higher mean than grand mean (3.30 g). The crosses, NDLH 1938 × SUVIN (6), H 1442 × SUVIN (12), ADB 542 × TCB 37 (17), ADB 532 × TCB 37 (23) and TSH 0250 × DB 11 (39) had low mean with IPCA score nearly zero. Bapatla location had high mean with high interaction effects (IPCA > 1) indicating suitability for specially adapted genotypes. Whereas, J M Puram location had high mean with high negative interaction effects suitable for poor environment adapted hybrids.

4.10.2.7 Lint index (g)

AMMI analysis of variance indicated that the genotypes, environments and genotype $\times$ environment interaction accounting for 51.75%, 16.48% and 31.75% of the total variance, respectively. Genotypes and environments components were significant. The ICPA I score was significant and exhibited 58.56% of total $G \times E$ interaction sum of squares.

In the biplot presentation (Fig. 4.17), NDLH 1938 $\times$ DB 16 (2), NDLH 1938 $\times$ DB 11 (3), H 1442 $\times$ TCB 37 (11), ADB 532 $\times$ GSB 41 (22), ADB 532 $\times$ SUVIN (24), WGCV 48 $\times$ DB 16 (26), WGCV 48 $\times$ DB 11 (27), MR 786 $\times$ TCB 37 (35), L 1058 $\times$ DB 11 (63), L 1058 $\times$ SUVIN (66), L 762 $\times$ DB 11 (69) and L 762 $\times$ GSB 41 (70) had above general mean (5.12 g) with ICPA score zero and were stable for this character. The hybrids, WGCV 48 $\times$ GSB 40 (25), WGCV 48 $\times$ GSB 41 (28), MR 786 $\times$ DB 11 (33), TSH 0250 $\times$ TCB 37 (41), BS 37 $\times$ DB 16 (44) and SCS 793 $\times$ GSB 40 (49) had low mean with IPCA score nearer to zero. J M Puram location had high mean with high interaction effects showed suitability for specially adapted hybrids. Bapatla location had IPCA score nearly zero with stable performance of all hybrids in this location.

4.10.2.8 Seed index (g)

AMMI analysis of variance partitioned the treatment sum of squares into genotypes, environments and genotype $\times$ environment interaction sum of squares. Genotypes and environments sum of squares were significant and explained 13.26% and 62.17% of total sum of variance. Genotype $\times$ environment interaction contributed 24.56% of total variance and ICPA I was significant with 51.79% of total $G \times E$ interaction sum of squares.

For this trait biplot interaction (Fig. 4.18) showed that the hybrids, MR 786 $\times$ DB 11 (33), BS 37 $\times$ GSB 41 (46), BS 37 $\times$ TCB 37 (47), SCS 793 $\times$ DB 16 (50), SCS 793 $\times$ GSB 41 (52), MCU 5 $\times$ DB 16 (56), and L 1058 $\times$ GSB 40 (61) were stable with ICPA score zero and above grand mean value (12.64 g). The hybrids, NDLH 1938 $\times$ GSB 40 (1), NDLH 1938 $\times$ DB 11 (3), H 1442 $\times$ DB 11 (9), ADB 542 $\times$ SUVIN (18), MCU 5 $\times$ DB 11 (57) and L 762 $\times$ GSB 40 (67) recorded low mean with IPCA score nearer to zero. J M Puram location had high mean for this trait with high interaction effects exhibiting suitability for specially adapted hybrids. IPCA score for Bapatla location was zero indicates the stable performance of all hybrids for seed index.

4.10.2.9 Ginning out-turn (%)

For ginning out-turn genotypes and environments were significant and expressed 51.54% and 23.18% of the total variation. Genotype $\times$ environment interaction contributed 25.27% of the total variation and expressed in one IPCA accounting for 51.12% of $G \times E$ sum of squares.

In AMMI I biplot (Fig. 4.19), NDLH 1938 $\times$ GSB 41 (4), ADB 542 $\times$ GSB 41 (16), WGCV 48 $\times$ SUVIN (30), L 1058 $\times$ SUVIN (66), L 762 $\times$ GSB 40 (67) and L 762 $\times$ GSB 41 (70) hybrids were stable with more than grand mean (29.03) and IPCA score zero. The hybrids, WGCV 48 $\times$ TCB 37 (29), MR 786 $\times$ TCB 37 (35), TSH 0250 $\times$ GSB 41 (40), MCU 5 $\times$ DB 16 (56) and MCU 5 $\times$ DB 11 (57) exhibited low mean and IPCA score near to zero. Lam Farm location had high mean for ginning out turn but exhibiting high interaction effects showed the suitability for specially adapted hybrids. IPCA score of Bapatla location was nearly zero with stable performance of all hybrids for ginning out-turn.

4.10.2.10 2.5% span length (mm)

The genotypes and environments were significant for 2.5% span length. They contributed 38.99% and 44.15% of total variation. Genotype $\times$ environment interaction was explained 16.84 % of total variance and IPCA I was significant and exhibited 65.34% of the total $G \times E$ interaction sum of squares.

According to AMMI I biplot (Fig. 4.20) the hybrids, NDLH 1938 $\times$ SUVIN (6), H 1442 $\times$ TCB 37 (11), ADB 542 $\times$ TCB 37 (17), SCS 793 $\times$ GSB 40 (49) and MCU 5 $\times$ GSB 40 (55) were stable with IPCA score zero and above grand mean (34.91). The hybrids, NDLH 1938 $\times$ DB 11 (3), NDLH 1938 $\times$ TCB 37 (5), WGCV 48 $\times$ GSB 41 (28), WGCV 48 $\times$ SUVIN (30), SCS 793 $\times$ DB 11 (51), L 1058 $\times$ DB 16 (62), L 762 $\times$ GSB 40 (67) and L 762 $\times$ SUVIN (72) showed low mean with IPCA score nearly zero. J M Puram location had high mean for 2.5% span length but high interaction effects showed the suitability for specially adapted hybrids. Interaction of H 1442 $\times$ SUVIN (12) hybrid with Bapatla location indicates the positive interaction of them. IPCA score of Bapatla was nearly zero with stable performance of all hybrids in this location for 2.5% span length and could be good enough for selection of genotypes with average adaptation.

4.10.2.11 Uniformity ratio

AMMI analysis for uniformity ratio showed that genotypes and environments were significant for this character. The genotypes, environments and genotype $\times$ environment interaction exhibited 56.38%, 1.42% and 42.19% of the total variation. IPCA I was significant and contributed 63.10% of the total $G \times E$ interaction sum of squares.

From Fig. 4.21 the hybrids, NDLH 1938 $\times$ DB 11 (3), ADB 542 $\times$ DB 11 (15), ADB 542 $\times$ GSB 41 (16), ADB 532 $\times$ GSB 40 (19) and ADB 532 $\times$ DB 11 (21) were identified as stable genotypes with zero IPCA I score and higher mean than grand mean (45.72). IPCA score near to zero and low mean performance was showed by H 1442 $\times$ SUVIN (12), MCU 5 $\times$ DB 11 (57), MCU 5 $\times$ TCB 37 (59), L 1058 $\times$ DB 16 (62), L 1058 $\times$ TCB 37 (65) and L 1058 $\times$ SUVIN (66).

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

AMMI analysis of variance indicated that the genotypes, environments and genotype $\times$ environment interaction accounting for 24.59%, 57.28% and 18.11% of the total variation. Genotypes and environment variances were significant and $G \times E$ interaction presented in one IPCA axis. IPCA I was significant with 78.65% of total $G \times E$ sum of squares.

In AMMI I biplot (Fig. 4.22) ADB 542 $\times$ GSB 41 (16), ADB 532 $\times$ TCB 37 (23), SCS 793 $\times$ GSB 40 (49) and L 762 $\times$ GSB 41 (70) were stable with IPCA score nearer to zero and above grand mean (2.85×10^{-6} g/inch). ADB 542 $\times$ DB 11 (15), SCS 793 $\times$ DB 16 (50), MCU 5 $\times$ TCB 37 (59), L 1058 $\times$ TCB 37 (65) and L 1058 $\times$ SUVIN (66) recorded low mean with IPCA score near to zero. Bapatla location showed favourable conditions for poor environment adapted hybrids with mean performance nearly equal to grand mean for this trait. Whereas, J M Puram location had high mean performance for hybrids but showing high interaction effects indicates the suitability for specially adapted hybrids.

4.10.2.13 Bundle strength (g/tex)

For bundle strength, genotypes and environments were significant and exhibited 32.68% and 45.21% of the total variation. Genotype $\times$ environment interaction explained 22.10% of total variance and presented in one IPCA axis which was significant and contributed 60.73% of $G \times E$ interaction sum of squares.

In AMMI I biplot presentation (Fig. 4.23) the hybrids, NDLH 1938 × GSB 41 (4), ADB 542 × SUVIN (18), ADB 532 × GSB 41 (22), ADB 532 × SUVIN (24), WGCV 48 × GSB 40 (25), WGCV 48 × DB 16 (26), WGCV 48 × TCB 37 (29), BS 37 × TCB 37 (47), SCS 793 × GSB 40 (49), MCU 5 × GSB 40 (55), L 1058 × DB 11 (63) and L 1058 × GSB 41 (64) were found to be stable as they had above grand mean (27.02 g/tex) with IPCA score nearly zero. Low mean with IPCA score nearly zero exhibited by L 1058 × DB 16 (62), L 762 × GSB 41 (70) and L 762 × TCB 37 (71). J M Puram location suitable for specially adapted hybrids as it had high mean with negative interaction effects. Bapatla location had stable performance of hybrids for bundle strength as its IPCA score was near to zero.

4.10.2.14 Fibre elongation (%)

Variation due to genotypes and environments was significant and showed 39.84% and 37.88% of the total variation, whereas, genotype × environment interaction was exhibited 22.27% of the total variation. IPCA I was significant and explained 56.89% of the total G × E interaction sum of squares.

According to AMMI I biplot (Fig. 4.24) NDLH 1938 × DB 16 (2), NDLH 1938 × GSB 41 (4), WGCV 48 × DB 11 (27), BS 37 × GSB 41 (46) and L 1058 × DB 11 (63) hybrids were stable with nearly zero IPCA score and higher mean than grand mean (4.93 %). The hybrids, NDLH 1938 × TCB 37 (5), H 1442 × TCB 37 (11), ADB 532 × TCB 37 (23), MR 786 × SUVIN (36), TSH 0250 × TCB 37 (41), MCU 5 × DB 11 (57) and L 1058 × GSB 41 (64) possessed low mean with IPCA score nearer to zero. IPCA score of J M Puram location was nearly zero with high mean indicated stable performance of genotypes.

4.10.2.15 Seed cotton yield plant⁻¹ (g)

AMMI analysis of variance indicated that the genotypes and environments main effects were significant and accounted for 50.96% and 10.29% of the total variation. Genotype × environment interaction exhibited 38.73% of the total variance and presented in IPCA I axis. IPCA I was significant and contributed 61.53% of the total G × E interaction sum of squares.

From the AMMI I biplot (Fig. 4.25) the hybrids, NDLH 1938 × GSB 41 (4), ADB 542 × GSB 41 (16), ADB 532 × DB 16 (20), WGCV 48 × DB 16 (26), MR 786 × DB 16 (32), MR 786 × SUVIN (36), TSH 0250 × GSB 40 (37) and SCS 793 × DB 11

(51) were stable with higher mean than grand mean (184.10 g) and IPCA score nearly zero. ADB 532 × GSB 41 (22), ADB 532 × SUVIN (24), TSH 0250 × GSB 41(40), MCU 5 × DB 16 (56) and L 762 × GSB 41 (70) showed low mean with IPCA score nearer to zero. J M Puram location with ICPA score nearer to zero and high mean value than grand mean showed favourable conditions for seed cotton yield plant⁻¹. Lam Farm location suitable for specially adapted hybrids as it had high mean with high negative interaction effects. These results are in accordance with the results of Riaz *et al.* (2013).

4.10.2.16 Lint yield plant⁻¹ (g)

Genotypes, environments variances were significant and accounted for 57.69% and 13.08% of the total variance. The genotype × environment interaction contributed 29.22% of total variance. IPCA I was significant and exhibited 59.89% of the total G × E interaction sum of squares.

In AMMI I biplot presentation (Fig. 4.26) the hybrids, NDLH 1938 × GSB 41 (4), ADB 542 × GSB 41 (16), WGCV 48 × DB 16 (26), MR 786 × DB 16 (32), BS 37 × GSB 41 (46), SCS 793 × DB 11 (51) and L 762 × DB 11 (69) recorded IPCA score close to zero and high mean than grand mean (53.90g) indicating stable performance of these hybrids over locations. ADB 542 × SUVIN (18), ADB 532 × SUVIN (24), WGCV 48 × TCB 37 (29), TSH 0250 × GSB 41 (40) and L 762 × GSB 40 (67) were recorded low mean with IPCA score near to zero. Lam Farm location had good potential for lint yield plant⁻¹ but exhibiting high interaction effects showed the suitability for specially adapted hybrids.

According to both the stability models the hybrid, L 762 × TCB 37 stable for days to 50% flowering whereas, BS 37 × DB 16, SCS 793 × DB 16 and L 762 × SUVIN were stable for plant height. For number of sympodia plant⁻¹ NDLH 1938 × SUVIN was stable while, H 1442 × DB 11 and L 762 × TCB 37 recorded stability for number of bolls plant⁻¹. The hybrid NDLH 1938 × GSB 41 exhibited stability for ginning out-turn. SCS 793 × GSB 40 registered stability for 2.5% span length while for bundle strength, ADB 542 × SUVIN, ADB 532 × GSB 41, WGCV 48 × DB 16 and SCS 793 × GSB 40 were recorded stable performance. Only one hybrid *i.e.*, NDLH 1938 × GSB 41 showed stability for fibre elongation ratio. For micronaire value ADB 532 × TCB 37 was stable. ADB 542 × GSB 41 registered stable performance for seed cotton yield plant⁻¹ whereas, NDLH 1938 × GSB 41 and ADB 542 × GSB 41 were exhibited stability for lint yield plant⁻¹ over locations (Table 4.49). List of superior and stable inter-specific hybrids for different characters was presented in the Table 4.50.

4.11 IDENTIFICATION OF FAVOURABLE ALLELES IN THE DONOR PARENTS

The widespread use of high speed spinning technology in the textile mills has increased the demand for raw cotton fibre with higher strength and length. Hence, cotton fibre quality must be improved to remain competitive with synthetic fibres and to meet the needs of new spinning and weaving methods (Kohel, 1999). In this day by day quality and quantity requirement changing scenario, the cotton hybrids usage in the present day agricultural production is limited. Therefore, they have to be replaced by new hybrids that will exceed the existing ones in their performance. Egyptian cotton genotypes may serve for the improvement of existing cotton hybrids in terms of important fibre quality traits viz., 2.5% span length and bundle strength as the donors of favourable alleles.

Dudley (1984) proposed a methodology for identification of unique favourable alleles in donor inbred lines of maize for improving the parental constituents in a desirable single cross. This method was followed by several modifications by him as well as by other workers (Dudley, 1987b, Zanoni and Dubley, 1989b and Bernardo, 1990) devising new parameters for evaluating the donor inbred lines from all aspects like frequency of favourable alleles present, frequency of alleles lacking in the parental parents, estimating the relative relationships of the donor inbred and also estimating the loss of alleles not only in the donor parents but also in the single cross hybrids of maize. In the present experiment, a target cross (NDLH 1938 $\times$ MCU 5) which has been a *priori* projected to be improved was considered based on its proven performance in the previous yield trials.

4.11.1 NDLH 1938 $\times$ MCU 5 (Target Cross)

The estimates of $\mu G'$ for the cross NDLH 1938 $\times$ MCU 5 for 2.5% span length and bundle strength were presented in the Table 4.51. For 2.5% span length, in combined analysis and at Lam Farm all the six donors recorded significant positive $\mu G'$ estimates. Only one donor *i.e.*, SUVIN exhibited significant $\mu G'$ estimates at J M Puram. All the donors registered significant $\mu G'$ values at Bapatla except DB 11 and SUVIN. The donor, SUVIN showed highest $\mu G'$ estimate at Lam Farm and J M Puram. Whereas, GSB 40 recorded the highest $\mu G'$ value at Bapatla. In combined analysis, SUVIN had shown the highest $\mu G'$ estimate followed by GSB 40 and TCB 37. However, DB 11 showed the lowest $\mu G'$ estimate among all donors.

For bundle strength, all the donors showed significant positive $\mu G'$ estimates in combined analysis, of which GSB 40 gave the highest $\mu G'$ estimate followed by SUVIN and DB 16. The donor, DB 11 recorded the lowest $\mu G'$ estimate in combined analysis. Considering the individual environments, all the six donors except DB 11 at Lam Farm; GSB 40 and DB 16 at Bapatla recorded significant positive $\mu G'$ estimates. It is interesting to note that at J M Puram, $\mu G'$ estimates could not be obtained for all the donors. The reasons may be due to the failure of the assumptions of complete dominance or epistasis (Dudley, 1988).

Considering the overall data, it may be inferred that estimates of $\mu G'$ in various donors greatly differed in different environments for the same trait. This may be attributed to the differential environmental effects on the same set of genes governing the expression of the same trait. It is also observed that almost all the donors showed significant positive $\mu G'$ estimates for the two characters studied in combined analysis indicating existence of favourable alleles for further improvement of the target hybrid.

However, further characterization of various donors and their genetic similarity estimates (Tables 4.52 and 4.53) have to be analyzed critically along with the other estimates ($\mu B'$ to $\mu G'$) to initiate the improvement programme for this cross. For this cross the genetic enhancement for 2.5% span length and bundle strength was considered.

A perusal of the results obtained with respect to the donors (Table 4.51) is quite encouraging. The donors viz., SUVIN, GSB 40 and TCB 37 gave the highest significant positive $\mu G'$ estimates indicating their worth in transferring favourable alleles in the target cross for 2.5% span length. In order to obtain further details about the nature and frequency of alleles in the donor parents *vis-a-vis* concerned target cross, the various parameters to represent the different classes and the relationship of the donors with the parents of the cross concerned are presented in the Table 4.52. Critical study of mean *per se* value of the crosses and different parameters of the model taken into consideration together indicates that the findings are not beyond expectations. For example, the donor, SUVIN showed the highest significant $\mu G'$ estimate (3.467*) among the donors and expectedly should have given higher mean value in its cross combinations with the constituents (NDLH 1938 and MCU 5) of the target cross.

The cross, MCU 5 (P_2) $\times$ P_w recorded high *per se* performance and higher $\mu F'$ values (class where P_1 and P_w have unfavourable alleles and P_2 has favourable alleles) indicating for further improvement of the target cross for 2.5% span length can be

possible through replacement of P_1 with the donor line if other yield contributing traits are unaltered. On the other hand, if the improvement of this cross is sought *via* parental improvement the genotype SUVIN can be used as donor for recycling as it showed high $\mu G'$ values compared with other donors. Considering the parameters $(\mu C' + \mu F')$ and $(\mu D' + \mu E')$, the donor has genetic affinity with NDLH 1938 and it may be summarized that enhancement of NDLH 1938 by this will not cause any canceling effect which usually emanate from wide diversity of alleles coming together causing disequilibrium in the degree of association of dominant genes acting in opposite directions.

For enhancing bundle strength in the target cross, NDLH 1938 $\times$ MCU 5 through parental improvement, GSB 40 (3.552*) could be suggested, as this donor recorded highest positive and significant $\mu G'$ value. This revealed its worth in transferring favourable alleles. The cross MCU 5 (P_2) $\times$ P_w had recorded high *per se* performance and at the same time it had also recorded high $\mu F'$ value (class where P_1 and P_w have unfavourable alleles and P_2 has favourable alleles) (Table 4.53). For increased bundle strength in elite hybrid, P_1 may be replaced by the donor line GSB 40 or otherwise improvement of elite hybrid may be possible through improving the parental line NDLH 1938(P_1) through back crossing with GSB 40 as the donor has high genetic affinity with NDLH 1938.

Similarly several workers (Bernardo, 1990; Dudley *et al.*, 1996; Malvar *et al.*, 1997 and Ayrault *et al.*, 1999) used this model for population improvement and several workers (Dudley, 1984; 1987a, Kumar *et al.*, 2003; Reddy *et al.*, 2003, 2004; Malvar *et al.*, 2004; Reddy *et al.*, 2005 and Rodriguez *et al.*, 2007) used this model for inbreds improvement and supported the contention that the single cross hybrid improvement could be possible by selecting donors with significant favourable alleles.

FUTURE LINE OF WORK

- ❖ The lines *viz.*, NDLH 1938, ADB 542, ADB 532, BS 37 and L 762 were identified as good general combiners for yield and fibre quality traits. These lines can be used as parents for development of high yielding superior fibre quality intra-specific hybrids. Among the testers, TCB 37 and SUVIN were found to be good general combiners for 2.5% span length indicating their usefulness as parents for developing high yielding extra-long staple inter-specific cotton hybrids.

- ❖ Study of segregating generations of hybrids viz., H 1442 × GSB 41, H 1442 × DB 16 and ADB 542 × DB 16 will be helpful to identify superior transgressive segregants as they have high *per se* performance and *sca* effects for seed cotton yield plant⁻¹ along with number of sympodia plant⁻¹, number of boll plant⁻¹, boll weight and ginning out-turn and fibre quality traits like 2.5% span length and micronaire value.
- ❖ The stable hybrid, ADB 542 × GSB 41 (in both models) along with TSH 0250 × GSB 40 (in AMMI analysis and *per se* performance, *sca* effects and standard heterosis) may be evaluated over large number of environments in different seasons for further confirmation of their performance before they are being commercially exploited.

Chapter V

SUMMARY AND CONCLUSIONS

The present investigation on “Genetic analysis of yield and fibre quality traits in inter-specific hybrids of cotton (*Gossypium hirsutum* L. × *Gossypium barbadense* L.)” was carried out by selecting twelve *hirsutum* lines viz., NDH 1938, H 1442, ADB 542, ADB 532, WGCV 48, MR 786, TSH 0250, BS 37, SCS 793, MCU 5, L 1058, L 762 and six *barbadense* testers viz., GSB 40, DB 16, DB 11, GSB 41, TCB 37 and SUVIN based on cluster mean and *per se* performance studies with 70 *hirsutum* and 20 *barbadense* genotypes, respectively during *kharif*, 2013-14. Seventy two inter-specific cross combinations were obtained by crossing the parents in a line × tester design during off season (2014) at RARS, Lam Farm, Guntur, Andhra Pradesh. The evaluation of these inter-specific cotton hybrids along with their parents and standard checks was done at three locations i.e., RARS, Lam Farm; ARS, J M Puram and Agricultural College Farm, Bapatla during *kharif*, 2014-15.

Data was collected on 16 characters viz., days to 50% flowering, plant height (cm), number of monopodia plant⁻¹, number of sympodia plant⁻¹, number of bolls plant⁻¹, boll weight (g), lint index (g), seed index (g), ginning out-turn (%), 2.5% span length (mm), micronaire value (10⁻⁶g/inch), bundle strength (g/tex), uniformity ratio, fibre elongation (%), seed cotton yield plant⁻¹(g) and lint yield plant⁻¹ (g). The data was subject to different statistical analysis as per the objectives.

The Analysis of variance for both the groups of genotypes revealed existence of significant differences among the genotypes for 16 characters indicating the presence of genetic variability in the material evaluated. The mean, genetic variability, heritability, genetic advance as per cent of mean and genetic divergence, were studied for 16 characters in 70 American and 20 Egyptian cotton genotypes during *kharif*, 2013-14. Variability studies for 70 *hirsutum* and 20 *barbadense* genotypes revealed that wider genetic variability was exhibited by number of monopodia plant⁻¹ in Egyptian cotton group whereas it was for number of monopodia plant⁻¹ and seed cotton yield plant⁻¹ in American cotton group. In case of *hirsutum* genotypes moderate variability was noticed for number of sympodia plant⁻¹, number of bolls plant⁻¹, lint index, seed index, ginning out-turn, micronaire value, seed cotton yield plant⁻¹ and lint yield plant⁻¹. While, in *barbadense* group moderate genetic variability was exhibited by number of sympodia plant⁻¹, number of bolls plant⁻¹, lint index and lint yield plant⁻¹.

High heritability coupled with high genetic advance as per cent of mean was observed for number of monopodia plant⁻¹, number of bolls plant⁻¹, lint index, seed index, micronaire value, seed cotton yield plant⁻¹ and lint yield plant⁻¹ in *hirsutum* while it was for number of monopodia plant⁻¹, number of sympodia plant⁻¹, number of bolls plant⁻¹, lint index, seed cotton yield plant⁻¹ and lint yield plant⁻¹ in *barbadense*. This indicates the operation of additive gene action in the inheritance of these traits. Directional selection could be profitably applied on these traits in the genetically diverse material.

Days to 50% flowering, number of sympodia plant⁻¹, boll weight, ginning out-turn, 2.5% span length and bundle strength recorded high heritability coupled with moderate genetic advance as per cent of mean in American cotton group while boll weight, seed index, 2.5% span length, micronaire value and bundle strength in Egyptian cotton group. This indicates involvement of both additive and non-additive gene actions in the inheritance of these traits. Improvement of these traits is possible by simultaneous exploitation of both additive and non-additive components by adopting breeding procedures like bi-parental mating, diallel selective mating system or cyclic hybridization.

D² analysis grouped the 70 American cotton genotypes into 13 clusters and 20 Egyptian cotton genotypes into seven clusters. In case of *hirsutum* cluster I was the largest with 33 genotypes followed by cluster IV (11 genotypes), cluster VII (7 genotypes), cluster III (6 genotypes), cluster X (5 genotypes) and clusters II, V, VI, VIII, IX, XI, XII and XIII with one genotype each. Whereas cluster II was the largest with six genotypes followed by cluster I and IV (5 genotypes each) and clusters III, V, VI and VII were monogenotypic in *barbadense*.

D² analysis revealed that micronaire value (21.33) followed by lint index (19.30), days to 50% flowering (16.40), number of monopodia plant⁻¹ (13.94) and seed index (13.29) in *hirsutum* while seed index (18.37) followed by fibre elongation (12.63), 2.5% span length (12.11), seed cotton yield plant⁻¹ (10.60) and number of monopodia plant⁻¹ (10.49) in *barbadense* contributed maximum for the divergence.

Principal component analysis identified six significant principal components (PCs) for both the groups of genotypes, which contributed 74.61 and 92.05 per cent of cumulative variance, respectively. The first principal component (PC₁) contributed maximum towards variability (19.82) and the characters viz., plant height (-0.342),

number of monopodia plant⁻¹ (-0.236), number of sympodia plant⁻¹ (-0.320), seed index (0.223), 2.5% span length (0.427), micronaire value (-0.338), fibre elongation (-0.255), uniformity ratio (0.223) and lint yield plant⁻¹ (-0.431) explained the maximum variance in the first principal component (PC₁) and signifying their importance in yield in *hirsutum*. In *barbadense* 30.21 per cent variance was contributed by the first principal component (PC₁) and the characters viz., number of sympodia plant⁻¹ (-0.346), boll weight (-0.307), lint index (-0.407), seed index (-0.416), ginning out-turn (-0.269), bundle strength (-0.281), fibre elongation (-0.216), seed cotton yield plant⁻¹ (0.285) and lint yield plant⁻¹ (0.240) explained the maximum variance in the first principal component (PC₁).

Based on cluster mean values and *per se* performance for important traits viz., number of bolls plant⁻¹, boll weight and seed cotton yield plant⁻¹ the genotypes, NDLH 1938, H 1442, ADB 542, ADB 532, WGCV 48, MR 786, TSH 0250, BS 37, SCS 793, MCU 5, L 1058 and L762, were selected as female parents (lines) from *hirsutum* group. On the other hand *barbadense* genotypes GSB 40, DB 16, DB 11, GSB 41, TCB 37 and SUVIN were identified as male parents (testers) as they have high cluster mean and *per se* performance values for 2.5% span length and bundle strength. Hence, these genotypes (12 lines + 6 testers) were taken for inter-specific hybrids production by crossing them in line × tester fashion to exploit heterosis.

The pooled estimates of variability, heritability ($h^2_{(b)}$) in broad sense and genetic advance as per cent of mean (GAM) for 72 inter-specific cotton hybrids indicated wide variability for number of monopodia plant⁻¹, number of bolls plant⁻¹, seed cotton yield plant⁻¹ and lint yield plant⁻¹ which reveals their amenability towards directional selection. The traits viz., plant height, number of sympodia plant⁻¹, boll weight and micronaire value recorded moderate variability.

High heritability coupled with high genetic advance as per cent of mean was observed for micronaire value, seed cotton yield plant⁻¹ and lint yield plant⁻¹ which suggests the role of additive gene action in the inheritance of these traits and directional selection could be profitably exploited for the improvement. High heritability and moderate genetic advance as per cent of mean were observed for boll weight, 2.5% span length and bundle strength revealing the involvement of both additive and non-additive gene actions in the inheritance of these traits. Further improvement of these traits would be possible through breeding procedures like bi-parental mating, diallel selective mating or cyclic hybridization.

The character association and path analysis studies revealed plant height, number of bolls plant⁻¹, boll weight, lint index, ginning out-turn, 2.5% span length, bundle strength, fibre elongation and lint yield plant⁻¹ showed direct positive effects and significant correlation with seed cotton yield plant⁻¹. Thus, the present study indicated that due weightage should be laid in selection process with more number of bolls plant⁻¹ and boll weight and there should be economic balance among these traits to get higher seed cotton yield plant⁻¹.

The pooled analysis of variance of 90 genotypes (12 lines, 6 testers and 72 hybrids) for combining ability showed significant differences due to locations, parents, hybrids and various interactions indicating the existence of sufficient variation in the material under study. The ratio of general combining ability component of variance to specific combining ability component of variance indicated the presence of additive gene action for number of bolls plant⁻¹, seed index, 2.5% span length, uniformity ratio and seed cotton yield plant⁻¹. The traits governed by additive gene action can be improved through hybridization followed by simple selection *i.e.*, pedigree method. Whereas, non-additive gene action was present for days to 50% flowering, plant height, number of monopodia plant⁻¹, number of sympodia plant⁻¹, lint index, ginning out-turn, micronaire value, bundle strength, fibre elongation and lint yield plant⁻¹. Bi-parental mating or diallel selective mating or heterosis breeding can be employed for the improvement of these traits. Whereas the character boll weight was controlled by both additive and non-additive gene actions. Further improvement of this trait can be possible through bi-parental mating or diallel selective mating or any form of recurrent selection in the early generations followed by single plant selection.

In pooled analysis, none of the lines and testers was found to exhibit significant *gca* effects for all the characters studied. The lines, NDLH 1938, H 1442, ADB 542, ADB 532, MR 786, BS 37, L 762 and testers, GSB 40, DB 16, DB 11 and GSB 41, were found to be promising general combiners for seed cotton yield plant⁻¹ and other traits. The crosses, H 1442 × GSB 41, TSH 0250 × GSB 40 and ADB 542 × DB 16, showed high *per se* performance and positive *sca* effects for seed cotton yield plant⁻¹ and also recorded significant *sca* effects for yield contributing and fibre quality traits like, number of sympodia plant⁻¹ (TSH 0250 × GSB 40, ADB 542 × DB 16), number of bolls plant⁻¹ (TSH 0250 × GSB 40, ADB 542 × DB 16), boll weight (H 1442 × GSB 41, TSH 0250 × GSB 40 and ADB 542 × DB 16), ginning out-turn (H 1442 × GSB 41, TSH 0250 × GSB 40 and ADB 542 × DB 16) and 2.5% span length (TSH 0250 × GSB 40).

Based on *per se* performance, *sca* effects and standard heterosis in pooled analysis, the cross combinations viz., H 1442 × GSB 41, H 1442 × DB 16 and TSH 0250 × GSB 40 were found to be promising for seed cotton yield plant⁻¹. Besides seed cotton yield plant⁻¹, the hybrids exhibited superior performance for other important yield contributing and quality characters viz., number of sympodia plant⁻¹, number of boll plant⁻¹, boll weight, and ginning out turn and quality traits like 2.5% span length and micronaire value.

Environmental index reveals the suitability of an environment for a particular trait. Based on the positive values of environmental index, Lam Farm location was found to be most favourable for seed cotton yield plant⁻¹ and other yield component characters viz., days to 50% flowering, plant height, number of sympodia plant⁻¹, number of bolls plant⁻¹, ginning out-turn and lint yield plant⁻¹.

Pooled analysis of variance for stability using Eberhart and Russell and AMMI models revealed significant differences among the genotypes and locations for all the yield and fibre quality traits. Results of the Eberhart and Russell model revealed that none of the hybrid had shown stable performance for all the characters studied, this may be attributed to the changes in the environments. The hybrid, ADB 542 × GSB 41, showed stability for seed cotton yield plant⁻¹ over locations.

AMMI analysis of variance revealed that ICPCA I was significant for all the traits and explained more than 50% of the total G × E interaction sum of squares. The interaction of seventy two hybrids over three locations was best predicted by first interaction principal component. Hybrids viz., NDLH 1938 × GSB 41, ADB 542 × GSB 41, ADB 532 × DB 16, WGCV 48 × DB 16, MR 786 × DB 16, MR 786 × SUVIN, TSH 0250 × GSB 40 and SCS 793 × DB 11, were found to be stable with higher mean than grand mean and IPCA score near zero.

When compared over both the stability models, the hybrid, ADB 542 × GSB 41, registered stable performance for seed cotton yield plant⁻¹ along with fibre elongation and lint yield plant⁻¹. Whereas, the hybrid, TSH 0250 × GSB 40, recorded significant *per se* performance, *sca* effect and standard heterosis, stable performance in AMMI analysis and suitable for unfavourable environments as per Eberhart and Russell model for seed cotton yield plant⁻¹ with desirable 2.5% span length and micronaire value. Hence, these hybrids may be considered for thorough testing over large number of seasons and locations for confirming their performance before they are being exploited for commercial cultivation.

The identification of favourable alleles in donor parents for improving target cross, NDLH 1938 $\times$ MCU 5 revealed that the donors, SUVIN, GSB 40 and TCB 37 for 2.5% span length and for bundle strength GSB 40, SUVIN and DB 16 recorded significant and positive $\mu G'$ estimates in combined analysis and exhibited their worth in transferring favourable alleles in the target cross. The cross, MCU 5 (P_2) $\times$ SUVIN (P_w) showed high *per se* performance and high $\mu F'$ value for 2.5% span length and indicated P_1 and P_w have unfavourable alleles and P_2 had favourable alleles and $(\mu C' + \mu F')$ and $(\mu D' + \mu E')$ values revealed the donor had high genetic affinity with NDLH 1938 (P_1). For bundle strength MCU 5 (P_2) $\times$ GSB 40 (P_w) exhibited high *per se* and $\mu F'$ value which revealed presence of unfavorable alleles in P_1 and P_w and favourable alleles in donor parent and $(\mu C' + \mu F')$ and $(\mu D' + \mu E')$ values indicated high genetic affinity of donor *i.e.*, GSB 40 with NDLH 1938. NDLH 1938 had unfavourable alleles for both the traits and had high genetic affinity with both the donors. Hence, NDLH 1938 can be improved by using these two donors and improved NDLH 1938 may be used to produce target cross with high seed cotton yield along with good quality fibre.

Table 2.6. Review of literature on gene action governing seed cotton yield and yield components in cotton hybrids

S.No.	Character	Additive	Non-additive	Additive and non-additive
1.	Days to 50% flowering	Reshmi <i>et al.</i> (2007) Kalpande <i>et al.</i> (2008) Wankhade <i>et al.</i> (2008) Ambhore <i>et al.</i> (2012) Shinde <i>et al.</i> (2012) Patel <i>et al.</i> (2014)	Kamboh <i>et al.</i> (2008) Preetha and Raveendran (2008) Deosarkar <i>et al.</i> (2009b) Patil <i>et al.</i> (2011) Sheraz <i>et al.</i> (2011) Amir <i>et al.</i> (2012) Vineela <i>et al.</i> (2012) Simon <i>et al.</i> (2013) Yanal <i>et al.</i> (2013) Deosarkar <i>et al.</i> (2014)	Laxman and Ganesh (2003) Sivaprasad <i>et al.</i> (2004) Gibri <i>et al.</i> (2006)
2.	Plant height (cm)	Patel <i>et al.</i> (2005) Ilyas <i>et al.</i> (2007) Bhaskaran and Ravikesavan (2008) Kalpande <i>et al.</i> (2008) Natera <i>et al.</i> (2011) Ambhore <i>et al.</i> (2012) Kumar <i>et al.</i> (2013) Mohammad <i>et al.</i> (2013) Patel <i>et al.</i> (2014) Usharani <i>et al.</i> (2014)	Kamboh <i>et al.</i> (2008) Deosarkar <i>et al.</i> (2009b) Mohammad <i>et al.</i> (2010) Patil <i>et al.</i> (2011) Patel <i>et al.</i> (2012) Vineela <i>et al.</i> (2012) Simon <i>et al.</i> (2013) Yanal <i>et al.</i> (2013) Deosarkar <i>et al.</i> (2014)	Rathore <i>et al.</i> (2004) Sundaravadivelu <i>et al.</i> (2005) Gibri <i>et al.</i> (2006) Ghaffar <i>et al.</i> (2007) Kumar <i>et al.</i> (2013) Shabana <i>et al.</i> (2014)
3.	Number of monopodia plant ⁻¹	Ghaffar <i>et al.</i> (2007) Kiani <i>et al.</i> (2007) Mohammad <i>et al.</i> (2010) Mohan (2011) Ambhore <i>et al.</i> (2012)	Deosarkar <i>et al.</i> (2009b) Mahantesh <i>et al.</i> (2010) Patil <i>et al.</i> (2011) Vineela <i>et al.</i> (2012) Tuteja and Banga (2013) Yanal <i>et al.</i> (2013) Deosarkar <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Rajamani <i>et al.</i> (2014)	Laxman and Ganesh (2003) Sundaravadivelu <i>et al.</i> (2005) Gibri <i>et al.</i> (2006) Wandhare <i>et al.</i> (2010) Tariq and Uzair (2012)

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Table 2.6 (cont.)

S.No.	Character	Additive	Non-additive	Additive and non-additive
4.	Number of sympodia plant ⁻¹	Bhaskaran and Ravikesavan (2008) Jatoi <i>et al.</i> (2011) Mohan (2011) Wajid <i>et al.</i> (2011) Ambhore <i>et al.</i> (2012) Shinde <i>et al.</i> (2012) Tariq and Uzair (2012) Mohammad <i>et al.</i> (2013) Usharani <i>et al.</i> (2014)	Kiani <i>et al.</i> (2007) Kamboh <i>et al.</i> (2008) Patel <i>et al.</i> (2009) Kumar <i>et al.</i> (2010) Mahantesh <i>et al.</i> (2010) Mohammad <i>et al.</i> (2010) Patil <i>et al.</i> (2011) Vineela <i>et al.</i> (2012) Kumar <i>et al.</i> (2013) Tuteja and Banga (2013) Yanal <i>et al.</i> (2013) Deosarkar <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Rajamani <i>et al.</i> (2014)	Rathore <i>et al.</i> (2004) Sundaravadivelu <i>et al.</i> (2005) Gibri <i>et al.</i> (2006) Wandhare <i>et al.</i> (2010) Shabana <i>et al.</i> (2014)
5.	Number of bolls plant ⁻¹	Sivaprasad <i>et al.</i> (2004) Iqbal <i>et al.</i> (2007) Bhaskaran and Ravikesavan (2008) Kalpande <i>et al.</i> (2008) Pole <i>et al.</i> (2008) Mohan (2011) Wajid <i>et al.</i> (2011) Ambhore <i>et al.</i> (2012) Tariq and Uzair (2012) Kumar <i>et al.</i> (2013) Simon <i>et al.</i> (2013)	Ilyas <i>et al.</i> (2007) Kamboh <i>et al.</i> (2008) Mahantesh <i>et al.</i> (2010) Mohammad <i>et al.</i> (2010) Patil <i>et al.</i> (2011) Imran <i>et al.</i> (2012) Patel <i>et al.</i> (2012) Vineela <i>et al.</i> (2012) Mohammad <i>et al.</i> (2013) Tuteja and Banga (2013) Yanal <i>et al.</i> (2013) Deosarkar <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Rajamani <i>et al.</i> (2014) Usharani <i>et al.</i> (2014)	Narisireddy and Satyanarayana (2004) Rathore <i>et al.</i> (2004) Sundaravadivelu <i>et al.</i> (2005) Gibri <i>et al.</i> (2006) Singh and Singh (2006) Ghaffar <i>et al.</i> (2007) Kiani <i>et al.</i> (2007) Panhwar <i>et al.</i> (2008) Bbebe <i>et al.</i> (2010) Wandhare <i>et al.</i> (2010) Kumar <i>et al.</i> (2013) Baloch <i>et al.</i> (2014) Patel and Jadon (2014)

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S.No.	Character	Additive	Non-additive	Additive and non-additive
6.	Boll weight (g)	Bhaskaran and Ravikesavan (2008) Kamboh <i>et al.</i> (2008) Mohammad <i>et al.</i> (2010) Singh <i>et al.</i> (2010) Natera <i>et al.</i> (2011) Ambhore <i>et al.</i> (2012) Amir <i>et al.</i> (2012) Patel <i>et al.</i> (2012) Tariq and Uzair (2012) Kumar <i>et al.</i> (2013) Mohammad <i>et al.</i> (2013) Patel <i>et al.</i> (2014) Usharani <i>et al.</i> (2014)	Ilyas <i>et al.</i> (2007) Iraddi and Kajjidoni (2009) Kumar <i>et al.</i> (2010) Mohan (2011) Patil <i>et al.</i> (2011) Vineela <i>et al.</i> (2012) Simon <i>et al.</i> (2013) Tuteja and Banga (2013) Yanal <i>et al.</i> (2013) Deosarkar <i>et al.</i> (2014) Rajamani <i>et al.</i> (2014)	Narisireddy and Satyanarayana (2004) Gibri <i>et al.</i> (2006) Ghaffar <i>et al.</i> (2007) Kiani <i>et al.</i> (2007) Panhwar <i>et al.</i> (2008) Gamal <i>et al.</i> (2009) Bbebe <i>et al.</i> (2010) Wandhare <i>et al.</i> (2010) Rajamani <i>et al.</i> (2012) Baloch <i>et al.</i> (2014) Patel and Jadon (2014)
8.	Lint index (g)	Rathore <i>et al.</i> (2004) Kalpande <i>et al.</i> (2008) Mohammad <i>et al.</i> (2009) Wandhare <i>et al.</i> (2010) Ambhore <i>et al.</i> (2012) Kumar <i>et al.</i> (2013) Usharani <i>et al.</i> (2014)	Preetha and Raveendran (2008) Basal <i>et al.</i> (2009) Iraddi and Kajjidoni (2009) Mahantesh <i>et al.</i> (2010) Mohan (2011) Patil <i>et al.</i> (2011) Vineela <i>et al.</i> (2012) Yanal <i>et al.</i> (2013) Patel <i>et al.</i> (2014) Rajamani <i>et al.</i> (2014)	Reddy (2001) Laxman and Ganesh (2003) Sundaravadivelu <i>et al.</i> (2005) Gibri <i>et al.</i> (2006) Gamal <i>et al.</i> (2009)

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S.No.	Character	Additive	Non-additive	Additive and non-additive
9.	Seed index (g)	Paulo <i>et al.</i> (2007) Kalpande <i>et al.</i> (2008) Pole <i>et al.</i> (2008) Mohammad <i>et al.</i> (2009) Wandhare <i>et al.</i> (2010) Ambhore <i>et al.</i> (2012) Kumar <i>et al.</i> (2013) Usharani <i>et al.</i> (2014)	Deosarkar <i>et al.</i> (2009b) Iraddi and Kajjidoni (2009) Mahantesh <i>et al.</i> (2010) Mohan (2011) Patil <i>et al.</i> (2011) Vineela <i>et al.</i> (2012) Yanal <i>et al.</i> (2013) Deosarkar <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Rajamani <i>et al.</i> (2014)	Sivaprasad <i>et al.</i> (2004) Sundaravadivelu <i>et al.</i> (2005) Gibri <i>et al.</i> (2006) Panhwar <i>et al.</i> (2008)
10.	Ginning out-turn (%)	Iqbal <i>et al.</i> (2007) Bhaskaran and Ravikesavan (2008) Kalpande <i>et al.</i> (2008) Pole <i>et al.</i> (2008) Deshmukh <i>et al.</i> (2010) Wandhare <i>et al.</i> (2010) Ambhore <i>et al.</i> (2012) Kumar <i>et al.</i> (2013) Usharani <i>et al.</i> (2014)	Karademir <i>et al.</i> (2009) Mahantesh <i>et al.</i> (2010) Singh <i>et al.</i> (2010) Mohan (2011) Patil <i>et al.</i> (2011) Patel <i>et al.</i> (2012) Vineela <i>et al.</i> (2012) Tuteja and Banga (2013) Yanal <i>et al.</i> (2013) Deosarkar <i>et al.</i> (2014) Patel <i>et al.</i> (2014)	Laxman and Ganesh (2003) Sivaprasad <i>et al.</i> (2004) Sundaravadivelu <i>et al.</i> (2005) Gibri <i>et al.</i> (2006) Singh and Singh (2006) Panhwar <i>et al.</i> (2008) Bbebe <i>et al.</i> (2010) Patel and Jadon (2014) Rajamani <i>et al.</i> (2014)
11.	2.5% span length (mm)	Iqbal <i>et al.</i> (2007) Paulo <i>et al.</i> (2007) Kalpande <i>et al.</i> (2008) Kamboh <i>et al.</i> (2008) Muhammad <i>et al.</i> (2008) Karademir <i>et al.</i> (2009) Wandhare <i>et al.</i> (2010) Mohan (2011)	Ilyas <i>et al.</i> (2007) Faqir and Muhammad (2008) Kumar and Ravikesavan (2008) Iraddi and Kajjidoni (2009) Mahantesh <i>et al.</i> (2010) Singh <i>et al.</i> (2010) Vineela <i>et al.</i> (2012) Tuteja and Banga (2013) Deosarkar <i>et al.</i> (2014)	Huseyin and Ismail (2003) Sivaprasad <i>et al.</i> (2004) Sundaravadivelu <i>et al.</i> (2005) Natera <i>et al.</i> (2012) Kumar <i>et al.</i> (2013) Baloch <i>et al.</i> (2014) Patel and Jadon (2014)

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S.No.	Character	Additive	Non-additive	Additive and non-additive
11.	2.5% span length (mm)	Patil <i>et al.</i> (2011) Ambhore <i>et al.</i> (2012) Amir <i>et al.</i> (2012) Kumar <i>et al.</i> (2013) Mohammad <i>et al.</i> (2013)	Patel <i>et al.</i> (2014) Rajamani <i>et al.</i> (2014)	----
12.	Uniformity ratio	Paulo <i>et al.</i> (2007) Mohammad <i>et al.</i> (2009) Deshmukh <i>et al.</i> (2010) Wandhare <i>et al.</i> (2010) Ambhore <i>et al.</i> (2012) Nimbalkar <i>et al.</i> (2014)	Muhammad <i>et al.</i> (2008) Preetha and Raveendran (2008) Basal <i>et al.</i> (2009) Iraddi and Kajjidoni (2009) Karademir <i>et al.</i> (2009) Hussain <i>et al.</i> (2010) Mohan (2011) Patil <i>et al.</i> (2011) Vineela <i>et al.</i> (2012) Deosarkar <i>et al.</i> (2014) Rajamani <i>et al.</i> (2014)	Karademir <i>et al.</i> (2007) Venkatesh (2012)
13.	Micronaire value (10 ⁻⁶ g/inch)	Naphade <i>et al.</i> (2004) Verma <i>et al.</i> (2004) Subramanian <i>et al.</i> (2005) Paulo <i>et al.</i> (2007) Kalpande <i>et al.</i> (2008) Kamboh <i>et al.</i> (2008) Karademir <i>et al.</i> (2009) Wandhare <i>et al.</i> (2010) Ambhore <i>et al.</i> (2012) Nimbalkar <i>et al.</i> (2014)	Mahantesh <i>et al.</i> (2010) Singh <i>et al.</i> (2010) Mohan (2011) Patil <i>et al.</i> (2011) Amir <i>et al.</i> (2012) Vineela <i>et al.</i> (2012) Kumar <i>et al.</i> (2013) Tuteja and Banga (2013) Deosarkar <i>et al.</i> (2014) Rajamani <i>et al.</i> (2014)	Huseyin and Ismail (2003) Sivaprasad <i>et al.</i> (2004) Natera <i>et al.</i> (2011) Kumar <i>et al.</i> (2013)

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S.No.	Character	Additive	Non-additive	Additive and non-additive
14.	Bundle strength (g/tex)	Huseyin and Ismail (2003) Paulo <i>et al.</i> (2007) Bhaskaran and Ravikesavan (2008) Kalpande <i>et al.</i> (2008) Basal <i>et al.</i> (2009) Wandhare <i>et al.</i> (2010) Ambhore <i>et al.</i> (2012) Amir <i>et al.</i> (2012) Mohammad <i>et al.</i> (2013) Nimbalkar <i>et al.</i> (2014) Patel <i>et al.</i> (2014) Rajamani <i>et al.</i> (2014)	Ilyas <i>et al.</i> (2007) Muhammad <i>et al.</i> (2008) Karademir <i>et al.</i> (2009) Hussain <i>et al.</i> (2010) Mahantesh <i>et al.</i> (2010) Mohan (2011) Vineela <i>et al.</i> (2012) Kumar <i>et al.</i> (2013) Tuteja and Banga (2013) Deosarkar <i>et al.</i> (2014)	Venkatesh (2012)
15.	Fibre elongation (%)	Karademir <i>et al.</i> (2007) Paulo <i>et al.</i> (2007) Bhaskaran and Ravikesavan (2008) Muhammad <i>et al.</i> (2008) Karademir <i>et al.</i> (2009) Singh <i>et al.</i> (2010) Mohan (2011)	Manickam and Gururajan (2004) Kumar and Ravikesavan (2008) Preetha and Raveendran (2008) Basal <i>et al.</i> (2009) Mahantesh <i>et al.</i> (2010) Vineela <i>et al.</i> (2012) Deosarkar <i>et al.</i> (2014)	Venkatesh (2012)
15.	Seed cotton yield plant ⁻¹ (g)	Paulo <i>et al.</i> (2007) Reshmi <i>et al.</i> (2007) Bbebe <i>et al.</i> (2010) Mohammad <i>et al.</i> (2010) Singh <i>et al.</i> (2010) Wandhare <i>et al.</i> (2010) Mohan (2011)	Ilyas <i>et al.</i> (2007) Kamboh <i>et al.</i> (2008) Deosarkar <i>et al.</i> (2009b) Karademir <i>et al.</i> (2009) Jyothiba <i>et al.</i> (2010) Mahantesh <i>et al.</i> (2010)	Huseyin and Ismail (2003) Rathore <i>et al.</i> (2004) Gibri <i>et al.</i> (2006) Singh and Singh (2006) Panhwar <i>et al.</i> (2008) Gamal <i>et al.</i> (2009) Wandhare <i>et al.</i> (2010)

Table 2.6 (cont.)

Table 2.6 (cont.)

S.No.	Character	Additive	Non-additive	Additive and non-additive
15.	Seed cotton yield plant ⁻¹ (g)	Wajid <i>et al.</i> (2011) Amir <i>et al.</i> (2012) Tariq and Uzair (2012) Mohammad <i>et al.</i> (2013) Simon <i>et al.</i> (2013) Patel <i>et al.</i> (2014) Usharani <i>et al.</i> (2014)	Patil <i>et al.</i> (2011) Sheraz <i>et al.</i> (2011) Imran <i>et al.</i> (2012) Patel <i>et al.</i> (2012) Kumar <i>et al.</i> (2013) Tuteja and Banga (2013) Yanal <i>et al.</i> (2013) Deosarkar <i>et al.</i> (2014) Patel <i>et al.</i> (2014)	Natera <i>et al.</i> (2011) Baloch <i>et al.</i> (2014) Shabana <i>et al.</i> (2014)
16.	Lint yield plant ⁻¹ (g)	Tomar and Singh (1996) Paulo <i>et al.</i> (2007) Pole <i>et al.</i> (2008) Simon <i>et al.</i> (2013)	Deosarkar <i>et al.</i> (2009b) Karademir <i>et al.</i> (2009) Sheraz <i>et al.</i> (2011) Imran <i>et al.</i> (2012) Patel <i>et al.</i> (2012) Vineela <i>et al.</i> (2012)	Dagaonkar and Malkhandale (1993) Huseyin and Ismail (2003) Gamal <i>et al.</i> (2009)

Table 2.7. Review of literature on heterosis over mid parent (relative heterosis), better parent (heterobeltiosis) and standard check (standard heterosis) for yield and yield components in cotton hybrids

S.No.	Character	Number of crosses	Range of heterosis (%)			References
			Mid parent heterosis	Better parent heterosis	Standard heterosis	
1.	Days to 50% flowering	56	-2.70 to 7.32	-	-	Dukre <i>et al.</i> (2007)
		21	-14.33 to 10.21	-8.07 to 11.62	-10.45 to 11.62	Deosarkar <i>et al.</i> (2009a)
		4	-3.79 to 0.90	-1.40 to 8.31	-	Haleem <i>et al.</i> (2010)
		15	0.77 to 6.52	1.49 to 7.58	-10.94 to -2.90	Amalabalu <i>et al.</i> (2012)
2.	Plant height (cm)	16	-	-24.24 to 14.54	-	Patel <i>et al.</i> (2005)
		56	-16.65 to 29.67	-	-	Dukre <i>et al.</i> (2007)
		15	23.80 to 32.77	- 32.24 to 22.92	-	Jesus <i>et al.</i> (2007)
		21	-32.81 to 21.51	-40.59 to 17.07	-22.76 to 37.70	Deosarkar <i>et al.</i> (2009a)
		15	-	-4.94 to 33.98	2.13 to 40.50	Wankhade <i>et al.</i> (2009)
		15	-66.98 to 46.48	-20.98 to 34.46	-13.94 to 19.77	Amalabalu <i>et al.</i> (2012)
		45	12.80 to 102.29	-4.03 to 77.38	-12.22 to 49.17	Patel <i>et al.</i> (2012)
		56	- 65.00 to 92.00	- 65.00 to 73.00	-	Punitha <i>et al.</i> (2012)
		52	-	-	-0.16 to 23.33	Kumar <i>et al.</i> (2013)
		45	-	-	- 2.12 to 21.82	Nirania <i>et al.</i> (2014)
3.	Number of monopodia plant ⁻¹	18	-35.62 to 81.52	-29.32 to 79.51	-32.10 to 80.51	Reddy (2001)
		21	-57.69 to 57.89	-60.71 to 29.16	-54.16 to 29.16	Deosarkar <i>et al.</i> (2009a)
		52	-	-	- 66.67 to 28.79	Kumar <i>et al.</i> (2013)
		45	-	-	- 14.63 to 178.05	Nirania <i>et al.</i> (2014)
		44	-	-	- 55.60 to 81.10	Tuteja (2014)
4.	Number of sympodia plant ⁻¹	15	-10.37 to 46.93	-	-	Potdukhe (2002)
		56	-37.52 to 29.74	-	-	Dukre <i>et al.</i> (2007)
		21	-25.84 to 55.13	-31.83 to 48.39	-38.54 to 30.26	Deosarkar <i>et al.</i> (2009a)
		15	-	-15.37 to 45.08	-15.09 to 37.69	Wankhade <i>et al.</i> (2009)

Table 2.7 (cont.)

Table 2.7 (cont.)

S.No.	Character	Number of crosses	Range of heterosis (%)			References
			Mid parent heterosis	Better parent heterosis	Standard heterosis	
4.	Number of sympodia plant ⁻¹	4	27.35 to 125.14	0.00 to 28.39	-	Haleem <i>et al.</i> (2010)
		15	-6.82 to 35.48	-9.52 to 29.03	2.00 to 22.58	Amalabalu <i>et al.</i> (2012)
		55	-	-6.09 to 46.14	-	Nidagundi <i>et al.</i> (2012)
		56	-63.00 to 38.00	-64.00 to 33.00	-	Punitha <i>et al.</i> (2012)
		45	-	-	-27.53 to 34.11	Nirania <i>et al.</i> (2014)
		44	-	-	-54.90 to -31.90	Tuteja (2014)
5.	Number of bolls plant ⁻¹	56	-23.28 to 56.92	-	-	Dukre <i>et al.</i> (2007)
		6	3.87 to 20.05	-7.23 to 17.27	-	Syed and Sajid (2008)
		21	-29.14 to 132.47	-46.26 to 119.52	-62.54 to 47.27	Deosarkar <i>et al.</i> (2009a)
		15	-	0.00 to 132.93	-48.65 to 10.11	Wankhade <i>et al.</i> (2009)
		4	20.80 to 59.35	0.00 to 49.39	-	Haleem <i>et al.</i> (2010)
		15	-24.19 to 145.74	-45.16 to 124.68	4.55 to 56.36	Amalabalu <i>et al.</i> (2012)
		55	-	-17.01 to 30.43	-	Nidagundi <i>et al.</i> (2012)
		45	-35.62 to 50.83	-48.24 to 47.08	-40.38 to 51.78	Patel <i>et al.</i> (2012)
		56	-61.00 to 129.00	-70.00 to 118.00	-	Punitha <i>et al.</i> (2012)
		52	-	-	-33.69 to 68.48	Kumar <i>et al.</i> (2013)
		50	-	-	- 32.50 to 17.90	Tuteja <i>et al.</i> (2013)
		45	-	-	-33.52 to 74.59	Nirania <i>et al.</i> (2014)
		28	-	- 23.84 to 76.00	-	Patil <i>et al.</i> (2014)
		9	-36.24 to 10.98	-39.79 to 4.25	-	Seoudy <i>et al.</i> (2014)
		44	-	-	- 53.10 to -12.70	Tuteja (2014)
6.	Boll weight (g)	6	-2.98 to 3.21	-7.54 to 3.81	-	Syed and Sajid (2008)
		21	-25.42 to 33.08	-61.41 to 17.85	-27.63 to 15.46	Deosarkar <i>et al.</i> (2009a)
		15	-	-21.45 to 22.74	-12.20 to 21.59	Wankhade <i>et al.</i> (2009)
		4	17.62 to 28.99	0.00 to 23.04	-	Haleem <i>et al.</i> (2010)
		15	-25.00 to 26.74	-39.29 to 11.63	-17.86 to 25.00	Amalabalu <i>et al.</i> (2012)

Table 2.7 (cont.)

Table 2.7 (cont.)

S.No.	Character	Number of crosses	Range of heterosis (%)			References
			Mid parent heterosis	Better parent heterosis	Standard heterosis	
6.	Boll weight (g)	55	-	-11.28 to 12.95	-	Nidagundi <i>et al.</i> (2012)
		45	-41.83 to 59.00	-56.05 to 29.02	-54.26 to 34.07	Patel <i>et al.</i> (2012)
		56	-65.60 to 33.30	-70.9 to 14.40	-	Punitha <i>et al.</i> (2012)
		52	-	-	-12.03 to 34.82	Kumar <i>et al.</i> (2013)
		50	-	-	-36.8 to -6.60	Tuteja <i>et al.</i> (2013)
		45	-	-	-9.04 to 26.91	Nirania <i>et al.</i> (2014)
		9	-10.17 to 22.60	-17.68 to 20.17	-	Seoudy <i>et al.</i> (2014)
		44	-	-	- 30.10 to 5.60	Tuteja (2014)
7.	Lint index (g)	56	-27.65 to 41.28	-	-	Dukre <i>et al.</i> (2007)
		15	-	-24.94 to 27.57	0.60 to 42.85	Wankhade <i>et al.</i> (2009)
		15	-15.38 to 25.15	-19.23 to 15.94	-20.69 to 33.30	Amalabalu <i>et al.</i> (2012)
		55	-	-11.71 to 11.43	-	Nidagundi <i>et al.</i> (2012)
		56	- 63.40 to 33.60	- 63.70 to 13.60	-	Punitha <i>et al.</i> (2012)
		52	-	-	0.19 to 35.04	Kumar <i>et al.</i> (2013)
		28	-	- 30.86 to 10.29	-	Patil <i>et al.</i> (2014)
		9	-8.37 to 5.27	-19.08 to -0.75	-	Seoudy <i>et al.</i> (2014)
8.	Seed index (g)	21	-11.81 to 18.85	-22.65 to 16.76	-	Pole <i>et al.</i> (2008)
		21	-9.68 to 8.57	-9.68 to 8.57	-9.68 to 8.57	Deosarkar <i>et al.</i> (2009a)
		15	-14.49 to 13.39	-19.05 to 10.24	-4.76 to 13.39	Amalabalu <i>et al.</i> (2012)
		55	-	-22.23 to 5.37	-	Nidagundi <i>et al.</i> (2012)
		56	- 63.80 to 21.20	-64.10 to 23.60	-	Punitha <i>et al.</i> (2012)
		52	-	-	-3.76 to 30.52	Kumar <i>et al.</i> (2013)
		45	-	-	-16.67 to 13.60	Nirania <i>et al.</i> (2014)
		28	-	- 18.94 to 4.24	-	Patil <i>et al.</i> (2014)
		9	-1.76 to 8.54	-8.28 to 8.19	-	Seoudy <i>et al.</i> (2014)
		44	-	-	- 36.70 to 15.90	Tuteja (2014)

Table 2.7 (cont.)

Table 2.7 (cont.)

S.No.	Character	Number of crosses	Range of heterosis (%)			References
			Mid parent heterosis	Better parent heterosis	Standard heterosis	
9.	Ginning out-turn (%)	21	-7.98 to 5.95	-9.61 to 6.24	-7.25 to 3.85	Deosarkar <i>et al.</i> (2009a)
		21	-10.75 to 14.08	-	-	Karademir <i>et al.</i> (2009)
		15	-	21.56 to 19.45	-13.58 to 9.64	Wankhade <i>et al.</i> (2009)
		4	1.22 to 17.88	-2.68 to 10.25	-	Haleem <i>et al.</i> (2010)
		15	-4.12 to 9.75	-7.32 to 7.69	9.76 to 20.22	Amalabalu <i>et al.</i> (2012)
		55	-	- 15.67 to 4.85	-	Nidagundi <i>et al.</i> (2012)
		45	-10.81 to 20.09	-20.73 to 19.86	-21.01 to 1.75	Patel <i>et al.</i> (2012)
		52	-	-	- 2.66 to 9.02	Kumar <i>et al.</i> (2013)
		50	-	-	- 3.50 to 13.10	Tuteja <i>et al.</i> (2013)
		45	-	-	- 7.64 to 6.42	Nirania <i>et al.</i> (2014)
		9	-8.67 to 3.37	-13.70 to -1.37	-	Seoudy <i>et al.</i> (2014)
		44	-	-	- 4.5 to 10.40	Tuteja (2014)
10.	2.5% span length (mm)	6	0.44 to 4.34	-1.98 to 4.18	-	Syed and Sajid (2008)
		21	-14.69 to 19.38	-	-	Karademir <i>et al.</i> (2009)
		9	-2.24 to 11.59	-8.55 to 9.99	-3.81 to 18.43	Rajamani <i>et al.</i> (2009)
		15	-	-5.47 to 14.90	0.82 to 22.47	Wankhade <i>et al.</i> (2009)
		15	-9.72 to 5.49	1.04 to 10.26	-15.52 to 6.84	Amalabalu <i>et al.</i> (2012)
		30	- 2.63 to 10.70	-5.38 to 7.59	-9.58 to 9.35	Patil <i>et al.</i> (2012)
		56	-54.70 to 20.50	-56.40 to 15.60	-	Punitha <i>et al.</i> (2012)
		50	-	-	- 7.50 to 5.30	Tuteja <i>et al.</i> (2013)
		54	-	- 13.06 to 28.78	-	Deshmukh <i>et al.</i> (2014)
		44	-	-	- 6.30 to 7.40	Tuteja (2014)
11.	Uniformity ratio	18	-17.75 to 22.30	-11.08 to 15.39	-10.56 to 31.05	Reddy (2001)
		21	-1.73 to 3.10	-	-	Karademir <i>et al.</i> (2009)
		9	-13.51 to -0.80	-17.55 to -2.79	-11.22 to 4.04	Rajamani <i>et al.</i> (2009)
		30	-1.95 to 5.37	- 3.21 to 4.67	- 0.67 to 6.00	Patil <i>et al.</i> (2012)

Table 2.7 (cont.)

Table 2.7 (cont.)

S.No.	Character	Number of crosses	Range of heterosis (%)			References
			Mid parent heterosis	Better parent heterosis	Standard heterosis	
12.	Micronaire value (10 ⁻⁶ g/inch)	56	-8.95 to 11.79	-	-	Dukre <i>et al.</i> (2007)
		15	23.8 to 32.77	- 32.24 to 22.92	-	Jesus <i>et al.</i> (2007)
		21	-17.57 to 3.03	-	-	Karademir <i>et al.</i> (2009)
		9	-17.53 to 4.60	-24.52 to 1.69	-4.58 to 7.81	Rajamani <i>et al.</i> (2009)
		30	- 2.28 to 5.37	- 1.98 to 5.37	- 7.58 to 11.36	Patil <i>et al.</i> (2012)
		50	-	-	- 25.80 to -3.80	Tuteja <i>et al.</i> (2013)
		54	-	- 23.27 to 21.83	-	Deshmukh <i>et al.</i> (2014)
		44	-	-	-19.20 to 0.00	Tuteja (2014)
13.	Bundle strength (g/tex)	21	-	-18.25 to 24.67	-	Karademir <i>et al.</i> (2009)
		9	-10.12 to 6.14	-10.41 to 3.73	-2.82 to 17.88	Rajamani <i>et al.</i> (2009)
		15	-	-10.45 to 6.13	0.77 to 16.88	Wankhade <i>et al.</i> (2009)
		30	- 8.18 to 11.48	-10.68 to 10.11	- 8.15 to 10.96	Patil <i>et al.</i> (2012)
		56	- 50.70 to 40.20	-51.80 to 23.20	-	Punitha <i>et al.</i> (2012)
		50	-	-	- 14.60 to 4.00	Tuteja <i>et al.</i> (2013)
		54	-	- 13.63 to 48.91	-	Deshmukh <i>et al.</i> (2014)
		44	-	-	- 9.40 to 13.40	Tuteja (2014)
14.	Fibre elongation (%)	6	6.79 to 33.11	0.04 to 28.92	-	Syed and Sajid (2008)
		21	-8.21 to 6.54	-	-	Karademir <i>et al.</i> (2009)
		9	-1.20 to 33.59	-7.54 to 28.34	-18.79 to 13.55	Rajamani <i>et al.</i> (2009)
		15	-	11.37 to 231.99	14.12 to 82.35	Wankhade <i>et al.</i> (2009)
		4	16.60 to 102.16	0.00 to 34.58	-	Haleem <i>et al.</i> (2010)
		15	-5.68 to 184.34	-18.71 to 156.79	-12.61 to 54.08	Amalabalu <i>et al.</i> (2012)
		55	-	-9.65 to 37.43	-	Nidagundi <i>et al.</i> (2012)
		45	-54.19 to 43.76	-71.71 to 14.65	-59.21 to 17.50	Patel <i>et al.</i> (2012)
		30	- 5.09 to 6.21	- 6.42 to 5.11	- 1.95 to 5.37	Patil <i>et al.</i> (2012)
		54	-	- 20.72 to 39.05	-	Deshmukh <i>et al.</i> (2014)

Table 2.7 (cont.)

Table 2.7 (cont.)

S.No.	Character	Number of crosses	Range of heterosis (%)			References
			Mid parent heterosis	Better parent heterosis	Standard heterosis	
15.	Seed cotton yield plant ⁻¹ (g)	30	- 15.52 to 44.54	- 18.30 to 44.20	- 15.48 to 27.70	Patil <i>et al.</i> (2012)
		56	- 67.90 to 122.20	-74.30 to 74.90	-	Punitha <i>et al.</i> (2012)
		52	-	-	- 23.03 to 68.98	Kumar <i>et al.</i> (2013)
		50	-	-	- 62.50 to 7.90	Tuteja <i>et al.</i> (2013)
		54	-	- 17.24 to 83.52	-	Deshmukh <i>et al.</i> (2014)
		45	-	-	- 12.38 to 89.59	Nirania <i>et al.</i> (2014)
		9	-40.36 to 18.75	-43.20 to 8.65	-	Seoudy <i>et al.</i> (2014)
		44	-	-	- 53.40 to 10.50	Tuteja (2014)
16.	Lint yield plant ⁻¹ (g)	49	-	-	-31.52 to 81.63	Tuteja <i>et al.</i> (2005)
		28	-9.70 to 29.80	-	-	Paulo <i>et al.</i> (2007)
		21	30.35 to 100.87	25.26 to 64.20	-	Pole <i>et al.</i> (2008)
		21	-544.70 to 226.70	-	-	Karademir <i>et al.</i> (2009)
		4	22.78 to 56.11	0.00 to 41.16	-	Haleem <i>et al.</i> (2010)
		55	-	-16.95 to 30.73	-	Nidagundi <i>et al.</i> (2012)
		45	-54.06 to 42.31	-71.37 to 16.40	-57.76 to 19.18	Patel <i>et al.</i> (2012)
		28	-	- 27.95 to 76.20	-	Patil <i>et al.</i> (2014)
		9	-38.58 to 15.44	-44.02 to 5.45	-	Seoudy <i>et al.</i> (2014)

Chapter II

REVIEW OF LITERATURE

Cotton (*Gossypium* spp.) is an important commercial crop of India. The literature on the main objectives of 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 Genetic diversity

2.4 Character association

2.5 Path analysis

2.6 Combining ability

2.7 Heterosis

2.8 Stability analysis

2.9 Identification of favourable alleles in the donor parents

2.1. GENETIC VARIABILITY

Genetic variability forms the basis for any crop improvement programme. Superior genotypes can be isolated by selection if considerable genetic variation was present within the population. Yield and its component characters are polygenically inherited which are greatly influenced by the environment. The phenotype of a character is the resultant of interaction between genotype and environment. Partitioning of observed variability into heritable and non-heritable components is essential to get a true indication of the genetic variation of the trait. The available published literature on the variability in respect of yield and its component traits of cotton are reviewed and presented in the Table 2.1.

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

The degree of success in a selection programme depends upon the magnitude of heritability present in the population. Heritability ($h^2_{(b)}$) measures the relative amount of the heritable portion of variation. Characters which show high heritability coupled with wider variability would be successfully improved by direct selection (Paul, 1978). Genetic advance helps to measure the amount of progress that could be achieved with selection intensity. The available literature on heritability and genetic advance as per cent of mean is reviewed and presented in the Table 2.2.

2.3. GENETIC DIVERGENCE

2.3.1 Mahalanobis' D^2 Analysis

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

Mahalanobis' 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).

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

Jain and Yadav (2001) reported variation in grouping of populations into clusters from environment to environment in their study on 44 genotypes of American cotton in two different locations.

Gururajan and Manickam (2002) reported maximum contribution of characters like yellowness followed by fibre length, fibre fineness and elongation towards genetic divergence in their study involving 85 genotypes of Egyptian cotton.

Altaher and Singh (2003b) assessed genetic divergence among 50 different upland cotton varieties collected from all the three cotton growing zones of India for different agronomical and fibre quality traits using D^2 statistic and principal component analysis. The genotypes were grouped into 6 clusters and genotypes from different agro-climatic zones were grouped together in the same cluster indicating that geographical diversity is not always necessarily associated with genetic diversity.

Sambamurthy *et al.* (2006) grouped 105 genotypes into eight clusters with variable number of genotypes per cluster based on D^2 estimates. The characters, number of bolls plant⁻¹ followed by seed cotton yield plant⁻¹ contributed maximum towards the 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.

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

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

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

Rao *et al.* (2009b) 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.

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

Srinivasulu *et al.* (2010b) carried out genetic divergence analysis with sixty genotypes of cotton based on sixteen characters and grouped them into eight clusters. Cluster I was the largest with 23 genotypes. Divergence studies indicated that geographical diversity is always not necessarily associated with 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 Mahalanobis D^2 statistic and grouped them into eight clusters. The contribution of various characters towards expression of genetic divergence indicated that the seed cotton yield (kg ha^{-1}) contributed highest followed by number of sympodia plant^{-1} , uniformity ratio, ginning out turn% and lint index, respectively.

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

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

Kavithamani *et al.* (2013) studied genetic diversity in 48 genotypes of *Gossypium barbadense* L. using multivariate Mahalanobis D^2 analysis and these genotypes were grouped into 13 clusters. Grouping of these genotypes into different clusters was

independent of their geographical origin indicating other forces are responsible for diversity. The mutual relationship between the clusters revealed that inter cluster distance values were greater the intra-cluster values.

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

Araujo *et al.* (2014) evaluated eleven cultivars of upland cotton for genetic diversity based on fifteen agronomic and quality characteristics of the fibre. The genotypes were grouped into four clusters. Mean boll weight contributed maximum towards genetic diversity.

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

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

Ravikesan *et al.* (2014) evaluated 142 cotton germplasm accessions (91 *Gossypium barabdense* L. + 51 *Gossypium hirsutum* L.) for genetic divergence. D^2 analysis revealed that the *Gossypium barabdense* L. and *Gossypium hirsutum* L. accessions were grouped into 32 and 6 clusters. In *Gossypium barabdense* L. highest inter-cluster distance was observed between cluster XVIII and XXIX. Whereas, in *Gossypium hirsutum* L. inter-cluster distance was maximum between cluster V and VI. They further observed accessions from different origin were arranged in same cluster and *vice-versa* and concluded that genetic diversity need not necessarily be related to geographical diversity.

Tulasi *et al.* (2014) studied genetic divergence with 40 genotypes of cotton based on 15 quantitative characters in upland cotton and grouped them into seven clusters based on Mahalanobis D^2 analysis. Cluster I and II were the largest with 13 genotypes each. Based on 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.

2.3.2 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).

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.

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.

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

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

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

2.4. CHARACTER ASSOCIATION

Yield is a complex and polygenically controlled character and highly influenced by the environment. Selection based on the component characters has been considered to be more effective compared to the selection based on yield alone. Knowledge on the association of the fibre characters with yield and other yield components is of paramount important while aiming for improvement in yield and quality simultaneously. Unfavourable associations between the desired attributes under selection may limit genetic advance. Hence, information on the association of the yield is a pre-requisite for taking up any breeding programme.

2.4.1 Association of Component Characters with Seed Cotton Yield

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

2.4.2 Association among the Yield Component Characters

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

2.5 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 yield components and fibre quality parameters on seed cotton yield are reviewed and presented in the Table 2.5.

2.6 COMBINING ABILITY

The concept of combining ability as a measure of gene action was proposed by Sprague and Tatum (1942). Combining ability refers to the ability of a parent to transmit desirable performance to its hybrid progeny or crosses. Combining ability analysis helps in the evaluation of inbreds in terms of their genetic value and in the selection of suitable parents for hybridization. The superior specific cross combinations were also identified by this technique.

General combining ability is the average performance of a genotype in cross combinations involving a set of other genotypes. It is specific for the set of lines and testing environment, whereas specific combining ability is the average performance of a specific cross combination expressed as deviation from the population mean (Sprague and Tatum, 1942).

The *gca* effect reflects the breeding value of the parental genotypes and assists in identifying genotypes to be used for developing superior populations. Specific combining ability effects represent the non-reliable component of the genotypic value arising due to contribution from dominance deviation and interaction deviation. Hence, *sca* effect is the main cause for superiority of a cross. It is inferred that superiority of a cross cannot be fixed through selection.

The available literature on combining ability studies in cotton is furnished in the Table 2.6.

2.7 HETEROSIS

Shull (1914) first coined the term heterosis. Heterosis is the superiority of F_1 over the mean of the parents (relative or mid parent heterosis) or over the better parent (heterobeltiosis) or over the standard check (standard heterosis) (Hayes and Foster, 1976) with respect to agriculturally useful traits. The primary objective of heterosis breeding is to achieve a quantum jump in yield and quality aspects of crop plants. Heterotic performance can be used as the measure of nicking ability of any inbred line when crossed with a common tester. Exploitation of heterosis to increase the yield of agricultural crops has become one of the most important techniques in plant breeding. The available literature on heterosis over mid parent, better parent and standard check in cotton were summarized and presented in the Table 2.7.

2.8 STABILITY ANALYSIS

Stable performance is one of the most desirable properties of a genotype to be released as a variety for wide cultivation (or) for use as a parent in crop improvement programmes. The phenotype is a product of genotype and environment. The phenotypic performance of a genotype is not necessarily being the same under diverse agro-ecological conditions and all genotypes may not reach the same level of phenotypic expression under all environmental conditions.

Allard and Bradshaw (1964) observed that the nature of genotype-environment interactions is extremely complex. Genotype-environment interaction is usually present irrespective of the fact whether the varieties are purelines, single cross or double cross hybrids, test crosses, S_1 lines, segregating populations or any other material with which the breeder is working.

In the past, the principal analytical approach has been used to estimate genotype-environment interaction from the pooled analysis of variance (Salman, 1951; Horner and Frey, 1957 and Sandison and Bartlett, 1958). These estimates were then used to locate those environmental factors which interacted more strongly with the genotypes so that subsequent experiments might be modified accordingly. This technique could provide information only on the existence of interaction between genotype and environment but failed to give any measurement of the interaction of the individual genotypes with the environment.

Lewis (1954) suggested a single measure of phenotypic stability termed as “Stability factor”. Plaisted and Peterson (1959) described a procedure to characterize the stability of the performance of several genotypes, but this method becomes cumbersome when a large number of genotypes are tested. Wricke (1962) developed a method to estimate the ecovalence of genotypes grown under different environments to measure the stability of performance. Jowett (1972) reported that Wricke’s method, based on single parameter called ecovalence, was least informative.

Later on information was centered mainly on regression technique as an alternative method of analysis of the genotype-environment interaction. One of the most essential features in developing this technique was to quantify the environmental effect on the basis of mean performance of the best material. This was originally suggested by Yates and Cochran (1938) and later modified by several workers for use in breeding

experiments (Finlay and Wilkinson, 1963; Eberhart and Russell, 1966; Perkins and Jinks, 1968; Breese, 1969 and Freeman and Perkins, 1971). The regression of genotype on environment provides two simple measures of genotypic changes over environments namely, regression coefficient and deviation from regression. For measuring the genotype-environment interactions through linear regression technique, Yates and Cochran (1938), Finlay and Wilkinson (1963), Eberhart and Russell (1966) and Perkins and Jinks (1968) used the mean obtained by averaging all the cultivars for a particular character at each location as the environmental index.

Though different stability models are available, the regression analysis of Eberhart and Russell (1966) has been widely used by many workers (Sharma *et al.*, 1980; Kandalkar and Sanghi, 1982; Bhatade and Bhale, 1983; Desai *et al.*, 1983 and Henry and Daulay, 1983). A number of studies have been carried out with varieties and hybrids to know $G \times E$ interaction and stability of performance over seasons and locations.

Singh *et al.* (2004) evaluated six *Gossypium arboreum* L. genotypes for phenotypic stability over five seasons and indicated significant varietal difference over all the years and also in pooled analysis using Eberhart and Russell model (1966). The partition of genotype $\times$ environment interaction into two components *i.e.*, genotype $\times$ environment (linear) and pooled deviation showed that, pooled deviation was significant for all the genotypes, implying that none of these varieties could give stable performance over the seasonal variations. The genotype, AKH 4, recorded highest mean seed cotton yield (6.83 q/ha) followed by AKH 8401 (5.14 q/ha) and NNA1 (5.08 q/ha).

Fatih and Eyup (2006) evaluated fourteen cotton genotypes at four locations to determine genotype $\times$ environment ($G \times E$) interaction and stability of cotton genotypes and effect of different environments on seed cotton yield to understand its adaptation to varying environments. Significant differences were observed for the mean yield in the eight environments. Genotypes showed significant interaction with environments. Regression coefficients ranged from 0.23 to 1.46 and deviations from regression were significant for only four genotypes. The study also identified three high yielding cotton genotypes, SG-1001, SG-125 and DLR 5409, as stable genotypes for seed cotton yield per plant.

Saini *et al.* (2008) assessed stability of 86 lines of cotton under four environments and revealed significant mean squares due to genotypes and environments. The genotypes $\times$ environment mean square was significant for all the characters.

Satish *et al.* (2009b) conducted stability analysis for seventy genotypes over three environments. Variance due to genotypes, environments and genotype $\times$ environment interaction were significant for all the characters. CNH-13 and PIL -8-5 were found to have desirable high mean, non significant S^2d_i value and significant b_i values for seed cotton yield in specific environments only. But none of the seventy genotypes were found stable for all the characters.

Patil and Patel (2010) tested 58 *Bt* cotton hybrids for their performance at four agro-climatic conditions and stability analysis was carried out to study the genotype $\times$ environment interaction for seed cotton yield and its component traits. The variance due to genotypes, environments, genotypes $\times$ environments and environments (linear) were significant for all the characters. The study also revealed that the *Bt* hybrids viz., PRCH-31, AKKA, RCH-2, MRC-6301, HM-322 and PCH-205, had regression coefficient around unity and least deviation from regression and thus appeared to exhibit stability with more responsiveness to wide range of environments for seed cotton yield, lint yield, ginning out turn, boll weight and number of bolls per plant. The hybrids KCH-707, VBCH-1010, NCEH-2R showed stability for seed index.

Basanagouda *et al.* (2011) studied the stability of twenty genotypes of *Gossypium hirsutum* L. in four diverse, locations over two seasons using Eberhart and Russell model (1966). The study revealed the presence of significant genotype $\times$ environment interactions for seed cotton yield, number of bolls per plant and boll weight. Heterogeneities between regressions (linear component of genotypes $\times$ environment interactions) were significant for seed cotton yield and number of bolls per plant. This study also indicated that genotypes, GSHV-97/612 L-762 and H-1250, were most productive with high mean yield and suitable for favourable environments. LH-1968 and CPD-371 displayed average stability; while, the genotype, VIKAS, was found to possess average yield but a high degree of stability coupled with non-significant S^2d_i values for seed cotton yield per plant, number of bolls per plant and boll weight.

Kavithamani *et al.* (2011) conducted Eberhart and Russell (1966) stability analysis for forty one accessions of *Gossypium barbadense* L. over three seasons. The variance due to genotypes, environments, genotypes $\times$ environments and environments

(linear) were significant for all the characters and also revealed that Barbadas, 6002-1, and Giza 70 and 17/3 A were appeared to exhibit good stability over environments for the characters viz., seed cotton yield, lint yield, ginning out turn, boll weight and number of bolls per plant.

Patel *et al.* (2011) evaluated 44 upland genotypes cotton entries to determine stability over three locations. $G \times E$ interaction component was of considerable magnitude for all the characters indicating that different genotypes reacted differently to varying environments for all the characters. The genotypes, LRK 516 and AKH 26, were found to be stable over locations. Hybrids, LRK 516 $\times$ AKH 26, LRK 516 $\times$ AKH 39, CAK 8835 $\times$ AKH 26 and CAK 3456 $\times$ AKH 39, had high mean values with stable performance.

Nidagundi *et al.* (2012) tested 66 cotton genotypes over three environments and revealed that the pooled analysis of variance for seed cotton yield, lint yield, ginning out turn, boll weight, seed index, lint index, sympodia per plant and number of bolls per plant were highly significant. The magnitude of variance for $G \times E$ interaction and environment were also significant.

Taranjit *et al.* (2012) evaluated fifteen cotton hybrids over nine environments to determine the stability for lint yield and fibre quality traits. The pooled analysis of variance revealed highly significant genotypic, environmental and genotype $\times$ environment ($G \times E$) interaction mean squares for all the traits. But the significance of deviation from regression for all the hybrids under test showed that none of the hybrids gave stable performance over environments for any fibre trait. Hybrids, MBC 6304 *Bt* and Bunny *Bt*, showed above average stability for lint yield, 2.5% span length and fibre strength showing greater resistance to environmental changes.

Dewdar (2013) used stability analysis to study the magnitude and nature of genotype $\times$ environment interaction and to determine stability of yield for five Egyptian cotton varieties. Stability analysis showed highly significant differences between the genotypes, environments and for $G \times E$ interaction for all traits under study. The genotypes, Giza 90 and Giza 80, were more stable genotypes for the traits seed cotton yield per plant, lint yield per plant, boll weight, number of open bolls per plant and lint index.

Patel *et al.* (2013a) assessed the stability of 22 released BG II hybrids over three locations to determine genotype $\times$ environment interaction. The pooled analysis of variance for stability parameters revealed that the mean difference between genotypes and environments was significant indicating that genotype as well as environment was different for each other for most of the characters. The study also revealed that the hybrid, ABCH-1085, with highest mean yield had better adaptability to better environment.

Riaz *et al.* (2013) evaluated nine cotton genotypes to determine the yield stability, adaptability and to analyze the $G \times E$ interaction in twelve environments. Additive main effects and multiplicative interactions (AMMI) analysis revealed that the major contributions to treatment sum of squares were environments (38.51%), $G \times E$ (35.27%) and genotypes (26.22%), respectively, suggesting that the seed cotton yield of genotypes was under the major influence of $G \times E$ interaction. Results also indicated the genotypes, BH-172, MNH-814 and NIAB-2009, had the lowest $G \times E$ interaction and were the most stable genotypes over locations. The first two principal component axes (PCA 1 and 2) cumulatively contributed to 64.34% of the total $G \times E$ interaction and were significant ($P \leq 0.01$).

Shaaraway *et al.* (2013) studied 36 cotton genotypes across five locations using additive main effects and multiplicative interaction model. Highly significant mean squares were obtained for genotypes, genotype-environment interaction and interaction principal component axis (IPCA 1), for all traits. The mean square for IPCA 2 was highly significant for all the traits except for seed index. The contribution of IPCA 1, for $G \times E$ sum squares was greater for lint percentage followed by seed cotton yield. The highest contribution for IPCA2 was from seed cotton yield. Most of $G \times E$ sum squares, for all traits, could be attributed to IPCA 1, IPCA 2 and IPCA 3. Stable genotypes were recorded for the traits viz., seed cotton yield per plant, lint yield, seed index, lint index and lint per cent.

Verma *et al.* (2013) evaluated seven *Gossypium arboreum* L. genotypes for different characters in three years. Based on the linear, non linear components and high mean performance the genotypes LD 861 and CISA 614 were found stable for seed cotton yield. While based on sustainability index and best performance, the only genotype, CISA 614, was found to be stable. For other traits like seed index, lint index, ginning out turn, number of bolls plant⁻¹, boll weight, micronaire value, the deviation from regression was non-significant.

Reddy and Sarma (2014) conducted an experiment to estimate the relative stability of *G. arboreum* L. cotton genotypes. Components of variation was significant for all the characters except for micronaire value, number of bolls per plant, boll weight, indicating the seasons were quite diverse with regarding to their effect on the performance of the genotypes for different traits studied. The study also identified stable hybrids for number of bolls per plant, boll weight, ginning out-turn and seed cotton yield per plant. Identification of favourable alleles in the donor parents.

2.9 IDENTIFICATION OF FAVOURABLE ALLELES IN THE DONOR PARENTS

The choice of parental genotypes is most important at the beginning of any breeding programme, since all selected elite, adapted inbreds / hybrids are not likely to contain all the favourable alleles. Often in a breeding programme which attempts to use the exotic germplasm to improve quantitative traits, the breeder needs to know which of several populations/inbreds carry favourable alleles that are not present in elite selected germplasm.

For qualitative traits *i.e.*, traits governed by a few major genes, the procedures are straight forward. Different sources are screened for the presence of favourable genes which are then immediately introduced into the breeding programme by crossing parents carrying them to an elite parent. For traits under polygenic control, the identification of useful source of genes is more difficult.

Dudley (1984) first developed the theory useful for identification of donor parents (I_w) with the largest number of favourable dominant alleles (μ_G) not found in either parent (I_1 or I_2) of the elite single cross. The theory was based on four assumptions namely i) μ constant at all loci ii) complete dominance iii) no epistasis iv) $\mu_A = \mu_H$. He also suggested that, the method for identifying inbred lines carrying alleles should be particularly useful for applied pedigree breeding programmes.

Dudley (1987b) further reported the modified method to identify donor inbreds by allowing partial relaxation of assumptions $\mu_A = \mu_H$ and, equal effects at loci. The minimally biased estimate μ_G' , could not be derived directly, since allele frequencies in various classes of loci were not immediately known. However, classes were arbitrarily set and used to estimate allele frequencies of remaining classes. Four different cases were described for establishing upper and lower limits of the allele frequencies based on the phenotype data being analysed. The cases, q_{j0} , q_{k1} ; q_{j0} , q_{j1} ; q_{j1} , q_{k0} ; and q_{kl} , q_{k0} were four methods of estimating the bias term in μ_G due to assumptions in the model.

Zanoni and Dudley (1989a) compared the minimally biased estimate of the number of favourable alleles present in an inbred but not present in an elite hybrid ($\mu G'$) with UBND, PTC and GCA. The $\mu G'$ estimates were highly correlated with PTC and UBND estimates for most of the traits.

Zanoni and Dudley (1989b) extended the theory for estimating the relative number of favourable alleles ($\mu G'$) from use of inbred and F_1 data to use of inbred and F_2 or F_1 and F_2 data and compared the three methods of evaluating donor inbreds and obtained the same results whether inbred and F_2 , F_1 and F_2 or inbred and F_1 data were used.

Bernardo (1990) presented an alternative statistic for identifying lines useful for improving parents of an elite single cross and also suggested that transferring the favourable alleles to new elite single cross, is important to consider both potential gains of favourable alleles from I_w (donor) and loss of favourable alleles already present in $I_1 \times I_2$. The study called the method as “Net Improvement (NI)” statistic. NI was also compared with $\mu G'$, UBND and TC (SC). Correlations among the four estimators were high but the rank order of donor lines differed depending on the statistic used.

Malvar *et al.* (1997) used Dudley's theory to identify US and European field corn inbreds, adapted to European conditions, as potential donors for improving agronomic performance of sweet corn hybrids. The relationships among different estimators of favourable alleles were estimated and found very high positive correlations between $\mu G'$, UBND, PTC, NI and GCA for all the traits.

Reddy *et al.* (2003) conducted experiments in maize in order to identify favourable alleles in inbred lines for the improvement of single cross hybrid in maize and estimated $\mu G'$ in the eight donor lines for grain yield per plant for individual environments as well as combined analysis and concluded that, IPA 3 and FSA 17 were the top two donor inbreds possessing high levels of positive favourable alleles not present in the constituent parents of the target hybrid.

Reddy *et al.* (2004) investigated with an aim to identify favourable alleles ($\mu G'$) in eight recycled inbred lines for the improvement of an elite single cross hybrid, IPA 3 $\times$ SC 7. Results indicated that, estimators of $\mu G'$ were able to detect the differences among the donor inbreds in the relative number of loci with favourable

alleles for the traits viz., grain yield, 100 kernel weight, ear length and ear diameter. The study also reported that the estimators of $\mu G'$ in various donor inbreds varied in different environments for the same trait.

Reddy *et al.* (2005) compared various statistical methods ($\mu G'$, NI, PTC and UBND) useful for identification of maize inbreds with favourable alleles and the results revealed that though each and every statistical method has its own conceptual and computational advantages as well as limitations, $\mu G'$, NI, PTC and UBND, have higher *inter se* correlations. Hence, the study concluded that any one of these methods could be successfully utilized for selecting the donor with the highest favourable alleles for the improvement of single cross hybrid.

Drazic *et al.* (2010) conducted an experiment in tobacco with four genotypes (SA 130, Bols 334, Berlej T and TN 90) to identify lines with favourable alleles ($\mu G'$) for the improvement of an elite single cross hybrid, Bols 335 $\times$ TN 86. The study also indicated that estimators of $\mu G'$ were highly significant for TN 90 and it can be used as donor parent for improvement of target cross for traits like number of leaves and total leaf area.

Goran *et al.* (2012) had taken up an experiment to improve an elite maize hybrid, ZPL 1 $\times$ ZPL 2 by using inbreds from different recurrent selection cycles and reported that inbreds belong to later cycles of recurrent selections proved to be better donors of favourable alleles than inbreds belonging to the earlier cycles of selection.

Naik (2012) evaluated eight (CM 119, CM 120, CM 131, CM 133, CM 210, CM 211, BML10 and BML13) maize inbreds to identify favourable alleles for improving yield in target cross DHM 117 (BML 6 $\times$ BML 7) and reported that inbreds BML 10 and CM 131 showed highest frequency of favourable alleles ($\mu G'$) for further improvement in yield performance.

Table 2.4. Review of literature on association among component characters of seed cotton yield in cotton

S.No.	Character	Association	S/NS	Reference
I. Days to 50% flowering with				
1.	Plant height	Positive	S	Erande <i>et al.</i> (2014)
			NS	Sangeetha (1998)
		Negative	S	Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011)
			NS	Sakthi <i>et al.</i> (2007)
2.	Number of monopodia plant ⁻¹	Positive	S	Muraleedhar (2005) Kaushik and Kapoor (2006) Vijayalaxmi <i>et al.</i> (2008) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)
			NS	Ladole and Meshram (2000)
		Negative	S	Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
			NS	Neelam <i>et al.</i> (2002) Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007)
3.	Number of sympodia plant ⁻¹	Positive	S	Ladole and Meshram (2000) Muraleedhar (2005)
			NS	Basha (1997) Erande <i>et al.</i> (2014)
		Negative	S	Altaher and Singh (2003a) Vijayalaxmi <i>et al.</i> (2008)
			NS	Kaushik and Kapoor (2006) Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
4.	Number of bolls plant ⁻¹	Positive	S	Muraleedhar (2005) Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)
			NS	Kaushik and Kapoor (2006) Kale <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011) Kumar <i>et al.</i> (2014)
		Negative	S	Reddy (2001)
			NS	Annapurve <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007) Rajamani <i>et al.</i> (2013)

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
5.	Boll weight	Positive	S	Altaher and Singh (2003a) Ranjan <i>et al.</i> (2014)
			NS	Erande <i>et al.</i> (2014)
		Negative	S	Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
			NS	Annapurve <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007)
6.	Lint index	Positive	S	Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)
			NS	Basha (1997) Neelam <i>et al.</i> (2002)
		Negative	S	Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011)
			NS	Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014)
7.	Seed index	Positive	S	Erande <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)
			NS	Kale <i>et al.</i> (2007) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
		Negative	S	Muraleedhar (2005) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011)
			NS	Neelam <i>et al.</i> (2002) Kaushik and Kapoor (2006)
8.	Ginning out-turn	Positive	S	Neelam <i>et al.</i> (2002)
			NS	Kaushik and Kapoor (2006) Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014)
		Negative	S	Pratap <i>et al.</i> (2007)
			NS	Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
9.	2.5% span length	Positive	S	Muraleedhar (2005)
			NS	Vijayalaxmi <i>et al.</i> (2008) Rajamani <i>et al.</i> (2013)
		Negative	NS	Kaushik and Kapoor (2006) Sakthi <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
10.	Uniformity ratio	Positive	S	Neelima <i>et al.</i> (2005)
			NS	Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014)
		Negative	S	Venkateswaralu <i>et al.</i> (2010a)
			NS	Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Kumar <i>et al.</i> (2014)
11.	Micronaire value	Positive	S	Pratap <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011)
			NS	Sangeetha (1998) Sakthi <i>et al.</i> (2007) Erande <i>et al.</i> (2014)
		Negative	S	Altaher and Singh (2003a) Muraleedhar (2005) Vijayalaxmi <i>et al.</i> (2008)
			NS	Neelam <i>et al.</i> (2002) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
12.	Bundle strength	Positive	S	Vijayalaxmi <i>et al.</i> (2008)
			NS	Neelam <i>et al.</i> (2002)
		Negative	S	Altaher and Singh (2003a)
			NS	Sakthi <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
13.	Fibre elongation	Positive	S	Muraleedhar (2005)
			NS	Rajanna (2010)
		Negative	S	Pratap <i>et al.</i> (2007) Vijayalakshmi <i>et al.</i> (2008)
			NS	Sakthi <i>et al.</i> (2007) Vijayalakshmi <i>et al.</i> (2008) Rajanna (2010)
14.	Lint yield plant ⁻¹	Positive	S	Patel <i>et al.</i> (2013)
			NS	Erande <i>et al.</i> (2014)
		Negative	S	Pratap <i>et al.</i> (2007)
			NS	Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011)
II. Plant height with				
1.	Number of monopodia plant ⁻¹	Positive	S	Kaushik and Kapoor (2006) Hafiz <i>et al.</i> (2013) Rajamani <i>et al.</i> (2013) Chitti <i>et al.</i> (2014)

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
	Number of monopodia plant ⁻¹	Positive	NS	Kumar <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Ranjan <i>et al.</i> (2014)
			NS	Pradeep and Sumalini (2005) Kale <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014)
2.	Number of sympodia plant ⁻¹	Positive	S	Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Hafiz <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014)
			NS	Kale <i>et al.</i> (2007) Khan <i>et al.</i> (2015)
3.	Number of bolls plant ⁻¹	Positive	S	Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)
			NS	Sangeetha (1998) Annapurve <i>et al.</i> (2007) Khan <i>et al.</i> (2015)
		Negative	NS	Sakthi <i>et al.</i> (2007)
4.	Boll weight	Positive	S	Rajamani <i>et al.</i> (2013) Farooq <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)
			NS	Pradeep and Sumalini (2005) Annapurve <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Chitti <i>et al.</i> (2014)
			NS	Sakthi <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011)

Table 2.4 (cont.)

Table 2.4 (cont.)

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

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
10.	Micronaire value	Positive	NS	Vijayalaxmi <i>et al.</i> (2008) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
			Negative	S
				NS
			11.	Bundle strength
NS	Kowsalya and Raveendran (1996) Rajanna <i>et al.</i> (2011) Vinodhana <i>et al.</i> (2013)			
Negative	NS	Sangeetha (1998) Sakthi <i>et al.</i> (2007) Rajamani <i>et al.</i> (2013)		
	12.	Fibre elongation		
Negative			NS	Rajanna (2010)
13.	Lint yield plant ⁻¹	Positive	S	Samanc and Ozkaynak (2000) Rajanna <i>et al.</i> (2011)
			NS	Erande <i>et al.</i> (2014)
		Negative	NS	Vijayalaxmi <i>et al.</i> (2008)
			III. No. of monopodia plant ⁻¹ with	
1.	Number of sympodia plant ⁻¹	Positive	S	Rajanna <i>et al.</i> (2011) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014)
			NS	Hafiz <i>et al.</i> (2013) Rajamani <i>et al.</i> (2013) Khan <i>et al.</i> (2015)
		Negative	S	Verma <i>et al.</i> (2006) Vijayalaxmi <i>et al.</i> (2008) Farooq <i>et al.</i> (2014)
			NS	Neelam <i>et al.</i> (2002) Pradeep and Sumalini (2005)
2.	Number of bolls plant ⁻¹	Positive	S	Verma <i>et al.</i> (2006) Vijayalaxmi <i>et al.</i> (2008) Kishore <i>et al.</i> (2011) Hafiz <i>et al.</i> (2013) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
			NS	Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011) Patel <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Khan <i>et al.</i> (2015)

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
2.	Number of bolls plant ⁻¹	Negative	S	Farooq <i>et al.</i> (2014)
			NS	Reddy (2001)
3.	Boll weight	Positive	S	Basha (1997)
			NS	Reddy (2001) Rajamani <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)
		Negative	S	Pratap <i>et al.</i> (2007) Kumar <i>et al.</i> (2014)
			NS	Annapurve <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Farooq <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
3.	Lint index	Positive	S	Rajanna (2010) Mahantesh (2009)
			NS	Ladole and Meshram (2000) Reddy (2001) Rajamani <i>et al.</i> (2013)
		Negative	NS	Kale <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008)
4.	Seed index	Positive	S	Mahantesh (2009)
			NS	Ladole and Meshram (2000) Reddy (2001) Rajanna (2010) Paramjit and Buttar (2013)
		Negative	S	Vijayalaxmi <i>et al.</i> (2008)
			NS	Kale <i>et al.</i> (2007) Rajamani <i>et al.</i> (2013)
5.	Ginning out-turn	Positive	S	Annapurve <i>et al.</i> (2007) Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)
			NS	Kale <i>et al.</i> (2007) Chitti <i>et al.</i> (2014) Farooq <i>et al.</i> (2014)
		Negative	S	Mohan (2011)
			NS	Neelam <i>et al.</i> (2002) Rajamani <i>et al.</i> (2013) Khan <i>et al.</i> (2015)
6.	2.5% span length	Positive	S	Mohan (2011) Hafiz <i>et al.</i> (2013)

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
6.	2.5% span length	Positive	NS	Neelam <i>et al.</i> (2002) Kale <i>et al.</i> (2007) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
		Negative	S	Rao <i>et al.</i> (2009a)
			NS	Verma <i>et al.</i> (2006) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
7.	Uniformity ratio	Positive	NS	Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Khan <i>et al.</i> (2015)
		Negative	S	Vijayalaxmi <i>et al.</i> (2008) Mahantesh (2009)
			NS	Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
8.	Micronaire value	Positive	NS	Rao <i>et al.</i> (2009a) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
		Negative	S	Muraleedhar (2005) Vijayalaxmi <i>et al.</i> (2008) Mahantesh (2009)
			NS	Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
9.	Bundle strength	Positive	S	Muraleedhar (2005) Mohan (2011)
			NS	Neelam <i>et al.</i> (2002) Vijayalaxmi <i>et al.</i> (2008) Kumar <i>et al.</i> (2014)
		Negative	NS	Reddy (2001) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
10.	Fibre elongation	Positive	S	Muraleedhar (2005) Mohan (2011)
			NS	Rao <i>et al.</i> (2009a)
		Negative	S	Vijayalaxmi <i>et al.</i> (2008) Venkatesh (2012)
			NS	Rajanna (2010)
11.	Lint yield plant ⁻¹	Positive	S	Rajanna <i>et al.</i> (2011) Patel <i>et al.</i> (2013) Erande <i>et al.</i> (2014)

Table 2.4 (cont.)

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	Salahuddin <i>et al.</i> (2010) Mohan (2011) Rajanna <i>et al.</i> (2011) Hafiz <i>et al.</i> (2013) Patel <i>et al.</i> (2013) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014)
			NS	Pradeep and Sumalini (2005) Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	NS	Vijayalaxmi <i>et al.</i> (2008)
2.	Boll weight	Positive	S	Sakthi <i>et al.</i> (2007) Salahuddin <i>et al.</i> (2010) Mohan (2011)
			NS	Vijayalaxmi <i>et al.</i> (2008) Rao <i>et al.</i> (2009a) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Pratap <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011) Vinodhana <i>et al.</i> (2013)
			NS	Pradeep and Sumalini (2005) Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Chitti <i>et al.</i> (2014)
3.	Lint index	Positive	S	Neelam <i>et al.</i> (2002) Muthu <i>et al.</i> (2004) Muraleedhar (2005) Neelima <i>et al.</i> (2005) Sakthi <i>et al.</i> (2007) Mahantesh (2009)
			NS	Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Khan <i>et al.</i> (2015)
		Negative	S	Muraleedhar (2005) Venkateswarlu <i>et al.</i> (2010a) Chitti <i>et al.</i> (2014)
			NS	Erande <i>et al.</i> (2014)

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
4.	Seed index	Positive	S	Muthu <i>et al.</i> (2004) Neelima <i>et al.</i> (2005) Mahantesh (2009) Mohan (2011) Rajanna <i>et al.</i> (2011)
			NS	Vijayalaxmi <i>et al.</i> (2008) Rao <i>et al.</i> (2009a) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Muthuswamy and Vivekanandan (2004) Muraleedhar (2005)
			NS	Kale <i>et al.</i> (2007) Chitti <i>et al.</i> (2014)
5.	Ginning out-turn	Positive	NS	Neelima <i>et al.</i> (2005) Sakthi <i>et al.</i> (2007) Rao <i>et al.</i> (2009a)
		Negative	S	Altaher and Singh (2003a) Chitti <i>et al.</i> (2014)
			NS	Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Khan <i>et al.</i> (2015)
6.	2.5% span length	Positive	S	Neelam <i>et al.</i> (2002) Sakthi <i>et al.</i> (2007) Mohan (2011) Vinodhana <i>et al.</i> (2013)
			NS	Verma <i>et al.</i> (2006)
		Negative	S	Kale <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rao <i>et al.</i> (2009a) Erande <i>et al.</i> (2014)
			NS	Muraleedhar (2005) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
7.	Uniformity ratio	Positive	S	Vijayalaxmi <i>et al.</i> (2008) Mohan (2011)
			NS	Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
5.	Uniformity ratio	Negative	S	Rao <i>et al.</i> (2009a) Venkateswarlu <i>et al.</i> (2010a)
			NS	Neelam <i>et al.</i> (2002) Sakthi <i>et al.</i> (2007) Khan <i>et al.</i> (2015)
6.	Micronaire value	Positive	S	Vijayalaxmi <i>et al.</i> (2008) Mohan (2011)
			NS	Neelam <i>et al.</i> (2002) Sakthi <i>et al.</i> (2007) Khan <i>et al.</i> (2015)
		Negative	S	Rajanna <i>et al.</i> (2011)
			NS	Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014)
7.	Bundle strength	Positive	S	Altaher and Singh (2003a) Muthu <i>et al.</i> (2004) Mohan (2011) Rajanna <i>et al.</i> (2011)
			NS	Sakthi <i>et al.</i> (2007) Rao <i>et al.</i> (2009a) Vinodhana <i>et al.</i> (2013)
		Negative	NS	Vijayalaxmi <i>et al.</i> (2008) Rajamani <i>et al.</i> (2013)
8.	Fibre elongation	Positive	NS	Vijayalaxmi <i>et al.</i> (2008) Rao <i>et al.</i> (2009a) Rajanna (2010)
		Negative	S	Muthu <i>et al.</i> (2004) Sakthi <i>et al.</i> (2007)
			NS	Muraleedhar (2005)
9.	Lint yield plant ⁻¹	Positive	S	Pratap <i>et al.</i> (2007) Rao <i>et al.</i> (2009a) Rajanna <i>et al.</i> (2011) Patel <i>et al.</i> (2013) Erande <i>et al.</i> (2014)
			NS	Vijayalaxmi <i>et al.</i> (2008)
V. Number of bolls plant ⁻¹ with				
1.	Boll weight	Positive	S	Altaher and Singh (2003a) Neelima <i>et al.</i> (2005) Sakthi <i>et al.</i> (2007) Salahuddin <i>et al.</i> (2010) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
1.	Boll weight	Positive	NS	Rao <i>et al.</i> (2009a) Rajamani <i>et al.</i> (2013) Khan <i>et al.</i> (2015)
		Negative	S	Rajanna <i>et al.</i> (2011) Kumar <i>et al.</i> (2014)
			NS	Kale <i>et al.</i> (2007) Vinodhana <i>et al.</i> (2013)
2.	Lint index	Positive	S	Muthu <i>et al.</i> (2004) Neelima <i>et al.</i> (2005) Chitti <i>et al.</i> (2014)
			NS	Sakthi <i>et al.</i> (2007) Mahantesh (2009) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Vijayalaxmi <i>et al.</i> (2008) Venkateswarlu <i>et al.</i> (2010a) Mohan (2011) Kumar <i>et al.</i> (2014)
			NS	Rao <i>et al.</i> (2009a) Rajanna <i>et al.</i> (2011) Vinodhana <i>et al.</i> (2013)
3.	Seed index	Positive	S	Neelima <i>et al.</i> (2005) Mahantesh (2009) Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014)
			NS	Ranjan <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Vijayalaxmi <i>et al.</i> (2008) Mohan (2011) Kumar <i>et al.</i> (2014)
			NS	Rao <i>et al.</i> (2009a) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
4.	Ginning out-turn	Positive	S	Muthu <i>et al.</i> (2004) Pratap <i>et al.</i> (2007) Salahuddin <i>et al.</i> (2010)
			NS	Kale <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajamani <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014) Khan <i>et al.</i> (2015)

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
4.	Ginning out-turn	Negative	S	Venkateswarlu <i>et al.</i> (2010a) Mohan (2011) Vinodhana <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
			NS	Sangeetha (1998) Rajanna <i>et al.</i> (2011)
5.	2.5% span length	Positive	S	Mohan (2011) Hafiz <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013)
			NS	Sakthi <i>et al.</i> (2007) Rao <i>et al.</i> (2009a) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
		Negative	S	Tyagi (1994) Muraleedhar (2005)
			NS	Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011)
6.	Uniformity ratio	Positive	S	Muthu <i>et al.</i> (2004)
			NS	Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
		Negative	S	Vijayalaxmi <i>et al.</i> (2008) Mohan (2011)
			NS	Sakthi <i>et al.</i> (2007) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
7.	Micronaire value	Positive	S	Muthu <i>et al.</i> (2004) Sakthi <i>et al.</i> (2007) Rao <i>et al.</i> (2009) Venkateswarlu <i>et al.</i> (2010a)
			NS	Neelam <i>et al.</i> (2002) Khan <i>et al.</i> (2015)
		Negative	S	Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Mohan (2011) Vinodhana <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
			NS	Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014)
8.	Bundle strength	Positive	S	Altaher and Singh (2003a) Muthu <i>et al.</i> (2004) Kumar <i>et al.</i> (2014)

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference		
8.	Bundle strength	Positive	NS	Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Vinodhana <i>et al.</i> (2013)		
				S	Sangeetha (1998)	
		Negative	NS	Rao <i>et al.</i> (2009a)		
9.	Fibre elongation		Negative	S	Muthu <i>et al.</i> (2004) Vijayalakshmi <i>et al.</i> (2008)	
		NS		Muraleedhar (2005) Sakthi <i>et al.</i> (2007) Rajanna (2010) Elango <i>et al.</i> (2012)		
		10.	Lint yield plant ⁻¹	Positive	S	Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rao <i>et al.</i> (2009a) Rajanna <i>et al.</i> (2011)
NS	Erande <i>et al.</i> (2014)					
VI. Boll weight with						
1.	Lint index	Positive	S	Vijayalaxmi <i>et al.</i> (2008) Venkateswarlu <i>et al.</i> (2010a) Mohan (2011) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)		
			NS	Erande <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014) Khan <i>et al.</i> (2015)		
2.	Seed index	Positive	S	Neelima <i>et al.</i> (2005) Venkateswarlu <i>et al.</i> (2010a) Mohan (2011) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)		
				NS	Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)	
				Negative	S	Rao <i>et al.</i> (2009a)
					NS	Chitti <i>et al.</i> (2014)

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
3.	Ginning out-turn	Positive	S	Muthuswamy and Vivekanandan (2004) Mohan (2011) Chitti <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
			NS	Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	NS	Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Ranjan <i>et al.</i> (2014)
4.	2.5% span length	Positive	S	Verma <i>et al.</i> (2006) Vijayalaxmi <i>et al.</i> (2008)
			NS	Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
		Negative	S	Mohan (2011)
			NS	Neelima <i>et al.</i> (2005)
5.	Uniformity ratio	Positive	NS	Rajanna <i>et al.</i> (2011) Khan <i>et al.</i> (2015)
		Negative	S	Muraleedhar (2005) Rajamani <i>et al.</i> (2013)
			NS	Sakthi <i>et al.</i> (2007) Rao <i>et al.</i> (2009a) Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014)
6.	Micronaire value	Positive	S	Tyagi (1994) Vinodhana <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
			NS	Sakthi <i>et al.</i> (2007) Rao <i>et al.</i> (2009a) Khan <i>et al.</i> (2015)
		Negative	S	Neelima <i>et al.</i> (2005) Erande <i>et al.</i> (2014)
			NS	Vijayalaxmi <i>et al.</i> (2008) Rajamani <i>et al.</i> (2013)
7.	Bundle strength	Positive	S	Muraleedhar (2005) Mahantesh (2009) Rao <i>et al.</i> (2009a) Rajamani <i>et al.</i> (2013)
			NS	Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008)

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
7.	Bundle strength	Negative	S	Mohan (2011) Vinodhana <i>et al.</i> (2013)
			NS	Rajanna <i>et al.</i> (2011) Kumar <i>et al.</i> (2014)
8.	Fibre elongation	Positive	S	Vijayalaxmi <i>et al.</i> (2008) Mahantesh (2009) Kumar <i>et al.</i> (2014)
			NS	Muraleedhar (2005) Rao <i>et al.</i> (2009a) Venkateswarlu <i>et al.</i> (2010a)
9.	Lint yield plant ⁻¹	Positive	S	Dedaniya and Pethani (1994) Rao <i>et al.</i> (2009a) Rajanna <i>et al.</i> (2011) Erande <i>et al.</i> (2014)
			NS	Patel <i>et al.</i> (2013)
VII. Lint index with				
1.	Seed index	Positive	S	Mahantesh (2009) Venkateswarlu <i>et al.</i> (2010a) Mohan (2011) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)
			NS	Neelam <i>et al.</i> (2002) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
2.	Ginning out-turn	Positive	S	Muthu <i>et al.</i> (2004) Pratap <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Mohan (2011) Rajanna <i>et al.</i> (2011) Chitti <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
			NS	Neelam <i>et al.</i> (2002) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
3.	2.5% span length	Positive	S	Muthu <i>et al.</i> (2004) Sambamurthy <i>et al.</i> (2006) Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
3.	2.5% span length	Positive	NS	Rajanna <i>et al.</i> (2011) Erande <i>et al.</i> (2014)
			S	Mohan (2011)
		Negative	NS	Mandloi <i>et al.</i> (2003) Vinodhana <i>et al.</i> (2013)
			S	Mohan (2011)
4.	Uniformity ratio	Positive	NS	Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
			S	Muthu <i>et al.</i> (2004) Sakthi <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011)
		Negative	S	Sangeetha (1998) Rao <i>et al.</i> (2009a) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
			NS	
			NS	Sakthi <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
			S	Mandloi <i>et al.</i> (2003) Mahantesh (2009) Kumar <i>et al.</i> (2014)
5.	Micronaire value	Positive	NS	Muthu <i>et al.</i> (2004)
			S	Sambamurthy <i>et al.</i> (2006)
		Negative	NS	Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008)
			S	Vinodhana <i>et al.</i> (2013)
6.	Bundle strength	Positive	S	Neelam <i>et al.</i> (2002) Mandloi <i>et al.</i> (2003) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
			NS	
		Negative	S	Mahantesh (2009) Rajanna <i>et al.</i> (2011)
			NS	Muraleedhar (2005) Vijayalaxmi <i>et al.</i> (2008)
			NS	Sakthi <i>et al.</i> (2007) Rao <i>et al.</i> (2009a)
			S	Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rao <i>et al.</i> (2009a) Rajanna <i>et al.</i> (2011) Patel <i>et al.</i> (2013)
7.	Fibre elongation	Positive	S	
			NS	
		Negative	NS	
			S	
8.	Lint yield plant ⁻¹	Positive	S	
			NS	

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
6.	Lint yield plant ⁻¹	Positive	NS	Dedaniya and Pethani (1994) Mandloi <i>et al.</i> (2003) Erande <i>et al.</i> (2014)
VIII. Seed index with				
1.	Ginning out-turn	Positive	S	Altaher and Singh (2003a)
			NS	Kale <i>et al.</i> (2007) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014)
		Negative	S	Rajanna <i>et al.</i> (2011) Mohan (2011) Kumar <i>et al.</i> (2014)
			NS	Chitti <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
2.	2.5% span length	Positive	S	Vijayalaxmi <i>et al.</i> (2008) Mohan (2011) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
			NS	Neelam <i>et al.</i> (2002)
		Negative	S	Kale <i>et al.</i> (2007)
			NS	Mandloi <i>et al.</i> (2003) Erande <i>et al.</i> (2014)
3.	Uniformity ratio	Positive	NS	Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Muraleedhar (2005) Rajanna <i>et al.</i> (2011) Kumar <i>et al.</i> (2014)
			NS	Rao <i>et al.</i> (2009a) Vijayalaxmi <i>et al.</i> (2008) Rajamani <i>et al.</i> (2013)
4.	Micronaire value	Positive	S	Vijayalaxmi <i>et al.</i> (2008) Rao <i>et al.</i> (2009a) Rajamani <i>et al.</i> (2013)
			NS	Neelam <i>et al.</i> (2002) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Rajanna <i>et al.</i> (2011) Mohan (2011) Kumar <i>et al.</i> (2014)
			NS	Vinodhana <i>et al.</i> (2013)
5.	Bundle strength	Positive	S	Muthu <i>et al.</i> (2004) Mohan (2011) Vinodhana <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
5.	Bundle strength	Positive	NS	Neelam <i>et al.</i> (2002) Altaher and Singh (2003a)
		Negative	S	Rajanna <i>et al.</i> (2011)
			NS	Vijayalaxmi <i>et al.</i> (2008) Rao <i>et al.</i> (2009a) Rajamani <i>et al.</i> (2013)
6.	Fibre elongation	Positive	S	Vijayalaxmi <i>et al.</i> (2008)
			NS	Rajanna <i>et al.</i> (2011)
		Negative	NS	Muthu <i>et al.</i> (2004) Muraleedhar (2005)
7.	Lint yield plant ⁻¹	Positive	NS	Rao <i>et al.</i> (2009a) Erande <i>et al.</i> (2014)
		Negative	NS	Mandloi <i>et al.</i> (2003) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011)
IX. Ginning out-turn with				
1.	2.5% span length	Positive	S	Kale <i>et al.</i> (2007)
			NS	Rajamani <i>et al.</i> (2013)
		Negative	S	Muthu <i>et al.</i> (2004) Sakthi <i>et al.</i> (2007) Mahantesh (2009) Mohan (2011) Kumar <i>et al.</i> (2014)
			NS	Neelam <i>et al.</i> (2002) Kale <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Erande <i>et al.</i> (2014)
2.	Uniformity ratio	Positive	S	Sakthi <i>et al.</i> (2007) Mohan (2011) Kumar <i>et al.</i> (2014)
			NS	Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Altaher and Singh (2003a)
			NS	Vijayalaxmi <i>et al.</i> (2008) Rao <i>et al.</i> (2009a)
3.	Micronaire value	Positive	S	Muthu <i>et al.</i> (2004) Mohan (2011)
			NS	Rao <i>et al.</i> (2009a) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Khan <i>et al.</i> (2015)

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
3.	Micronaire value	Negative	S	Vijayalaxmi <i>et al.</i> (2008)
			NS	Mandloi <i>et al.</i> (2003)
4.	Bundle strength	Positive	S	Mandloi <i>et al.</i> (2003) Sambamurthy <i>et al.</i> (2006) Rao <i>et al.</i> (2009a)
			NS	Vijayalaxmi <i>et al.</i> (2008)
		Negative	S	Neelam <i>et al.</i> (2002) Mahantesh (2009) Mohan (2011) Vinodhana <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
			NS	Sakthi <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013)
5.	Fibre elongation	Positive	S	Mahantesh (2009) Rajanna <i>et al.</i> (2011)
			NS	Muraleedhar (2005) Vijayalaxmi <i>et al.</i> (2008)
		Negative	NS	Sakthi <i>et al.</i> (2007) Rao <i>et al.</i> (2009a)
6.	Lint yield plant ⁻¹	Positive	S	Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rao <i>et al.</i> (2009a) Rajanna <i>et al.</i> (2011) Patel <i>et al.</i> (2013)
			NS	Dedaniya and Pethani (1994) Mandloi <i>et al.</i> (2003) Erande <i>et al.</i> (2014)
X. 2.5% span length with				
1.	Uniformity ratio	Positive	S	Venkateswarlu <i>et al.</i> (2010a)
			NS	Rajanna <i>et al.</i> (2011)
		Negative	S	Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rao <i>et al.</i> (2009a) Venkateswarlu <i>et al.</i> (2010a) Mohan (2011) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
			NS	Muthu <i>et al.</i> (2004) Tuteja <i>et al.</i> (2005) Erande <i>et al.</i> (2014)
2.	Micronaire value	Positive	S	Mandloi <i>et al.</i> (2003) Muthuswamy and Vivekanandan (2004)

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
2.	Micronaire value	Negative	S	Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Venkateswarlu <i>et al.</i> (2010a) Mohan (2011) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
			NS	Sakthi <i>et al.</i> (2007) Rao <i>et al.</i> (2009a)
3.	Bundle strength	Positive	S	Rathore <i>et al.</i> (2004) Tuteja <i>et al.</i> (2005) Vijayalaxmi <i>et al.</i> (2008) Mohan (2011) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
			NS	Mohan (2011) Rajanna <i>et al.</i> (2011)
		Negative	S	Rao <i>et al.</i> (2009a)
4.	Fibre elongation	Positive	S	Muraleedhar (2005) Vijayalaxmi <i>et al.</i> (2008) Mahantesh (2009) Mohan (2011) Rajanna <i>et al.</i> (2011)
		Negative	S	Muthuswamy and Vivekanandan (2004)
5.	Lint yield plant ⁻¹	Positive	NS	Dedaniya and Pethani (1994) Mandloi <i>et al.</i> (2003) Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014)
		Negative	NS	Rao <i>et al.</i> (2009a)
			S	Rajanna <i>et al.</i> (2011)
XI. Uniformity ratio with				
1.	Micronaire value	Positive	S	Rathore <i>et al.</i> (2004) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
			NS	Muthu <i>et al.</i> (2004) Khan <i>et al.</i> (2015)
		Negative	S	Tuteja <i>et al.</i> (2005)
			NS	Sangeetha (1998)

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
2.	Bundle strength	Positive	S	Rajan (1997)
		Negative	S	Tuteja <i>et al.</i> (2005) Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
			NS	Rathore <i>et al.</i> (2004)
3.	Fibre elongation	Positive	S	Sakthi <i>et al.</i> (2007) Mohan (2011)
			NS	Rajanna <i>et al.</i> (2011)
		Negative	S	Muraleedhar (2005)
4.	Lint yield plant ⁻¹	Positive	S	Rajanna <i>et al.</i> (2011)
		Negative	NS	Dedaniya and Pethani (1994) Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014)
XII. Micronaire value with				
1.	Bundle strength	Positive	S	Mahantesh (2009)
			NS	Rao <i>et al.</i> (2009a) Vijayalaxmi <i>et al.</i> (2008) Mohan (2011) Vinodhana <i>et al.</i> (2013)
		Negative	S	Kumar <i>et al.</i> (2014)
2.	Fibre elongation	Positive	S	Rao <i>et al.</i> (2009a)
		Negative	S	Muraleedhar (2005) Mahantesh (2009) Mohan (2011) Rajanna <i>et al.</i> (2011)
3.	Lint yield plant ⁻¹	Positive	S	Rao <i>et al.</i> (2009a)
			NS	Mandloi <i>et al.</i> (2003)
		Negative	S	Rajanna <i>et al.</i> (2011) Erande <i>et al.</i> (2014)
			NS	Dedaniya and Pethani (1994)
XIII. Bundle strength with				
1.	Fibre elongation	Positive	S	Muraleedhar (2005) Vijayalaxmi <i>et al.</i> (2008) Mohan (2011) Rajanna <i>et al.</i> (2011)
				S
		Negative	NS	Rajanna <i>et al.</i> (2011)

Table 2.4 (cont.)

Table 2.4 (cont.)

S.No.	Character	Association	S/NS	Reference
2.	Lint yield plant ⁻¹	Positive	S	Dedaniya and Pethani (1994)
		Negative	S	Mandloi <i>et al.</i> (2003)
			NS	Rao <i>et al.</i> (2009a) Rajanna <i>et al.</i> (2011)
XIV. Fibre elongation with				
1.	Lint yield plant ⁻¹	Positive	S	Rao <i>et al.</i> (2009a)
		Negative	NS	Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011)

Note: S- Significant

NS- Non-significant

Table 2.1. Review of literature on genetic variability in cotton

S.No.	Character	Wider genetic variability	Narrow genetic variability
1.	Days to 50% flowering	Ahuja and Tuteja (2000) Neelima <i>et al.</i> (2005)	Neelam <i>et al.</i> (2002) Altaher and Singh (2003a) Narisireddy and Ratnakumari (2004) Kaushik and Kapoor (2006) Neelima <i>et al.</i> (2008) Sarada <i>et al.</i> (2010) Kulkarni <i>et al.</i> (2011) Asha <i>et al.</i> (2013a) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014)
2.	Plant height (cm)	Neelam <i>et al.</i> (2002) Tuteja <i>et al.</i> (2006) Patnaik and Sial (2010) Sarada <i>et al.</i> (2010) Hafiz <i>et al.</i> (2013) Paramjit and Buttar (2013) Dhivya <i>et al.</i> (2014) Khan <i>et al.</i> (2015)	Kaushik and Kapoor (2006) Kale <i>et al.</i> (2007) Neelima <i>et al.</i> (2008) Rajanna (2010) Kulkarni <i>et al.</i> (2011) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015)
3.	Number of monopodia plant ⁻¹	Kaushik and Kapoor (2006) Tuteja <i>et al.</i> (2006) Verma <i>et al.</i> (2006) Neelima <i>et al.</i> (2008) Kishore <i>et al.</i> (2011) Kulkarni <i>et al.</i> (2011) Mohan (2011) Hafiz <i>et al.</i> (2013) Paramjit and Buttar (2013) Khan <i>et al.</i> (2015)	Ahuja and Tuteja (2000) Gururajan (2000) Girase and Mehetre (2002) Erande <i>et al.</i> (2014)
4.	Number of sympodia plant ⁻¹	Gururajan (2000) Neelam <i>et al.</i> (2002) Kaushik and Kapoor (2006) Tuteja <i>et al.</i> (2006) Neelima <i>et al.</i> (2008) Kulkarni <i>et al.</i> (2011) Hafiz <i>et al.</i> (2013) Paramjit and Buttar (2013) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)	Girase and Mehetre (2002) Vinodhana <i>et al.</i> (2013) Farooq <i>et al.</i> (2014)

Table 2.1 (cont.)

Table 2.1 (cont.)

S.No.	Character	Wider genetic variability	Narrow genetic variability
5.	Number of bolls plant ⁻¹	Gururajan and Sundar (2004) Narisireddy and Ratnakumari (2004) Kaushik and Kapoor (2006) Tuteja <i>et al.</i> (2006) Neelima <i>et al.</i> (2008) Kishore <i>et al.</i> (2011) Mohan (2011) Paramjit and Buttar (2013) Vinodhana <i>et al.</i> (2013) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015) Khan <i>et al.</i> (2015)	Girase and Mehetre (2002) An <i>et al.</i> (2008) Vijayalakshmi <i>et al.</i> (2008) Mahantesh (2009) Rajanna (2010) Hafiz <i>et al.</i> (2013)
6.	Boll weight (g)	Gururajan and Sundar (2004) Tuteja <i>et al.</i> (2006) Kulkarni <i>et al.</i> (2011) Mohan (2011) Paramjit and Buttar (2013)	Reddy (2001) Altaher and Singh (2003a) Neelima <i>et al.</i> (2008) Bazi (2011) Vinodhana <i>et al.</i> (2013) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014)
7.	Lint index (g)	Gururajan and Sundar (2004) Kaushik and Kapoor (2006) Kishore <i>et al.</i> (2011) Kulkarni <i>et al.</i> (2011) Asha <i>et al.</i> (2013a) Dhivya <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015) Khan <i>et al.</i> (2015)	Altaher and Singh (2003a) Neelima <i>et al.</i> (2008) Kulkarni <i>et al.</i> (2010) Naqib <i>et al.</i> (2010) Rajanna (2010) Vinodhana <i>et al.</i> (2013)
8.	Seed index (g)	Gururajan and Sundar (2004) Kumar (2004) Kaushik and Kapoor (2006) Kishore <i>et al.</i> (2011) Dhivya <i>et al.</i> (2014) Khan <i>et al.</i> (2015)	Neelam <i>et al.</i> (2002) Altaher and Singh (2003a) Neelima <i>et al.</i> (2008) Srinivasulu (2009) Rajanna (2010) Paramjit and Buttar (2013) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015)
9.	Ginning out- turn (%)	Tuteja <i>et al.</i> (2006) Naqib <i>et al.</i> (2010)	Muraleedhar (2005) Kaushik and Kapoor (2006) Neelima <i>et al.</i> (2008) Sarada <i>et al.</i> (2010) Mohan (2011) Vinodhana <i>et al.</i> (2013) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Khan <i>et al.</i> (2015)

Table 2.1 (cont.)

Table 2.1 (cont.)

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

Table 2.1 (cont.)

Table 2.1 (cont.)

S.No.	Character	Wider genetic variability	Narrow genetic variability
14.	Fibre elongation (%)	Srinivasulu <i>et al.</i> (2010a)	Rajanna (2010) Bazi (2011) Kulkarni <i>et al.</i> (2011) Elango <i>et al.</i> (2012) Asha <i>et al.</i> (2013a)
15.	Seed cotton yield plant ⁻¹ (g)	Kaushik and Kapoor (2006) Verma <i>et al.</i> (2006) Naqib <i>et al.</i> (2010) Sarada <i>et al.</i> (2010) Srinivasulu <i>et al.</i> (2010a) Kishore <i>et al.</i> (2011) Kulkarni <i>et al.</i> (2011) Mohan (2011) Asha <i>et al.</i> (2013a) Vinodhana <i>et al.</i> (2013) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015) Khan <i>et al.</i> (2015)	An <i>et al.</i> (2008) Mahantesh (2009) Rajanna (2010) Bazi (2011)
16.	Lint yield plant ⁻¹ (g)	Patnaik <i>et al.</i> (2004) Rajanna (2010) Erande <i>et al.</i> (2014)	Mahantesh (2009) Rajanna (2010) Lakshmi <i>et al.</i> (2012)

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

S.No.	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
1.	Days to 50% flowering	Neelam <i>et al.</i> (2002) Mahantesh (2009) Rao <i>et al.</i> (2009a) Hafiz <i>et al.</i> (2013)	Muraleedhar (2005) Kale <i>et al.</i> (2007) An <i>et al.</i> (2008) Ravikesavan <i>et al.</i> (2008) Mahantesh (2009) Rajanna (2010) Asha <i>et al.</i> (2013a) Patel <i>et al.</i> (2013b) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014)	Vijayalaxmi <i>et al.</i> (2008)	Neelima <i>et al.</i> (2002) Rao <i>et al.</i> (2009a) Kulkarni <i>et al.</i> (2011)
2.	Plant height (cm)	Neelam <i>et al.</i> (2002) Kale <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007) An <i>et al.</i> (2008) Ravikesavan <i>et al.</i> (2008) Kulkarni <i>et al.</i> (2011) Haritha <i>et al.</i> (2012) Lakshmi <i>et al.</i> (2012) Asha <i>et al.</i> (2013a) Hafiz <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Khan <i>et al.</i> (2015)	Kaushik and Kapoor (2006) Verma <i>et al.</i> (2006) Mahantesh (2009)	----	Rajanna (2010) Paramjit and Buttar (2013)

Table 2.2 (cont.)

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	Kaushik and Kapoor (2006) Mahantesh (2009) Rao <i>et al.</i> (2009a) Lakshmi <i>et al.</i> (2012) Asha <i>et al.</i> (2013a) Hafiz <i>et al.</i> (2013) Paramjit and Buttar (2013) Patel <i>et al.</i> (2013b) Erande <i>et al.</i> (2014)	Kulkarni <i>et al.</i> (2011) Farooq <i>et al.</i> (2014) Khan <i>et al.</i> (2015)	Neelima <i>et al.</i> (2002)	Kale <i>et al.</i> (2007) Rajamani and Rao (2009) Rajanna (2010)
4.	Number of sympodia plant ⁻¹	Girase and Mehetre (2002) Neelam <i>et al.</i> (2002) Kaushik and Kapoor (2006) Verma <i>et al.</i> (2006) Sakthi <i>et al.</i> (2007) An <i>et al.</i> (2008) Ravikesavan <i>et al.</i> (2008) Rajanna (2010) Haritha <i>et al.</i> (2012) Lakshmi <i>et al.</i> (2012) Asha <i>et al.</i> (2013a) Hafiz <i>et al.</i> (2013) Paramjit and Buttar (2013) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)	Gururajan (2000) Reddy (2001) Kulkarni <i>et al.</i> (2011) Vinodhana <i>et al.</i> (2013) Farooq <i>et al.</i> (2014)	Mahantesh (2009)	Bazi (2011) Patel <i>et al.</i> (2013b)

Table 2.2 (cont.)

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 and Kapoor (2006) Kale <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007) An <i>et al.</i> (2008) Mahantesh (2009) Rajanna (2010) Bazi (2011) Elango <i>et al.</i> (2012) Lakshmi <i>et al.</i> (2012) Asha <i>et al.</i> (2013a) Hafiz <i>et al.</i> (2013) Paramjit and Buttar (2013) Vinodhana <i>et al.</i> (2013) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015) Khan <i>et al.</i> (2015)	Gururajan and Sundar (2004) Patel <i>et al.</i> (2013b) Farooq <i>et al.</i> (2014)	----	Rajamani and Rao (2009)

Table 2.2 (cont.)

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)	Sakthi <i>et al.</i> (2007) An <i>et al.</i> (2008) Ravikesavan <i>et al.</i> (2008) Rajanna (2010) Bazi (2011) Elango <i>et al.</i> (2012) Haritha <i>et al.</i> (2012) Lakshmi <i>et al.</i> (2012) Asha <i>et al.</i> (2013a) Paramjit and Buttar (2013) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015) Khan <i>et al.</i> (2015)	Gururajan (2000) Gururajan and Sundar (2004) Kale <i>et al.</i> (2007) Mahantesh (2009) Farooq <i>et al.</i> (2014)	Dhivya <i>et al.</i> (2014)	Rajamani and Rao (2009)
7.	Lint index (g)	Kaushik and Kapoor (2006) Sambamurthy <i>et al.</i> (2006) An <i>et al.</i> (2008) Ravikesavan <i>et al.</i> (2008) Mahantesh (2009) Naqib <i>et al.</i> (2010) Bazi (2011) Haritha <i>et al.</i> (2012) Lakshmi <i>et al.</i> (2012) Asha <i>et al.</i> (2013a) Vinodhana <i>et al.</i> (2013) Dhivya <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015)	Sakthi <i>et al.</i> (2007) Rajanna (2010) Kulkarni <i>et al.</i> (2011) Khan <i>et al.</i> (2015)	Erande <i>et al.</i> (2014)	Srinivasulu (2009)

Table 2.2 (cont.)

Table 2.2 (cont.)

S.No.	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
8.	Seed index (g)	Kaushik and Kapoor (2006) An <i>et al.</i> (2008) Ravikesavan <i>et al.</i> (2008) Mahantesh (2009) Naqib <i>et al.</i> (2010) Bazi (2011) Asha <i>et al.</i> (2013a) Paramjit and Buttar (2013) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015)	Gururajan (2000) Neelam <i>et al.</i> (2002) Sakthi <i>et al.</i> (2007) Kulkarni <i>et al.</i> (2011) Rajanna (2010) Haritha <i>et al.</i> (2012) Vinodhana <i>et al.</i> (2013) Khan <i>et al.</i> (2015)	----	Gururajan and Sundar (2004)
9.	Ginning out-turn (%)	Gururajan and Sundar (2004) Ravikesavan <i>et al.</i> (2008) Elango <i>et al.</i> (2012) Haritha <i>et al.</i> (2012) Ahsan <i>et al.</i> (2015)	An <i>et al.</i> (2008) Mahantesh (2009) Rajanna (2010) Bazi (2011) Asha <i>et al.</i> (2013a) Paramjit and Buttar (2013) Patel <i>et al.</i> (2013b) Vinodhana <i>et al.</i> (2013) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Khan <i>et al.</i> (2015)	----	Srinivasulu (2009)

Table 2.2 (cont.)

Table 2.2 (cont.)

S.No.	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
10.	2.5% span length (mm)	Rao and Reddy (2001) Gururajan and Sundar (2004) Bazi (2011) Elango <i>et al.</i> (2012) Asha <i>et al.</i> (2013a) Hafiz <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014)	Sakthi <i>et al.</i> (2007) An <i>et al.</i> (2008) Ravikesavan <i>et al.</i> (2008) Mahantesh (2009) Rajamani and Rao (2009) Kulkarni <i>et al.</i> (2011) Rajanna (2010)	----	Haritha <i>et al.</i> (2012)
11.	Uniformity ratio	Muhammad <i>et al.</i> (2008) Haritha <i>et al.</i> (2012)	Sakthi <i>et al.</i> (2007) Mahantesh (2009) Bazi (2011) Elango <i>et al.</i> (2012) Haritha <i>et al.</i> (2012) Asha <i>et al.</i> (2013a) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)	Neelima <i>et al.</i> (2002)	Muraleedhar (2005) Rajamani and Rao (2009) Rajanna (2010)
12.	Micronaire value (10 ⁻⁶ g/inch)	Rao and Reddy (2001) An <i>et al.</i> (2008) Ravikesavan <i>et al.</i> (2008) Bazi (2011) Asha <i>et al.</i> (2013a) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014)	Sakthi <i>et al.</i> (2007) Mahantesh (2009) Elango <i>et al.</i> (2012) Haritha <i>et al.</i> (2012) Khan <i>et al.</i> (2015)	----	Rajamani and Rao (2009) Rajanna (2010)
13.	Bundle strength (g/tex)	Sambamurthy <i>et al.</i> (2006) An <i>et al.</i> (2008) Ravikesavan <i>et al.</i> (2008) Asha <i>et al.</i> (2013a) Vinodhana <i>et al.</i> (2013)	Rao and Reddy (2001) Sakthi <i>et al.</i> (2007) Kulkarni <i>et al.</i> (2011) Rajanna (2010)	----	Rao <i>et al.</i> (2009a) Mahantesh (2009) Rajamani and Rao (2009) Bazi (2011)

Table 2.2 (cont.)

Table 2.2 (cont.)

S.No.	Character	High heritability and high genetic advance	High heritability and low genetic advance	Low heritability and high genetic advance	Low heritability and low genetic advance
14.	Fibre elongation (%)	Valarmathi and Jehangir (1998) Sakthi <i>et al.</i> (2007)	Vijayalakshmi <i>et al.</i> (2008) Kulkarni <i>et al.</i> (2011) Elango <i>et al.</i> (2012) Venkatesh (2012) Asha <i>et al.</i> (2013a)	----	Muraleedhar (2005) Mahantesh (2009) Rajanna (2010) Bazi (2011)
15.	Seed cotton yield plant ⁻¹ (g)	An <i>et al.</i> (2008) Mahantesh (2009) Rajanna (2010) Bazi (2011) Elango <i>et al.</i> (2012) Haritha <i>et al.</i> (2012) Asha <i>et al.</i> (2013a) Paramjit and Buttar (2013) Vinodhana <i>et al.</i> (2013) Dhivya <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Ahsan <i>et al.</i> (2015) Khan <i>et al.</i> (2015)	Gururajan and Sundar (2004) Kale <i>et al.</i> (2007)	----	Rajamani and Rao (2009)
16.	Lint yield plant ⁻¹ (g)	Mahantesh (2009) Rajanna (2010) Elango <i>et al.</i> (2012) Erande <i>et al.</i> (2014)	Muhammad <i>et al.</i> (2008)	----	Rao <i>et al.</i> (2009a) Bazi (2011)

Table 2.5. Review of literature on direct effects of component characters on seed cotton yield in cotton

S.No.	Character	Positive Direct effect	Negative Direct effect
1.	Days to 50% flowering	Sangeetha (1998) Tuteja <i>et al.</i> (2006) Rajanna <i>et al.</i> (2011) Patel <i>et al.</i> (2013b) Rajamani <i>et al.</i> (2013) Ranjan <i>et al.</i> (2014)	Gururajan (2000) Muthu <i>et al.</i> (2004) Kaushik and Kapoor (2006) Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
2.	Plant height (cm)	Neelima <i>et al.</i> (2002) Altaher and Singh (2003a) Muthu <i>et al.</i> (2004) Kaushik and Kapoor (2006) Sakthi <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011) Venkatesh (2012) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)	Verma <i>et al.</i> (2006) Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
3.	Number of monopodia plant ⁻¹	Vijayalaxmi <i>et al.</i> (2008) Ekinci <i>et al.</i> (2010) Salahuddin <i>et al.</i> (2010) Srinivasulu <i>et al.</i> (2010a) Mohan (2011) Rajanna <i>et al.</i> (2011) Chitti <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)	Kaushik and Kapoor (2006) Tuteja <i>et al.</i> (2006) Verma <i>et al.</i> (2006) Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
4.	Number of sympodia plant ⁻¹	Vijayalaxmi <i>et al.</i> (2008) Ekinci <i>et al.</i> (2010) Salahuddin <i>et al.</i> (2010) Srinivasulu <i>et al.</i> (2010a) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014)	Gururajan (2000) Muthu <i>et al.</i> (2004) Tuteja <i>et al.</i> (2006) Venkateswarlu <i>et al.</i> (2010a)
5.	Number of bolls plant ⁻¹	Vijayalaxmi <i>et al.</i> (2008) Ekinci <i>et al.</i> (2010) Salahuddin <i>et al.</i> (2010) Srinivasulu <i>et al.</i> (2010a) Mohan (2011) Lakshmi <i>et al.</i> (2012) Rajamani <i>et al.</i> (2013)	Tuteja <i>et al.</i> (2006) Farooq <i>et al.</i> (2014)

Table 2.5 (cont.)

Table 2.5 (cont.)

S.No.	Character	Positive Direct effect	Negative Direct effect
5.	Number of bolls plant ⁻¹	Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)	----
6.	Boll weight (g)	Vijayalaxmi <i>et al.</i> (2008) Ekinci <i>et al.</i> (2010) Salahuddin <i>et al.</i> (2010) Srinivasulu <i>et al.</i> (2010a) Mohan (2011) Lakshmi <i>et al.</i> (2012) Patel <i>et al.</i> (2013b) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)	Ladole and Meshram (2000) Verma <i>et al.</i> (2006) Chitti <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
7.	Lint index (g)	Vijayalaxmi <i>et al.</i> (2008) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)	Muthu <i>et al.</i> (2004) Kaushik and Kapoor (2006) Pratap <i>et al.</i> (2007) Venkateswarlu <i>et al.</i> (2010a) Farooq <i>et al.</i> (2014)
8.	Seed index (g)	Vijayalaxmi <i>et al.</i> (2008) Mohan (2011) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)	Ladole and Meshram (2000) Neelima <i>et al.</i> (2002) Altaher and Singh (2003a) Gururajan and Sundar (2004) Kale <i>et al.</i> (2007) Farooq <i>et al.</i> (2014)
9.	Ginning out-turn (%)	Gururajan (2000) Muthu <i>et al.</i> (2004) Kaushik and Kapoor (2006) Tuteja <i>et al.</i> (2006) Verma <i>et al.</i> (2006) Kale <i>et al.</i> (2007) Pratap <i>et al.</i> (2007) Mohan (2011) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)	Vijayalaxmi <i>et al.</i> (2008) Salahuddin <i>et al.</i> (2010) Venkateswarlu <i>et al.</i> (2010a) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Chitti <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
10.	2.5% span length (mm)	Kaushik and Kapoor (2006) Tuteja <i>et al.</i> (2006) Kale <i>et al.</i> (2007) Mohan (2011) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)	Muhammad <i>et al.</i> (2003) Neelima <i>et al.</i> (2005) Sakthi <i>et al.</i> (2007) Venkateswarlu <i>et al.</i> (2010a) Vinodhana <i>et al.</i> (2013) Farooq <i>et al.</i> (2014)

Table 2.5 (cont.)

Table 2.5 (cont.)

S.No.	Character	Positive Direct effect	Negative Direct effect
11.	Uniformity ratio	Sambamurthy <i>et al.</i> (2006) Vijayalaxmi <i>et al.</i> (2008) Srinivasulu <i>et al.</i> (2010a) Mohan (2011) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)	Muthu <i>et al.</i> (2004) Neelima <i>et al.</i> (2005) Pratap <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007) Anandan (2009) Venkateswarulu <i>et al.</i> (2010a)
12.	Micronaire value (10 ⁻⁶ g/inch)	Neelima <i>et al.</i> (2005) Sambamurthy <i>et al.</i> (2006) Pratap <i>et al.</i> (2007) Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Mohan (2011) Rajanna <i>et al.</i> (2011) Rajamani <i>et al.</i> (2013) Erande <i>et al.</i> (2014)	Gururajan and Sundar (2004) Verma <i>et al.</i> (2006) Venkateswarlu <i>et al.</i> (2010a) Vinodhana <i>et al.</i> (2013) Kumar <i>et al.</i> (2014)
13.	Bundle strength (g/tex)	Neelima <i>et al.</i> (2005) Sambamurthy <i>et al.</i> (2006) Sakthi <i>et al.</i> (2007) Rajanna <i>et al.</i> (2011)	Vijayalaxmi <i>et al.</i> (2008) Venkateswarlu <i>et al.</i> (2010a) Rajamani <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013) Farooq <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
14.	Fibre elongation (%)	Muthu <i>et al.</i> (2004) Sakthi <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Srinivasulu <i>et al.</i> (2010a) Mohan (2011)	Muraleedhar (2005) Vijayalaxmi <i>et al.</i> (2008) Anandan (2009) Srinivasulu (2009) Mahantesh <i>et al.</i> (2010)
15.	Lint yield plant ⁻¹ (g)	Dedaniya and Pethani (1994) Tomar and Singh (1996) Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011)	----

Table 2.3. Review of literature on association of component characters with seed cotton yield in cotton

S.No.	Character	Association	S/NS	Reference
1.	Days to 50% flowering	Positive	S	Tuteja <i>et al.</i> (2006) Lakshmi <i>et al.</i> (2012) Ranjan <i>et al.</i> (2014)
			NS	Kaushik and Kapoor (2006) Kale <i>et al.</i> (2007) Erande <i>et al.</i> (2014)
		Negative	S	Neelima <i>et al.</i> (2005)
			NS	Annapurve <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rao <i>et al.</i> (2009a) Rajanna <i>et al.</i> (2011) Kumar <i>et al.</i> (2014)
2.	Plant height	Positive	S	Kaushik and Kapoor (2006) Rao <i>et al.</i> (2009a) Kishore <i>et al.</i> (2011) Rajanna <i>et al.</i> (2011) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)
			NS	Murthy (1997) Paramjit and Buttar (2013) Khan <i>et al.</i> (2015)
		Negative	S	Pratap <i>et al.</i> (2007)
			NS	Kaushik <i>et al.</i> (2003) Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Farooq <i>et al.</i> (2013) Vinodhana <i>et al.</i> (2013)
3.	Number of monopodia plant ⁻¹	Positive	S	Mahantesh (2009) Mohan (2011) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)
			NS	Annapurve <i>et al.</i> (2007) Kale <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Kishore <i>et al.</i> (2011) Rajanna <i>et al.</i> (2011) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
		Negative	S	Batool <i>et al.</i> (2010)
			NS	Rao <i>et al.</i> (2009a) Venkateswarlu <i>et al.</i> (2010a) Farooq <i>et al.</i> (2013) Paramjit and Buttar (2013) Farooq <i>et al.</i> (2014)

Table 2.3 (cont.)

Table 2.3 (cont.)

S.No.	Character	Association	S/NS	Reference
4.	Number of sympodia plant ⁻¹	Positive	S	Vijayalaxmi <i>et al.</i> (2008) Batoool <i>et al.</i> (2010) Ekinici <i>et al.</i> (2010) Patnaik and Sial (2010) Mohan (2011) Rajanna <i>et al.</i> (2011) Paramjit and Buttar (2013) Erande <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
			NS	Neelam <i>et al.</i> (2002) Pradeep and Sumalini (2005) Kishore <i>et al.</i> (2011) Farooq <i>et al.</i> (2014)
		Negative	NS	Rao <i>et al.</i> (2009a) Vinodhana <i>et al.</i> (2013) Farooq <i>et al.</i> (2014)
5.	Number of bolls plant ⁻¹	Positive	S	Makhdoom <i>et al.</i> (2010) Patnaik and Sial (2010) Kishore <i>et al.</i> (2011) Mohan (2011) Imran <i>et al.</i> (2012) Lakshmi <i>et al.</i> (2012) Paramjit and Buttar (2013) Vinodhana <i>et al.</i> (2013) Erande <i>et al.</i> (2014) Farooq <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014)
			NS	Pradeep and Sumalini (2005) Annapurve <i>et al.</i> (2007)
		Negative	NS	Farooq <i>et al.</i> (2013)
6.	Boll weight	Positive	S	Batoool <i>et al.</i> (2010) Kishore <i>et al.</i> (2011) Mohan (2011) Paramjit and Buttar (2013) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014) Ranjan <i>et al.</i> (2014) Khan <i>et al.</i> (2015)
			NS	Kaushik <i>et al.</i> (2003) Vijayalaxmi <i>et al.</i> (2008) Vinodhana <i>et al.</i> (2013) Farooq <i>et al.</i> (2014)
		Negative	S	Gururajan (2000)
			NS	Farooq <i>et al.</i> (2013)

Table 2.3 (cont.)

Table 2.3 (cont.)

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

Table 2.3 (cont.)

Table 2.3 (cont.)

S.No.	Character	Association	S/NS	Reference
10.	2.5% span length	Positive	S	Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
			NS	Mandloi <i>et al.</i> (2003) Vinodhana <i>et al.</i> (2013)
		Negative	S	Gururajan and Sundar (2004) Venkateswarlu <i>et al.</i> (2010a) Kishore <i>et al.</i> (2011) Mohan (2011)
			NS	Kale <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rao <i>et al.</i> (2009a) Rajanna <i>et al.</i> (2011) Farooq <i>et al.</i> (2014)
11.	Uniformity ratio	Positive	S	Neelima <i>et al.</i> (2005) Khan <i>et al.</i> (2015)
			NS	Kishore <i>et al.</i> (2011)
		Negative	S	Vijayalaxmi <i>et al.</i> (2008) Erande <i>et al.</i> (2014)
			NS	Tuteja <i>et al.</i> (2006) Kishore <i>et al.</i> (2011) Mohan (2011) Rajanna <i>et al.</i> (2011) Kumar <i>et al.</i> (2014)
12.	Micronaire value	Positive	S	Neelima <i>et al.</i> (2005) Sambamurthy <i>et al.</i> (2006) Kumar and Ravikesavan (2008) Venkateswarlu <i>et al.</i> (2010a) Khan <i>et al.</i> (2015)
		Negative	S	Rajanna <i>et al.</i> (2011) Erande <i>et al.</i> (2014) Kumar <i>et al.</i> (2014)
			NS	Mohan (2011) Vinodhana <i>et al.</i> (2013) Farooq <i>et al.</i> (2014)
13.	Bundle strength	Positive	S	Bazi (2011) Kumar <i>et al.</i> (2014)
			NS	Neelam <i>et al.</i> (2002) Mandloi <i>et al.</i> (2003) Mohan (2011) Venkatesh (2012)
		Negative	S	Vinodhana <i>et al.</i> (2013) Farooq <i>et al.</i> (2014)
14.	Fibre elongation	Positive	S	Rao <i>et al.</i> (2009a)
			NS	Muraleedhar (2005)
		Negative	S	Kishore <i>et al.</i> (2011)
			NS	Vijayalakshmi <i>et al.</i> (2008) Rajanna (2010) Elango <i>et al.</i> (2012)

Table 2.3 (cont.)

Table 2.3 (cont.)

S.No.	Character	Association	S/NS	Reference
15.	Lint yield plant ⁻¹	Positive	S	Mandloi <i>et al.</i> (2003) Pratap <i>et al.</i> (2007) Vijayalaxmi <i>et al.</i> (2008) Rajanna <i>et al.</i> (2011) Lakshmi <i>et al.</i> (2012) Venkatesh (2012) Erande <i>et al.</i> (2014)

Note: S - Significant

NS- Non-significant

Table 4.48. Analysis of variance for different characters in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) as per AMMI model during *kharif*, 2014-15

Source of variation	d.f	Days to 50 % flowering		Plant height (cm)		No. of monopodia plant ⁻¹		No. of sympodia plant ⁻¹	
		MSS	% explained	MSS	% explained	MSS	% explained	MSS	% explained
Trials	215	13.14**		327.53**		0.49		20.33**	
Genotypes	71	17.48**	43.93	271.90**	27.41	0.54	36.10	10.87**	17.65
Environments	2	353.94**	25.05	15243.13**	43.29	5.01**	9.52	1402.78**	64.20
G × E interaction	142	6.17	31.00	145.27	29.29	0.40	54.37	5.59	18.15
PCA I	72	7.72**	63.47	165.43**	57.74	0.44**	55.68	7.12**	64.63
Residual	70	4.57**		124.54**		0.36**		4.01**	
Error	432	1.15		39.48		0.02		0.63	
Total	647	5.13		135.20		0.17		7.17	

Source of variation	d.f	No. of bolls plant ⁻¹		Boll weight (g)		Lint index (g)		Seed index (g)	
		MSS	% explained	MSS	% explained	MSS	% explained	MSS	% explained
Trials	215	203.06**		0.20**		0.42**		3.91**	
Genotypes	71	193.74*	31.50	0.31**	51.26	0.66**	51.75	1.57	13.26
Environments	2	5882.86**	26.95	3.25**	15.10	7.42**	16.48	261.43**	62.17
G × E interaction	142	127.72	41.54	0.10	33.63	0.20	31.75	1.45	24.56
PCA I	72	174.20**	69.16	0.12**	61.74	0.23**	58.56	1.49**	51.79
Residual	70	79.91**		0.08**		0.17**		1.42**	
Error	432	4.14		0.01		0.01		0.07	
Total	647	70.24		0.07		0.15		1.35	

Table 4.48 (cont.)

Table 4.48 (cont.)

Source of variation	d.f	Ginning out-turn (%)		2.5% span length (mm)		Uniformity ratio		Micronaire value (10 ⁻⁶ g/inch)	
		MSS	% explained	MSS	% explained	MSS	% explained	MSS	% explained
Trials	215	9.24**		3.90**		1.24**		0.13**	
Genotypes	71	14.42**	51.54	4.60**	38.99	2.13**	56.38	0.10**	24.59
Environments	2	230.30**	23.18	185.06**	44.15	1.90	1.42	7.91**	57.28
G × E interaction	142	3.53	25.27	0.99	16.84	0.79	42.19	0.04	18.11
PCA I	72	3.56**	51.12	1.28**	65.34	0.99**	63.10	0.05**	78.65
Residual	70	3.51**		0.70**		0.59		0.02**	
Error	432	0.34		0.39		0.47		0.00	
Total	647	3.29		1.55		0.73		0.04	

Source of variation	d.f	Bundle strength (g/tex)		Fibre elongation (%)		Seed cotton yield plant ⁻¹ (g)		Lint yield plant ⁻¹ (g)	
		MSS	% explained	MSS	% explained	MSS	% explained	MSS	% explained
Trials	215	3.16**		0.04**		2109.72**		263.89**	
Genotypes	71	3.12**	32.68	0.10**	39.84	3255.72**	50.96	461.01**	57.69
Environments	2	153.38**	45.21	1.71**	37.88	23357.95**	10.29	3711.95**	13.08
G × E interaction	142	1.06	22.10	0.01	22.27	1237.45	38.73	116.76	29.22
PCA I	72	1.26**	60.73	0.02**	56.89	1501.62**	61.53	137.93**	59.89
Residual	70	0.84**		0.01**		965.74**		95.00**	
Error	432	0.24		0.01		73.90		7.24	
Total	647	1.21		0.02		750.41		92.52	

*Significant at 5 % level

** Significant at 1 % level

Table 4.2. Analysis of variance for different characters in Egyptian cotton (*Gossypium barbadense* L.)

Source of variation	d.f	Days to 50% flowering	Plant height (cm)	No. of monopodia plant ⁻¹	No. of sympodia plant ⁻¹	No. of bolls plant ⁻¹	Boll weight (g)	Lint index (g)	Seed index (g)
		Mean squares							
Replications	2	0.60	13.11	0.00	0.19	9.35	0.02	0.01	0.10
Treatments	19	17.07**	290.33**	0.36**	11.87**	131.42**	0.17**	1.10**	2.69**
Error	38	1.20	69.95	0.01	1.27	8.50	0.01	0.03	0.07

Source of variation	d.f	Ginning out-turn (%)	2.5% span length (mm)	Uniformity ratio	Micronaire value (10 ⁻⁶ g/inch)	Bundle strength (g/tex)	Fibre elongation (%)	Seed cotton yield plant ⁻¹ (g)	Lint yield plant ⁻¹ (g)
		Mean squares							
Replications	2	1.13	0.09	0.51	0.01	0.41	0.02	29.50	11.68
Treatments	19	9.13**	20.49**	7.78**	0.10**	9.59**	0.10**	1004.96**	125.07**
Error	38	1.37	0.86	1.77	0.01	0.72	0.02	56.54	6.64

** Significant at 1% level

Table 4.4. Mean, genetic variability, heritability (broad sense) and genetic advance as per cent of mean for different characters in Egyptian cotton (*Gossypium barbadense* L.)

S.No.	Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance as per cent of mean
			Minimum	Maximum	PCV (%)	GCV (%)		
1	Days to 50% flowering	72.50	68.00	77.00	3.51	3.17	81.60	5.90
2	Plant height (cm)	138.33	125.00	156.83	8.65	6.19	51.20	9.13
3	No. of monopodia plant ⁻¹	1.32	0.67	2.00	26.73	25.69	92.40	50.87
4	No. of sympodia plant ⁻¹	16.49	12.21	20.11	13.28	11.39	73.60	20.14
5	No. of bolls plant ⁻¹	44.18	32.80	57.22	15.91	14.48	82.80	27.15
6	Boll weight (g)	2.61	2.10	3.10	9.87	8.84	80.30	16.32
7	Lint index (g)	4.39	3.36	5.66	14.13	13.60	92.60	26.97
8	Seed index (g)	9.31	7.40	11.20	10.45	10.00	92.30	19.86
9	Ginning out-turn (%)	31.96	28.77	34.75	6.22	5.03	65.40	8.38
10	2.5% span length (mm)	32.58	28.27	37.82	8.35	7.85	88.40	15.20
11	Uniformity ratio	46.76	44.18	50.05	4.15	3.02	53.10	4.54
12	Micronaire value (10 ⁻⁶ g/inch)	2.84	2.40	3.20	7.27	6.16	71.80	10.75
13	Bundle strength (g/tex)	25.19	21.73	29.49	7.60	6.82	80.50	12.62
14	Fibre elongation (%)	5.25	4.90	5.53	3.96	3.17	63.90	5.22
15	Seed cotton yield plant ⁻¹ (g)	98.52	66.88	133.20	19.59	18.04	84.80	34.23
16	Lint yield plant ⁻¹ (g)	31.59	20.86	41.59	21.49	19.88	85.60	37.90

PCV: Phenotypic co-efficient of variation

GCV: Genotypic co-efficient of variation

Table 4.10. Contribution of different characters towards genetic divergence in 20 Egyptian cotton (*Gossypium barbadense* L.) genotypes

S.No.	Source	Times Ranked first	Contribution %
1	Days to 50 % flowering	4	2.11
2	Plant height (cm)	0	0.00
3	No. of monopodia plant ⁻¹	20	10.49
4	No. of sympodia plant ⁻¹	5	2.65
5	No.of bolls plant ⁻¹	4	2.11
6	Boll weight (g)	5	2.63
7	Lint index (g)	8	4.21
8	Seed index (g)	35	18.37
9	Ginning out-tum (%)	12	6.32
10	2.5% span length (mm)	23	12.11
11	Uniformity ratio	5	2.63
12	Micronaire value (10 ⁻⁶ g/inch)	15	7.87
13	Bundle strength (g/tex)	1	0.53
14	Fibre elongation (%)	24	12.63
15	Seed cotton yield plant ⁻¹ (g)	20	10.60
16	Lint yield plant ⁻¹ (g)	9	4.74

Table 4.11. Clustering of 20 genotypes of Egyptian cotton (*Gossypium barbadense* L.) by Tocher's method

Cluster No.	No. of genotypes	Name of genotype(s)
I	5	GSB 40, DB 11, GSB 21, GSB 41, RAB 8
II	6	GSB 43, ARBD 27, DB 14, TCB 26, CCB 33, DB 40
III	1	GSB 39
IV	5	CCB 30, DB 39, CCB 11, SUVIN, DB 16
V	1	TCB 51
VI	1	TCB 37
VII	1	RhCB 011

Table 4.12. Average intra and inter-cluster D² values among seven clusters in 20 Egyptian cotton (*Gossypium barbadense* L.) genotypes

Cluster No.	I	II	III	IV	V	VI	VII
I	38.76	78.56	148.77	128.73	133.68	69.32	86.62
II		42.93	82.27	105.98	71.97	168.26	100.52
III			0.00	57.57	175.60	263.35	98.92
IV				55.49	212.57	236.01	132.23
V					0.00	208.17	203.82
VI						0.00	181.54
VII							0.00

Note: Bold and diagonal values indicate intra-cluster D² distance

Table 4.13. The nearest and the farthest cluster from each cluster based on D² values using Tocher's method in 20 genotypes of Egyptian cotton (*Gossypium barbadense* L.)

Cluster No.	Nearest cluster with D ² values	Farthest cluster with D ² values
I	VI (69.32)	III (148.77)
II	V (71.97)	VI (168.26)
III	IV (57.57)	VI (263.35)
IV	III (57.57)	VI (236.01)
V	II (71.97)	IV (212.57)
VI	I (69.32)	III (263.35)
VII	I (86.62)	V (203.82)

Note: Values in parentheses indicate D² values

Table 4.14. Mean values of seven clusters estimated by Tocher's method from 20 genotypes of Egyptian cotton (*Gossypium barbadense* L.)

Cluster No.	Days to 50% flowering	Plant height (cm)	No. of monopodia plant ⁻¹	No. of sympodia a plant ⁻¹	No. of bolls plant ⁻¹	Boll weight (g)	Lint index (g)	Seed index (g)	Ginning out-turn (%)	2.5% span length (mm)	Uniformity ratio	Micronaire value (10 ⁻⁶ g/inch)	Bundles strength (g/tex)	Fibre elongation (%)	Seed cotton yield plant ⁻¹ (g)	Lint yield plant ⁻¹ (g)
I	72.40	147.33	1.29	18.58	43.43	2.84	4.99	9.86	33.63	33.34	46.42	2.86	25.66	5.28	104.87	35.33
II	72.83	130.87	1.52	15.79	45.55	2.70	4.23	9.45	30.95	31.04	47.18	2.86	24.28	5.25	104.91	32.68
III	73.00	130.29	1.22	12.21	48.90	2.37	3.53	8.67	28.96	30.57	45.80	2.83	23.17	5.21	98.48	28.65
IV	72.93	137.60	1.07	15.91	42.15	2.37	3.85	8.11	32.14	34.58	46.48	2.73	26.20	5.21	84.42	27.21
V	70.00	146.63	2.00	15.83	35.77	2.55	4.57	10.17	30.98	28.27	48.31	2.67	21.73	4.90	77.37	23.96
VI	72.00	130.44	1.67	18.00	40.67	2.48	5.67	11.20	33.61	37.83	45.56	3.09	29.49	5.54	85.61	28.81
VII	71.33	149.34	0.67	16.55	57.22	2.75	4.43	9.77	31.22	29.18	48.03	3.20	24.42	5.52	133.20	41.59

Note: Bold figures are minimum and maximum values

Table 4.16. Eigen values, proportion of the total variance represented by first six principal components, cumulative percent variance and component loading of different characters in Egyptian cotton (*Gossypium barbadense* L.)

	PC ₁	PC ₂	PC ₃	PC ₄	PC ₅	PC ₆
Eigene Value (Root)	4.84	3.03	2.29	2.17	1.42	1.02
% Var. Exp.	30.22	18.92	14.29	13.56	8.88	6.20
Cum. Var. Exp.	30.22	49.13	63.42	76.98	85.85	92.05
Days to 50 % flowering	0.15	0.01	0.03	0.52	0.34	0.19
Plant height (cm)	-0.11	-0.25	0.28	-0.07	-0.37	0.51
No. of monopodia plant ⁻¹	-0.19	0.39	-0.29	-0.05	0.24	0.16
No. of sympodia plant ⁻¹	-0.35	-0.18	-0.01	0.17	-0.26	-0.05
No. of bolls plant ⁻¹	0.14	-0.17	0.44	-0.28	0.31	0.11
Boll weight (g)	-0.31	0.09	0.33	0.12	0.14	0.27
Lint index (g)	-0.41	-0.02	0.03	-0.12	0.23	0.04
Seed index (g)	-0.42	-0.02	0.15	-0.14	0.01	-0.04
Ginning out-turn (%)	-0.27	0.39	0.02	-0.08	0.04	0.33
2.5% span length (mm)	-0.08	-0.49	-0.21	0.18	0.00	0.09
Uniformity ratio	-0.01	0.27	0.28	0.15	-0.51	-0.32
Micronaire value (10 ⁻⁶ g/inch)	-0.12	0.12	0.49	0.26	0.06	-0.29
Bundle strength (g/tex)	-0.28	-0.09	-0.01	0.32	0.34	-0.38
Fibre elongation (%)	-0.22	-0.46	-0.01	-0.16	0.07	-0.16
Seed cotton yield plant ⁻¹ (g)	0.28	-0.09	0.24	0.38	0.08	0.26
Lint yield plant ⁻¹ (g)	0.24	-0.01	0.28	-0.41	0.26	-0.20

PC= Principal component

Table 4.18. PCA scores of 20 genotypes of Egyptian cotton (*Gossypium barbadense* L.)

S.No.	GENOTYPE	PCA I X VECTOR	PCA II Y VECTOR	PCA III Z VECTOR
1	GSB 43	-104.61	103.16	26.53
2	ARBD 27	-104.09	104.06	27.76
3	DB 40	-99.34	100.59	27.72
4	CCB 30	-96.32	98.60	23.93
5	SUVIN	-97.75	96.83	21.59
6	CCB 33	-103.74	103.39	23.60
7	DB 39	-95.61	100.58	23.39
8	GSB 21	-107.28	100.16	24.68
9	DB 16	-100.10	96.09	25.90
10	CCB 11	-100.72	98.89	23.91
11	GSB 40	-106.37	98.02	25.76
12	TCB 37	-110.49	96.72	23.67
13	DB 11	-106.00	99.07	25.84
14	RAB 8	-105.06	99.45	29.16
15	GSB 41	-107.84	95.89	26.18
16	RhCB 011	-101.89	98.08	32.22
17	DB 14	-103.30	105.13	25.72
18	GSB 39	-96.26	100.77	26.03
19	TCB 51	-105.96	108.36	24.81
20	TCB 26	-101.07	104.89	27.52

Table 4.19. Analysis of variance for different characters in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) over three locations (pooled) during *kharif*, 2014-15

Source of variation	d.f	Days to 50% flowering	Plant height (cm)	No. of monopodia plant ⁻¹	No. of sympodia plant ⁻¹	No. of bolls plant ⁻¹	Boll weight (g)	Lint index (g)	Seed index (g)
Replications	2	0.55	12.87	0.01	1.75	6.53	0.03	0.01	0.14
Locations	2	989.97**	27421.73**	6.83**	3763.12**	13552.86**	7.24**	21.02**	794.63**
Interactions	4	1.86	87.39	0.02	1.23	18.03	0.01	0.02	0.12
Overall Sum	8	248.56**	6902.35**	1.71**	941.88**	3398.86**	1.82**	5.27**	198.76**
Treatments	89	120.90**	3391.81**	2.45**	94.79**	1316.79**	1.48**	2.23**	13.73**
Error	712	6.70	235.67	0.34	6.96		0.09	0.17	1.31

Source of variation	d.f	Ginning out-turn (%)	2.5% span length (mm)	Uniformity ratio	Micronaire value (10 ⁻⁶ g/inch)	Bundle strength (g/tex)	Fibre elongation (%)	Seed cotton yield plant ⁻¹ (g)	Lint yield plant ⁻¹ (g)
Replications	2	0.88	0.13	0.79	0.003	0.39	0.03	17.03	2.60
Locations	2	849.38**	692.79**	6.97**	31.880**	514.82**	5.55**	50063.40**	10799.23**
Interactions	4	0.78	0.97	0.51	0.006	1.10	0.01	52.96	9.46
Overall Sum	8	212.96**	173.72**	2.19	7.974**	129.35**	1.40**	12546.59**	2705.19**
Treatments	89	47.86**	66.82**	15.70**	1.692**	47.17**	0.20**	13620.91**	1495.51**
Error	712	3.64	1.74	1.74	0.043	1.42	0.03	996.85	92.83

* Significant at 5% level

** Significant at 1% level

Table 4.24. Analysis of variance of combining ability for different characters in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) over three locations (pooled) during *kharif*, 2014-15

Source of variation	d.f	Days to 50% flowering	Plant height (cm)	No. of monopodia plant ⁻¹	No. of sympodia plant ⁻¹	No. of bolls plant ⁻¹	Boll weight (g)	Lint index (g)	Seed index (g)
Replications	2	0.55	12.87	0.02	1.75	6.53	0.03	0.01	0.14
Environments	2	989.97**	27421.73**	6.83**	3763.31**	13552.86**	7.24**	21.02**	794.63**
Rep × Env.	4	1.86	87.39	0.00	1.23	18.03	0.01	0.02	0.12
Treatments	89	120.90**	3391.81**	2.45**	94.80**	1316.79**	1.48**	2.23**	13.73**
Parents	17	397.79**	1024.64**	0.97**	14.62**	390.94**	3.59**	1.96**	9.82**
Parents (Line)	11	145.89**	471.73**	1.06**	15.55**	371.73**	0.16**	0.85**	3.66**
Parents(Testers)	5	32.79**	730.54**	0.88**	13.62**	164.07**	0.35**	2.69**	3.41**
Parents (L vs T)	1	4993.78**	8577.13**	0.33**	9.33*	1736.48**	57.55**	10.51**	109.56**
Parent vs Crosses	1	275.04**	226538.63**	87.55**	5874.75**	69282.50**	4.12**	25.12**	720.54**
Crosses	71	52.43**	815.68**	1.61**	32.59**	581.21**	0.93**	1.97**	4.71**
Line effect	11	110.73**	1548.47**	3.52**	54.00*	1880.81**	1.87**	4.38**	11.73**
Tester effect	5	67.41	2364.03**	0.56	74.91*	691.19	3.34**	6.00**	5.41
Line × Tester effect	55	39.41**	528.37**	1.32**	24.45**	311.29**	0.53**	1.12**	3.25**
Env × Treatments	178	17.55**	618.07**	1.21**	22.67**	372.60**	0.30**	0.57**	4.64**
Env × Parents	34	8.51**	144.54	0.59**	12.17**	77.93**	0.14**	0.36**	2.73**
Env × Parents (L)	22	4.38	126.41	0.38**	11.53**	78.65**	0.14**	0.19**	0.99**
Env × Parents (T)	10	3.02	207.80*	0.67**	12.40**	85.92**	0.14**	0.71**	4.05**
Env × PAR (L vs T)	2	81.33**	27.69	2.40**	18.18**	30.10	0.06*	0.58**	15.26**
Env × Parent vs Cross	2	103.56**	21608.40**	12.05**	620.45**	4632.61**	2.61**	1.92**	56.53**
Env × Crosses	142	18.51**	435.81**	1.21**	16.76**	383.15**	0.31**	0.60**	4.36**
Env × Line effect	22	29.24*	1022.23**	2.20**	27.13*	749.16**	0.29	0.65	3.55
Env × Tester effect	10	18.04	127.42	1.90*	19.30	540.70	0.49	0.60	6.29
Env × L × T effect	110	16.40***	346.56**	0.95**	14.45**	295.63**	0.29**	0.59**	4.35**
Error	534	3.08	108.21	0.05	1.73	11.02	0.02	0.03	0.20

Table 4.24 (cont.)

Table 4.24 (cont.)

Source of variation	d.f	Ginning out-turn (%)	2.5% span length (mm)	Uniformity ratio	Micronaire value (10 ⁻⁶ g/inch)	Budnle strength (g/tex)	Fibre elongation (%)	Seed cotton yield plant ⁻¹ (g)	Lint yield plant ⁻¹ (g)
Replications	2	0.88	0.13	0.79	0.01	0.39	0.03	17.03	2.60
Environments	2	849.38**	692.79**	6.97*	31.88**	514.82**	5.55**	50063.40**	10799.23**
Rep × Env.	4	0.78	0.97	0.51	0.01	1.10	0.01	52.96	9.46
Treatments	89	47.86**	66.82**	15.70**	1.69**	47.17**	0.20**	13620.91**	1495.51**
Parents	17	24.09**	107.59**	22.83**	1.75**	108.06**	0.41**	3930.51**	463.16**
Parents (Line)	11	12.17**	18.23**	21.53**	1.48**	11.03**	0.16**	2614.58**	238.17**
Parents(Testers)	5	46.68**	16.88**	4.04*	0.86**	13.51**	0.04	1471.83**	246.46**
Parents (L vs T)	1	42.29**	1544.10**	131.12**	9.07**	1648.09**	5.05**	30699.13**	4021.53**
Parent vs Crosses	1	777.65**	3137.13**	556.85**	100.57**	1695.58**	0.09	451974.84**	27031.85**
Crosses	71	43.27**	13.81**	6.38**	0.29**	9.37**	0.15**	9767.15**	1383.02**
Line effect	11	106.79**	43.95**	15.84**	0.78**	17.77*	0.24*	27448.06**	3511.55**
Tester effect	5	107.24**	35.63**	22.27**	0.35	4.92	0.38**	25580.27**	4095.10**
Line × Tester effect	55	24.75**	5.80**	3.04**	0.18**	8.09**	0.11**	4793.40**	710.76**
Env × Treatments	178	11.37**	3.72**	2.37**	0.14**	3.56**	0.04**	3385.54**	311.68**
Env × Parents	34	12.00**	5.84**	2.44*	0.27**	5.02**	0.04**	670.42**	78.56**
Env × Parents (L)	22	9.33**	3.85**	2.38	0.26**	2.13**	0.03	774.10**	94.83**
Env × Parents (T)	10	17.34**	5.97**	2.48	0.24**	7.03**	0.06**	512.51**	44.49*
Env × PAR (L vs T)	2	14.77**	27.15**	3.03	0.52**	26.77**	0.03	319.42	69.84*
Env × Parent vs Cross	2	54.76**	20.05**	0.11	0.20**	6.96**	0.17**	26339.47**	1533.48**
Env × Crosses	142	10.61**	2.98**	2.39**	0.11**	3.17**	0.04**	3712.35**	350.29**
Env × Line effect	22	12.89	2.03	1.71	0.23**	2.88	0.04	6011.89*	615.49**
Env × Tester effect	10	9.93	6.85*	2.10	0.03	5.54	0.05	4450.07	478.99
Env × L × T effect	110	10.21**	2.82**	2.55**	0.09**	3.01**	0.04**	3185.38**	285.55**
Error	534	1.06	1.07	1.53	0.01	0.71	0.02	200.62	19.88

* Significant at 5% level

**Significant at 1% level

Table 4.25. General combining ability effects of parents for different characters in cotton over three locations (pooled) during *kharif*, 2014-15

	Days to 50% flowering	Plant height (cm)	No. of monopodia plant ⁻¹	No. of sympodia plant ⁻¹	No. of bolls plant ⁻¹	Boll weight (g)	Lint index (g)	Seed index (g)
LINES								
NDLH 1938	-0.64*	9.32**	-0.31**	0.40*	6.43**	0.14**	-0.04	-0.49**
H 1442	-1.90**	-0.28	-0.22**	0.91**	6.54**	0.12**	0.10**	-0.49**
ADB 542	0.96**	3.32*	0.10**	0.11	1.16*	0.13**	0.03	-0.23**
ADB 532	-0.12	-5.21**	0.18**	-0.99**	-2.49**	0.21**	0.15**	0.89**
WGCV 48	0.12	-7.63**	0.36**	-0.48*	-1.16*	-0.05**	0.03	0.04
MR 786	-0.28	7.35**	-0.15**	1.72**	1.60**	0.23**	0.29**	0.22**
TSH 0250	-0.27	0.17	-0.24**	-1.01**	-4.43**	-0.15**	-0.18**	-0.13*
BS 37	2.12**	-0.42	0.51**	0.14	2.68**	0.08**	-0.45**	-0.01
SCS 793	-0.14	-0.67	0.03	1.06**	3.68**	-0.30**	-0.37**	0.21**
MCU 5	1.23**	-8.56**	-0.12**	-1.91**	-14.61**	-0.33**	-0.31**	0.50**
L 1058	1.77**	0.73	0.07*	0.14	-3.81**	-0.02	0.50**	0.28**
L 762	-2.88**	1.89	-0.21**	-0.12	4.41**	-0.07**	0.24**	-0.79**
SE (gi)	0.25	1.49	0.03	0.19	0.48	0.02	0.02	0.06
TESTERS								
GSB 40	0.25	5.96**	0.07**	0.33*	-1.05**	0.20**	0.06**	0.28**
DB 16	-1.09**	1.84	-0.09**	0.95**	2.46**	0.16**	0.38**	0.06
DB 11	-0.34	2.00	-0.08**	-0.07	1.42**	0.03*	-0.14**	-0.08
GSB 41	-0.45*	1.50	0.04*	0.69**	2.71**	0.01	0.12**	-0.38**
TCB 37	1.15**	-5.18**	-0.01	-1.24**	-2.95**	-0.13**	-0.16**	0.15**
SUVIN	0.48**	-6.12**	0.07**	-0.66**	-2.59**	-0.27**	-0.26**	-0.03
SE (gi)	0.18	1.05	0.02	0.13	0.34	0.01	0.02	0.04

Table 4.25 (cont.)

Table 4.25 (cont.)

	Ginning out- turn (%)	2.5% span length (mm)	Uniformity ratio	Micronaire value (10 ⁻⁶ g/inch)	Bundle strength (g/tex)	Fibre elongation (%)	Seed cotton yield plant ⁻¹ (g)	Lint yield plant ⁻¹ (g)
LINES								
NDLH 1938	0.65**	-0.92**	0.52**	0.11**	0.17	0.08**	25.23**	8.97**
H 1442	1.21**	-0.24	0.32	0.15**	0.15	-0.01	25.40**	9.87**
ADB 542	0.58**	0.17	0.10	0.14**	-0.23*	0.06**	11.21**	4.16**
ADB 532	-0.80**	0.48**	-0.26	-0.13**	0.82**	0.03	4.22*	-0.47
WGCV 48	0.23	0.01	-0.03	0.12**	-0.06	-0.01	-7.19**	-1.64*
MR 786	0.73**	-1.54**	0.93**	-0.02	-1.15**	-0.01	16.75**	6.08**
TSH 0250	-0.56**	0.42**	-0.79**	-0.13**	0.05	-0.14**	-20.20**	-6.12**
BS 37	-1.84**	0.90**	-0.02	-0.03*	0.34**	0.05*	10.51**	-0.39
SCS 793	-1.73**	-0.54**	0.61**	-0.10**	0.34**	0.02	-7.09**	-5.75**
MCU 5	-2.15**	1.56**	-0.78**	-0.16**	0.42**	-0.11**	-55.60**	-19.40**
L 1058	1.45**	0.76**	-0.55**	-0.07**	0.19	-0.02	-10.81**	-1.00
L 762	2.22**	-1.07**	-0.05	0.12**	-1.03**	0.05*	7.56**	5.69**
SE (gi)	0.14	0.15	0.16	0.01	0.11	0.02	2.03	0.64
TESTERS								
GSB 40	-0.16	0.07	0.36**	0.03**	0.12	0.01	7.58**	2.12**
DB 16	1.35**	-0.06	-0.11	0.08**	0.14	0.09**	16.62**	7.26**
DB 11	-0.38**	-0.74**	0.53**	-0.06**	-0.40**	0.01	4.83**	0.75
GSB 41	1.08**	-0.54**	0.25*	0.03**	-0.08	0.03*	8.90**	4.58**
TCB 37	-0.84**	0.68**	-0.41**	-0.03**	0.11	-0.07**	-15.20**	-6.21**
SUVIN	-1.05**	0.59**	-0.62**	-0.06**	0.12	-0.06**	-22.73**	-8.50**
SE (gj)	0.10	0.10	0.12	0.01	0.08	0.01	1.43	0.45

* Significant at 5% level

**Significant at 1% level

Table 4.29. Estimates of *gca* and *sca* variances for different characters in inter- specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) over three locations (pooled) during *kharif*, 2014-15

	Days to 50% flowering	Plant height (cm)	No. of monopodia plant⁻¹	No. of sympodia plant⁻¹	No. of bolls plant⁻¹	Boll weight (g)	Lint index (g)	Seed index (g)
σ^2_{gca}	0.523*	14.810*	-0.005	0.385*	7.721	0.024*	0.049*	0.058
σ^2_{sca}	2.557**	20.200*	0.041	1.111*	1.740	0.025*	0.058**	-0.122
$\sigma^2_{gca}/\sigma^2_{sca}$	0.204	0.733	-0.121	0.346	4.437	0.96	0.844	-0.475

	Ginning out-turn (%)	2.5% span length (mm)	Micronaire value (10⁻⁶ g/inch)	Bundle strength (g/tex)	Uniformity ratio	Fibre elongation (%)	Seed cotton yield plant⁻¹ (g)	Lint yield plant⁻¹ (g)
σ^2_{gca}	1.000**	0.399**	0.004**	0.025	0.205	0.002**	242.903**	34.949**
σ^2_{sca}	1.615**	0.331**	0.010**	0.564**	0.054	0.008**	178.669*	47.246**
$\sigma^2_{gca}/\sigma^2_{sca}$	0.619	1.205	0.400	0.044	3.796	0.300	1.359	0.739

*Significant at 5% level

**Significant at 1% level

Table 4.26. Specific combining ability effects of 72 inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) for days to 50% flowering, plant height, no. of monopodia plant⁻¹, no. of sympodia plant⁻¹, no. of bolls plant⁻¹ and boll weight over three locations (pooled) during *kharif*, 2014-15

	Days to 50% flowering	Plant height (cm)	No. of monopodia plant ⁻¹	No. of sympodia plant ⁻¹	No. of bolls plant ⁻¹	Boll weight (g)
NDLH 1938 × GSB 40	1.43*	7.70*	0.15*	-0.83	0.01	0.08
NDLH 1938 × DB 16	0.55	-6.17	0.46**	-0.33	-1.39	0.06
NDLH 1938 × DB 11	-2.42**	-20.14**	0.07	-1.48**	-1.55	0.09*
NDLH 1938 × GSB 41	0.69	8.21*	-0.42**	1.22**	2.14	0.03
NDLH 1938 × TCB 37	1.76**	9.36*	-0.07	0.34	4.90**	-0.18**
NDLH 1938 × SUVIN	-2.01**	1.04	-0.18*	1.09*	-4.12**	-0.07
H 1442 × GSB 40	1.80**	7.32*	0.35**	0.06	2.61*	-0.26**
H 1442 × DB 16	-1.85**	-19.10**	-0.34**	2.03**	4.27**	0.16**
H 1442 × DB 11	1.84**	16.57**	0.35**	-0.90	1.66	-0.33**
H 1442 × GSB 41	-5.72**	-0.54	0.08	0.15	0.30	0.54**
H 1442 × TCB 37	0.90	1.33	0.13	-0.78	-6.72**	0.02
H 1442 × SUVIN	3.02**	-5.57	-0.57**	-0.55	-2.12	-0.10*
ADB 542 × GSB 40	0.28	-5.96	-0.78**	-1.88**	6.49**	-0.33**
ADB 542 × DB 16	-1.93**	6.52	0.26**	3.55**	7.25**	0.11*
ADB 542 × DB 11	-0.01	3.08	0.44**	-0.14	1.84	0.32**
ADB 542 × GSB 41	1.43*	0.18	0.02	-0.14	-9.14**	0.17**
ADB 542 × TCB 37	-0.73	4.81	0.18*	0.37	6.06**	-0.14**
ADB 542 × SUVIN	0.95	-8.63*	-0.12	-1.75**	-12.50**	-0.13**
ADB 532 × GSB 40	-2.31**	-0.51	-0.17*	1.79**	4.86**	0.13**
ADB 532 × DB 16	-0.63	19.74**	-0.67**	1.81**	-6.84**	0.14**
ADB 532 × DB 11	-0.94	3.43	0.06	0.64	1.36	-0.07
ADB 532 × GSB 41	1.17	-5.81	0.55**	-2.76**	-2.79*	-0.09*
ADB 532 × TCB 37	2.79**	-11.39**	0.21**	-1.09*	2.89*	-0.16**
ADB 532 × SUVIN	-0.09	-5.45	0.02	-0.39	0.52	0.05
WGCV 48 × GSB 40	-0.77	-1.38	-0.49**	1.46**	-0.73	0.05
WGCV 48 × DB 16	-1.10	9.13*	0.30**	0.88	0.07	-0.03
WGCV 48 × DB 11	-0.29	-0.70	0.14	1.91**	8.23**	-0.07
WGCV 48 × GSB 41	2.04**	-2.03	-0.02	-2.91**	0.70	-0.09*
WGCV 48 × TCB 37	0.11	-3.22	0.26***	0.38	0.52	-0.01
WGCV 48 × SUVIN	0.01	-1.78	-0.19**	-1.74**	-8.79**	0.14**
MR 786 × GSB 40	0.41	5.19	-0.17*	-1.19**	-4.56***	-0.06
MR 786 × DB 16	0.09	-4.15	-0.04	-2.70**	-2.46*	-0.01
MR 786 × DB 11	0.67	-1.31	0.13	-0.76	-0.44	-0.12**
MR 786 × GSB 41	-2.10**	-2.39	-0.11	5.60**	2.73*	0.09*
MR 786 × TCB 37	-1.93**	0.41	-0.05	0.06	4.73**	-0.02
MR 786 × SUVIN	2.86**	2.25	0.24**	-1.00*	0.01	0.13**

Table 4.26 (cont.)

Table 4.26 (cont.)

	Days to 50% flowering	Plant height (cm)	No. of monopodia plant⁻¹	No. of sympodia plant⁻¹	No. of bolls plant⁻¹	Boll weight (g)
TSH 0250 × GSB 40	-4.27**	10.79**	0.74**	1.94**	9.14**	0.86**
TSH 0250 × DB 16	0.40	3.84	0.46**	-1.44**	-0.65	-0.25**
TSH 0250 × DB 11	1.43*	-2.66	-0.44**	1.02*	3.58**	-0.25**
TSH 0250 × GSB 41	1.99**	-6.12	-0.05	-0.17	2.92*	-0.26**
TSH 0250 × TCB 37	1.50*	-8.22*	-0.73**	-0.82	-13.96**	0.01
TSH 0250 × SUVIN	-1.05	2.37	0.02	-0.53	-1.02	-0.11*
BS 37 × GSB 40	2.12**	-6.82	0.18*	0.29	0.58	0.12**
BS 37 × DB 16	-0.87	1.05	-0.03	-0.46	-4.56**	-0.16**
BS 37 × DB 11	0.38	-1.99	-0.17*	-2.08**	-10.99**	0.24**
BS 37 × GSB 41	-1.51*	2.29	-0.09	1.57**	6.86**	-0.03
BS 37 × TCB 37	-0.11	-1.67	0.04	0.58	-6.16**	-0.02
BS 37 × SUVIN	0.01	7.14	0.07	0.11	14.26**	-0.14**
SCS 793 × GSB 40	2.60**	-4.53	-0.23**	-0.17	-9.31**	-0.15**
SCS 793 × DB 16	1.72**	4.85	-0.33**	-2.12**	1.04	0.16**
SCS 793 × DB 11	-1.25*	2.57	0.25**	-0.29	2.80*	0.18**
SCS 793 × GSB 41	-2.03**	1.37	-0.02	-1.13*	3.72**	0.12**
SCS 793 × TCB 37	-1.19	0.65	-0.04	0.49	-4.25**	-0.26**
SCS 793 × SUVIN	0.15	-4.91	0.36**	3.22**	6.00**	-0.05
MCU 5 × GSB 40	1.56*	-3.66	0.58**	0.41	-3.67**	-0.06
MCU 5 × DB 16	-0.43	1.80	0.04	0.14	1.11	0.18**
MCU 5 × DB 11	1.60*	-1.87	-0.53**	0.56	-6.84**	-0.17**
MCU 5 × GSB 41	1.49*	4.97	-0.80**	-1.18*	-0.39	-0.06
MCU 5 × TCB 37	-3.11**	0.15	0.59**	-0.19	5.27**	0.16**
MCU 5 × SUVIN	-1.10	-1.39	0.13	0.25	4.52**	-0.05
L 1058 × GSB 40	-2.42**	-4.28	0.17*	-1.88**	-1.46	-0.24**
L 1058 × DB 16	5.70**	-11.79**	0.11	-0.37	-0.53	-0.24**
L 1058 × DB 11	-1.83**	1.68	-0.42**	0.18	-0.01	0.21**
L 1058 × GSB 41	0.06	-3.56	0.38**	0.47	-1.24	0.11*
L 1058 × TCB 37	0.24	7.58*	-0.15*	0.45	0.74	0.06
L 1058 × SUVIN	-1.75**	10.37**	-0.09	1.14*	2.51*	0.10*
L 762 × GSB 40	-0.44	-3.85	-0.33**	0.10	-3.96**	-0.14**
L 762 × DB 16	-1.65**	-5.73	-0.21**	-0.98*	2.69*	-0.12**
L 762 × DB 11	0.82	1.35	0.12	1.33**	0.37	-0.03
L 762 × GSB 41	2.49**	3.44	0.48**	-0.73	-5.80**	-0.53**
L 762 × TCB 37	-0.23	0.21	-0.36**	0.21	5.96**	0.57**
L 762 × SUVIN	-0.99	4.58	0.30**	0.16	0.73	0.24**
SE (S _{ij})	0.62	3.64	0.07	0.46	1.17	0.04

*Significant at 5% level

**Significant at 1% level

Table 4.27. Specific combining ability effects of 72 inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) for lint index, seed index, ginning out-turn, 2.5% span length, uniformity ratio and micronaire value over three locations (pooled) during *kharif*, 2014-15

	Lint index (g)	Seed index (g)	Ginning out- turn (%)	2.5% span length (mm)	Uniformity ratio	Micronaire value (10 ⁻⁶ g/inch)
NDLH 1938 × GSB 40	-0.05	-0.44**	0.28	-0.08	0.11	0.04
NDLH 1938 × DB 16	-0.34**	0.19	-1.57**	-0.44	0.61	0.22**
NDLH 1938 × DB 11	0.30**	-0.65**	2.42**	-0.28	-0.47	0.23**
NDLH 1938 × GSB 41	0.18**	0.05	0.57	0.02	-0.04	-0.25**
NDLH 1938 × TCB 37	0.35**	0.08	1.43**	0.07	-0.02	-0.28**
NDLH 1938 × SUVIN	-0.43**	0.77**	-3.14**	0.74*	-0.20	0.05
H 1442 × GSB 40	-0.02	0.62**	-0.79*	-0.45	-0.06	0.02
H 1442 × DB 16	-0.27**	-0.37*	-0.51	2.08**	0.29	-0.28**
H 1442 × DB 11	-0.14*	-0.16	-0.31	-0.71	-0.51	-0.10**
H 1442 × GSB 41	0.37**	-0.16	1.67**	-0.18	0.15	0.28**
H 1442 × TCB 37	0.13*	-0.08	0.51	-0.40	0.24	0.02
H 1442 × SUVIN	-0.07	0.14	-0.57	-0.34	-0.10	0.06
ADB 542 × GSB 40	-0.06	0.22	-0.59	-1.08**	-0.32	0.02
ADB 542 × DB 16	0.19**	-0.88**	2.13**	-0.04	0.24	0.33**
ADB 542 × DB 11	-0.18**	0.42**	-1.24**	0.48	-0.05	-0.21**
ADB 542 × GSB 41	0.33**	0.78**	-0.06	0.34	-0.02	-0.18**
ADB 542 × TCB 37	-0.23**	-0.11	-0.80*	-0.69	0.32	-0.12**
ADB 542 × SUVIN	-0.05	-0.41**	0.56	0.99**	-0.17	0.18**
ADB 532 × GSB 40	0.33**	0.53**	0.42	-0.70	0.27	-0.18**
ADB 532 × DB 16	0.36**	0.62**	0.21	0.28	-0.31	0.02
ADB 532 × DB 11	-0.39**	-0.57**	-0.71*	-0.72*	0.33	0.03
ADB 532 × GSB 41	0.04	-0.42**	0.68*	0.64	0.05	-0.04
ADB 532 × TCB 37	-0.37**	-0.18	-0.95**	-0.15	-0.19	0.21**
ADB 532 × SUVIN	0.03	0.02	0.34	0.65	-0.15	-0.05
WGCV 48 × GSB 40	-0.20**	0.18	-0.99**	0.76*	-0.72	-0.04
WGCV 48 × DB 16	-0.28**	0.03	-1.21**	-0.17	-0.34	-0.14**
WGCV 48 × DB 11	0.19**	-0.54**	1.77**	0.16	1.20**	0.09**
WGCV 48 × GSB 41	-0.38**	-0.37*	-0.95**	-0.54	-0.06	0.06
WGCV 48 × TCB 37	0.07	-0.05	0.14	0.53	-0.73	-0.04
WGCV 48 × SUVIN	0.61**	0.76**	1.23**	-0.74*	0.64	0.07*
MR 786 × GSB 40	-0.04	0.16	-0.51	-0.80*	0.25	-0.06
MR 786 × DB 16	0.09	0.15	0.09	-0.24	-0.17	0.03
MR 786 × DB 11	-0.65**	0.01	-2.77**	0.08	-0.74	-0.07*
MR 786 × GSB 41	0.18**	-0.95**	2.29**	0.99**	0.57	0.17**
MR 786 × TCB 37	0.13*	1.18**	-1.23**	0.16	1.26**	0.12**
MR 786 × SUVIN	0.30**	-0.55**	2.13**	-0.19	-1.16**	-0.19**

Table 4.27 (cont.)

Table 4.27 (cont.)

	Lint index (g)	Seed index (g)	Ginning out turn (%)	2.5% span length (mm)	Uniformity ratio	Micronaire value (10 ⁻⁶ g/inch)
TSH 0250 × GSB 40	0.92**	-1.00**	5.17**	1.38**	-0.49	0.25**
TSH 0250 × DB 16	0.06	0.09	0.26	0.18	0.49	0.01
TSH 0250 × DB 11	0.18**	0.85**	-0.43	-0.07	0.36	0.01
TSH 0250 × GSB 41	-0.16**	-0.05	-0.49	-1.50**	-0.17	-0.22**
TSH 0250 × TCB 37	-0.39**	-0.20	-1.32**	0.57	-0.08	0.03
TSH 0250 × SUVIN	-0.62**	0.31*	-3.20**	-0.56	-0.11	-0.06
BS 37 × GSB 40	0.44**	-0.29	2.56**	0.75*	1.16**	-0.01
BS 37 × DB 16	-0.11	0.21	-0.78*	-0.31	-0.76	0.06
BS 37 × DB 11	-0.17**	0.05	-1.01**	0.54	0.16	-0.07*
BS 37 × GSB 41	0.32**	0.74**	0.19	-0.13	-0.12	0.03
BS 37 × TCB 37	-0.32**	0.80**	-2.56**	0.41	-0.44	-0.11**
BS 37 × SUVIN	-0.16**	-1.52**	1.60**	-1.27**	-0.01	0.12**
SCS 793 × GSB 40	-0.47**	-0.56**	-0.62	1.25**	-0.76	0.09**
SCS 793 × DB 16	0.36**	0.14	1.14**	-0.61	0.14	-0.06
SCS 793 × DB 11	0.50**	0.55**	1.10**	0.21	0.25	-0.03
SCS 793 × GSB 41	-0.36**	0.63**	-2.30**	-0.52	0.67	0.03
SCS 793 × TCB 37	0.33**	-0.24	1.62**	0.84*	0.22	0.03
SCS 793 × SUVIN	-0.37**	-0.51**	-0.93**	-1.16**	-0.52	-0.06
MCU 5 × GSB 40	-0.53**	-0.19	-2.17**	0.75*	0.80*	-0.05
MCU 5 × DB 16	0.17**	0.97**	-0.81*	0.16	-0.96*	-0.12**
MCU 5 × DB 11	0.09	-0.76**	1.64**	-1.24**	0.21	-0.01
MCU 5 × GSB 41	0.02	-0.03	0.07	-0.33	-0.01	0.03
MCU 5 × TCB 37	-0.04	-0.55**	0.77*	-0.23	-0.58	0.13**
MCU 5 × SUVIN	0.29**	0.56**	0.50	0.90*	0.54	0.02
L 1058 × GSB 40	0.03	0.75**	-1.18**	-1.00**	0.03	0.01
L 1058 × DB 16	0.07	-0.69**	1.40**	-1.00**	-0.15	-0.10**
L 1058 × DB 11	0.06	0.15	-0.14	0.92*	0.20	0.06
L 1058 × GSB 41	-0.36**	-0.22	-1.07**	0.73*	-0.72	0.06
L 1058 × TCB 37	0.20**	-0.01	0.67*	-0.40	-0.21	-0.04
L 1058 × SUVIN	0.00	0.02	0.32	0.76*	0.85*	0.02
L 762 × GSB 40	-0.35**	0.03	-1.58**	-0.76*	-0.28	-0.07*
L 762 × DB 16	-0.32**	-0.45**	-0.36	0.10	0.93*	0.05
L 762 × DB 11	0.23**	0.64**	-0.32	0.63	-0.94*	0.09**
L 762 × GSB 41	-0.17**	-0.01	-0.58	0.50	-0.31	0.03
L 762 × TCB 37	0.14*	-0.64**	1.71**	-0.69	0.22	0.05
L 762 × SUVIN	0.47**	0.43**	1.13**	0.22	0.38	-0.14**
SE (s _{ij})	0.06	0.16	0.34	0.36	0.40	0.03

*Significant at 5% level

**Significant at 1% level

Table 4.28. Specific combining ability effects of 72 inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) for bundle strength, fibre elongation, seed cotton yield plant⁻¹ and lint yield plant⁻¹ over three locations (pooled) during *kharif*, 2014-15

	Bundle strength (g/tex)	Fibre elongation (%)	Seed cotton yield plant⁻¹ (g)	Lint yield plant⁻¹ (g)
NDLH 1938 × GSB 40	-0.06	0.03	6.26	1.04
NDLH 1938 × DB 16	0.07	0.14**	0.57	-1.97
NDLH 1938 × DB 11	-0.62*	-0.03	-0.14	6.61**
NDLH 1938 × GSB 41	-0.07	-0.09	7.00	2.86
NDLH 1938 × TCB 37	-0.11	-0.15**	1.01	2.19
NDLH 1938 × SUVIN	0.80**	0.10	-14.71**	-10.72**
H 1442 × GSB 40	-0.80**	-0.01	-10.38*	-5.67**
H 1442 × DB 16	2.36**	-0.04	25.28**	7.33**
H 1442 × DB 11	-0.64*	0.05	-16.70**	-5.90**
H 1442 × GSB 41	-0.16	-0.01	34.97**	15.37**
H 1442 × TCB 37	-0.48	-0.11*	-21.01**	-5.39**
H 1442 × SUVIN	-0.27	0.11*	-12.15*	-5.72**
ADB 542 × GSB 40	-1.32**	-0.05	-0.50	-1.63
ADB 542 × DB 16	0.32	0.07	28.56**	14.28**
ADB 542 × DB 11	0.48	-0.11*	24.33**	4.94**
ADB 542 × GSB 41	1.09**	0.03	-19.14**	-6.44**
ADB 542 × TCB 37	-0.88**	-0.07	7.63	-0.07
ADB 542 × SUVIN	0.31	0.13*	-40.88**	-11.08**
ADB 532 × GSB 40	0.23	-0.09	23.70**	8.34**
ADB 532 × DB 16	0.35	0.08	-15.22**	-4.25**
ADB 532 × DB 11	-1.29**	0.03	2.43	-0.68*
ADB 532 × GSB 41	0.73**	0.04	-14.10**	-3.17*
ADB 532 × TCB 37	0.50	0.02	-0.69	-2.35
ADB 532 × SUVIN	-0.52	-0.03	3.89	2.11
WGCV 48 × GSB 40	0.08	-0.05	-3.85	-2.92
WGCV 48 × DB 16	0.27	-0.06	-1.48	-3.38*
WGCV 48 × DB 11	-0.19	0.03	20.56**	9.56**
WGCV 48 × GSB 41	-0.76**	0.12*	-4.52	-3.06*
WGCV 48 × TCB 37	0.45	-0.07	1.42	1.17
WGCV 48 × SUVIN	0.15	0.03	-12.12*	-1.36
MR 786 × GSB 40	-0.78**	-0.11*	-19.65**	-7.62**
MR 786 × DB 16	0.30	0.09	-7.02	-1.48
MR 786 × DB 11	-0.47	-0.23**	-6.70	-7.33**
MR 786 × GSB 41	0.69*	0.20**	14.50**	10.21**
MR 786 × TCB 37	1.18**	0.18**	10.26*	0.90
MR 786 × SUVIN	-0.92**	-0.13*	8.60	5.31**

Table 4.28 (cont.)

Table 4.28 (cont.)

	Bundle strength (g/tex)	Fibre elongation (%)	Seed cotton yield plant⁻¹ (g)	Lint yield plant⁻¹ (g)
TSH 0250 × GSB 40	0.48	0.02	76.56**	33.18**
TSH 0250 × DB 16	0.30	0.16**	-14.42**	-5.33**
TSH 0250 × DB 11	0.18	0.06	-4.08	-3.10*
TSH 0250 × GSB 41	-0.57*	0.02	-7.36	-4.05**
TSH 0250 × TCB 37	-0.09	-0.07	-41.37**	-13.46**
TSH 0250 × SUVIN	-0.30	-0.19**	-9.33	-7.24**
BS 37 × GSB 40	1.78**	0.19**	11.66*	8.00**
BS 37 × DB 16	-1.08**	-0.21**	-22.53**	-8.52**
BS 37 × DB 11	0.42	-0.02	-23.42**	-9.10**
BS 37 × GSB 41	0.44	-0.01	18.96**	5.72**
BS 37 × TCB 37	0.30	0.10*	-13.30**	-6.84**
BS 37 × SUVIN	-1.86**	-0.06	28.63**	10.73**
SCS 793 × GSB 40	-0.14	0.07	-30.63**	-9.40**
SCS 793 × DB 16	-0.62*	-0.03	11.52*	5.26**
SCS 793 × DB 11	1.46**	0.04	16.08**	6.34**
SCS 793 × GSB 41	-0.54	0.01	16.64**	-0.31
SCS 793 × TCB 37	0.10	0.02	-24.02**	-4.15**
SCS 793 × SUVIN	-0.25	-0.11*	10.40*	2.27
MCU 5 × GSB 40	2.61**	0.13*	-17.65**	-7.65**
MCU 5 × DB 16	-0.88**	-0.15**	7.89	0.11
MCU 5 × DB 11	-0.66*	-0.05	-23.98**	-4.60**
MCU 5 × GSB 41	-1.04**	-0.11*	-4.25	-1.43
MCU 5 × TCB 37	-0.72*	0.11*	23.91**	8.28**
MCU 5 × SUVIN	0.69*	0.07	14.08**	5.30**
L 1058 × GSB 40	-1.39**	-0.01	-17.38**	-7.36**
L 1058 × DB 16	-1.19**	-0.10	-13.36**	-1.74
L 1058 × DB 11	0.97**	0.13*	13.11**	4.13**
L 1058 × GSB 41	0.58*	-0.14**	0.53	-1.43
L 1058 × TCB 37	-0.19	0.02	6.59	2.36
L 1058 × SUVIN	1.23**	0.09	10.50*	4.04**
L 762 × GSB 40	-0.69*	-0.13*	-18.14**	-8.31**
L 762 × DB 16	-0.19	0.04	0.22	-0.31
L 762 × DB 11	0.37	0.13*	-1.50	-0.87
L 762 × GSB 41	-0.37	-0.06	-43.25**	-14.25**
L 762 × TCB 37	-0.05	0.02	49.58**	17.38**
L 762 × SUVIN	0.94**	-0.01	13.08**	6.36**
SE (S _{ij})	0.28	0.05	4.98	1.56

*Significant at 5% level

**Significant at 1% level

Table 4.21. Phenotypic (above diagonal) and genotypic (below diagonal) correlations for different characters in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) over three locations (pooled) during *kharif*, 2014-15

Character	Days to 50% flowering	Plant height	No. of monopodia plant ⁻¹	No. of sympodia plant ⁻¹	No. of bolls plant ⁻¹	Boll weight	Lint index	Seed index
Days to 50% flowering	--	-0.0360	-0.0121	-0.1375**	-0.1031**	-0.4391**	-0.0517	0.0581
Plant height	-0.0919*	--	0.2988**	0.6930**	0.6842**	-0.0851*	0.3075**	0.4667**
No. of monopodia plant ⁻¹	-0.0214	0.6043**	--	0.3064**	0.3393**	-0.0223	0.1996**	0.3784**
No. of sympodia plant ⁻¹	-0.2368**	0.8647**	0.5872**	--	0.6713**	-0.0069	0.3232**	0.4553**
No. of bolls plant ⁻¹	-0.2298**	0.8233**	0.5827**	0.8672**	--	-0.0830*	0.2578**	0.3137**
Boll weight	-0.6085**	-0.1332**	-0.1082**	-0.0291**	-0.0814*	--	0.1012**	-0.1321**
Lint index	-0.0641	0.5191**	0.1939**	0.4847**	0.4447**	0.1307**	--	0.4075**
Seed index	0.1921**	0.7469**	0.5851**	0.6457**	0.5363**	-0.3710**	0.3738**	--
Ginning out-turn	-0.2403**	-0.2650**	-0.3864**	-0.2038**	-0.1332**	0.4652**	0.5016**	-0.6123**
2.5% span length	0.3362**	0.6727**	0.5770**	0.5903**	0.5019**	-0.5355**	0.3289**	0.8153**
Uniformity ratio	-0.3074**	-0.5528**	-0.4527**	-0.4414**	-0.3566**	0.5040**	-0.2228**	-0.6799**
Micronaire value	-0.1310**	-0.7752**	-0.5277**	-0.6462**	-0.5906**	0.4036**	-0.2629**	-0.8114**
Bundle strength	0.3613**	0.6495**	0.5155**	0.5841**	0.5474**	-0.5332**	0.3678**	0.7713**
Fibre elongation	0.3037**	0.1387**	0.0625	0.1271**	0.2266**	-0.1702**	0.3103**	0.0514
Lint yield plant ⁻¹	-0.5206**	0.5600**	0.3278**	0.6699**	0.7564**	0.5147**	0.6133**	0.1142**
Seed cotton yield plant ⁻¹ (P)	-0.2890**	0.5815**	0.2957**	0.6027**	0.8539**	0.4115**	0.3146**	0.2382**
Seed cotton yield plant ⁻¹ (G)	-0.4835**	0.6917**	0.4712**	0.7804**	0.8693**	0.4136**	0.5070**	0.3129**

Table 4.21 (cont.)

Table 4.21 (cont.)

Character	Ginning out-turn	2.5% span length	Uniformity ratio	Micronaire value	Bundle strength	Fibre elongation	Lint yield plant ⁻¹
Days to 50% Flowering	-0.1260**	0.2380**	-0.1775**	-0.0977**	0.2373**	0.1570**	-0.3124**
Plant height	-0.2138**	0.4518**	-0.2877**	-0.5493**	0.4425**	0.0585	0.4929**
No. of monopodia plant ⁻¹	-0.1805**	0.3486**	-0.1577**	-0.3602**	0.3139**	0.0405	0.2249**
No. of sympodia plant ⁻¹	-0.1783**	0.3940**	-0.2254**	-0.4663**	0.3913**	0.0343	0.5270**
No. of bolls plant ⁻¹	-0.1000**	0.3194**	-0.1768**	-0.4020**	0.3547**	0.1001**	0.7735**
Boll weight	0.2348**	-0.3753**	0.2927**	0.2670**	-0.3431**	-0.0455	0.4541**
Lint index	0.4747**	0.2503**	-0.1019**	-0.1926**	0.2416**	0.1643**	0.4366**
Seed index	-0.5977**	0.5629**	-0.3162**	-0.5299**	0.5186**	0.0381	0.0476
Ginning out-turn	--	-0.3435**	0.2373**	0.3529**	-0.3052**	0.1072**	0.3238**
2.5% span length	-0.4875**	--	-0.5609**	-0.6567**	0.8456**	0.1105**	0.0519
Uniformity ratio	0.4598**	-0.8612**	--	0.5172**	-0.3935**	0.1815**	0.0251
Micronaire value	0.5370**	-0.8126**	0.7726**	--	-0.5980**	0.1037**	-0.1304**
Bundle strength	-0.4128**	0.9371**	-0.6856**	-0.7591**	--	0.3185**	0.1058**
Elongation	0.2143**	0.1633**	0.1747**	0.0820*	0.3879**	--	0.1211**
Lint yield plant ⁻¹	0.4082**	0.0843*	0.0368	-0.1599**	0.1503**	0.2101**	--
Seed cotton yield plant ⁻¹ (P)	0.0341	0.1476**	-0.0333	-0.2447**	0.2005**	0.0959**	0.9488**
Seed cotton yield plant ⁻¹ (G)	0.1330**	0.2269**	-0.0878*	-0.3394**	0.2781**	0.1664**	0.9566**

*significant at 5% level

**significant at 1% level

Table 4.22. Direct and indirect effects (phenotypic) of yield components on seed cotton yield in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) over three locations (pooled) during *kharif*, 2014-15

Character	Days to 50% flowering	Plant height	No. of monopodia plant ⁻¹	No. of sympodia plant ⁻¹	No. of bolls plant ⁻¹	Boll weight (g)	Lint index (g)	Seed index (g)
Days to 50% Flowering	0.0106	-0.0004	-0.0001	-0.0015	-0.0011	-0.0047	-0.0006	0.0006
Plant height (cm)	0.0001	-0.0020	-0.0006	-0.0014	-0.0014	0.0002	-0.0006	-0.0009
No. of monopodia plant ⁻¹	0.0001	-0.0013	-0.0045	-0.0014	-0.0015	0.0001	-0.0009	-0.0017
No. of sympodia plant ⁻¹	0.0024	-0.0118	-0.0052	-0.0171	-0.0115	0.0001	-0.0055	-0.0078
No. of bolls plant ⁻¹	-0.0299	0.1984	0.0984	0.1946	0.2899	-0.0241	0.0748	0.0909
Boll weight (g)	-0.0695	-0.0135	-0.0035	-0.0011	-0.0131	0.1582	0.0160	-0.0209
Lint index (g)	0.0051	-0.0305	-0.0198	-0.0321	-0.0256	-0.0100	-0.0993	-0.0405
Seed index (g)	0.0073	0.0586	0.0475	0.0571	0.0394	-0.0166	0.0511	0.1255
Ginning out-turn (%)	0.0112	0.0189	0.0160	0.0158	0.0089	-0.0208	-0.0421	0.0530
2.5% span length (mm)	-0.0029	-0.0056	-0.0043	-0.0048	-0.0039	0.0046	-0.0031	-0.0069
Uniformity ratio	-0.0008	0.0013	-0.0007	-0.0010	-0.0008	0.0013	-0.0004	-0.0014
Micronaire value (10 ⁻⁶ g/inch)	0.0002	0.0009	0.0006	0.0008	0.0006	-0.0004	0.0003	0.0009
Bundle strength (g/tex)	0.0058	0.0108	0.0077	0.0096	0.0087	-0.0084	0.0059	0.0127
Fibre elongation (%)	-0.0002	-0.0001	0.0000	0.0000	-0.0001	0.0001	-0.0002	0.000
Lint yield plant ⁻¹ (g)	-0.2284	0.3603	0.1644	0.3852	0.5654	0.3320	0.3192	0.0348
Seed cotton yield plant ⁻¹ (g)	-0.2890**	0.5815**	0.2957**	0.6027**	0.8539**	0.4115**	0.3146**	0.2382**

Table 4.22 (cont.)

Table 4.22 (cont.)

Character	Ginning out-turn (%)	2.5% span length (mm)	Uniformity ratio	Micronaire value (10 ⁻⁶ g/inch)	Bundle strength (g/tex)	Fibre elongation (%)	Lint yield plant ⁻¹ (g)
Days to 50 % Flowering	-0.0013	0.0025	-0.0019	-0.0010	0.0025	0.0017	-0.0033
Plant height (cm)	0.0004	-0.0009	0.0006	0.0011	-0.0009	-0.0001	-0.0010
No. of monopodia plant ⁻¹	0.0008	-0.0016	0.0007	0.0016	-0.0014	-0.0002	-0.0010
No. of sympodia plant ⁻¹	0.0030	-0.0067	0.0039	0.0080	-0.0067	-0.0006	-0.0090
No. of bolls plant ⁻¹	-0.0290	0.0926	-0.0512	-0.1165	0.1028	0.0290	0.2242
Boll weight (g)	0.0371	-0.0594	0.0463	0.0422	-0.0543	-0.0072	0.0718
Lint index (g)	-0.0471	-0.0249	0.0101	0.0191	-0.0240	-0.0163	-0.0434
Seed index (g)	-0.0750	0.0706	-0.0397	-0.0665	0.0651	0.0048	0.0060
Ginning out-turn (%)	-0.0886	0.0304	-0.0210	-0.0313	0.0270	-0.0095	-0.0287
2.5% span length (mm)	0.0042	-0.0123	0.0069	0.0081	-0.0104	-0.0014	-0.0006
Uniformity ratio	0.0010	-0.0025	0.0044	0.0023	-0.0017	0.0008	0.0001
Micronaire value (10 ⁻⁶ g/inch)	-0.0006	0.0011	-0.0008	-0.0016	0.0010	-0.0002	0.0002
Bundle strength (g/tex)	-0.0075	0.0207	-0.0096	-0.0146	0.0244	0.0078	0.0026
Fibre elongation (%)	-0.0001	-0.0001	-0.0002	-0.0001	-0.0004	-0.0012	-0.0001
Lint yield plant ⁻¹ (g)	0.2367	0.0380	0.0184	-0.0953	0.0774	0.0885	0.7310
Seed cotton yield plant ⁻¹ (g)	0.0341	0.1476**	-0.0333	-0.2447**	0.2005**	0.0959**	0.9488**

Residual effect = 0.104

*Significant at 5% level

**Significant at 1% level

Note: Bold and diagonal values indicate direct effects

Table 4.23. Direct and indirect effects (genotypic) of yield components on seed cotton yield in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) over three locations (pooled) during *kharif*, 2014-15

Character	Days to 50% flowering	Plant height (cm)	No. of monopodia plant ⁻¹	No. of sympodia plant ⁻¹	No. of bolls plant ⁻¹	Boll weight (g)	Lint index(g)	Seed index (g)
Days to 50% Flowering	0.0178	-0.0016	-0.0004	-0.0042	-0.0041	-0.0108	-0.0011	0.0034
Plant height (cm)	-0.0021	0.0227	0.0137	0.0196	0.0187	-0.0030	0.0118	0.0169
No. of monopodia plant ⁻¹	0.0004	-0.0104	-0.0173	-0.0101	-0.0101	0.0019	-0.0033	-0.0101
No. of sympodia plant ⁻¹	0.0068	-0.0248	-0.0169	-0.0287	-0.0249	0.0008	-0.0139	-0.0185
No. of bolls plant ⁻¹	-0.1227	0.4394	0.3110	0.4629	0.5337	-0.0434	0.2374	0.2863
Boll weight (g)	-0.1812	-0.0397	-0.0322	-0.0087	-0.0242	0.2977	0.0389	-0.1105
Lint index(g)	0.0067	-0.0540	-0.0202	-0.0504	-0.0462	-0.0136	-0.1040	-0.0389
Seed index(g)	0.0209	0.0814	0.0638	0.0704	0.0585	-0.0404	0.0408	0.1090
Ginning out-turn (%)	-0.0009	-0.0010	-0.0015	-0.0008	-0.0005	0.0018	0.0019	-0.0024
2.5% span length (mm)	0.0190	0.0380	0.0326	0.0334	0.0284	-0.0303	0.0186	0.0461
Uniformity ratio	-0.0082	-0.0147	-0.0120	-0.0117	-0.0095	0.0134	-0.0059	-0.0180
Micronaire value (10 ⁻⁶ g/inch)	-0.0021	-0.0122	-0.0083	-0.0102	-0.0093	0.0064	-0.0041	-0.0128
Bundle strength (g/tex)	0.0043	0.0077	0.0061	0.0069	0.0065	-0.0063	0.0044	0.0092
Fibre elongation (%)	0.0002	0.0001	0.0000	0.0001	0.0001	-0.0001	0.0002	0.000
Lint yield plant ⁻¹ (g)	-0.2424	0.2608	0.1526	0.3120	0.3523	0.2397	0.2856	0.0532
Seed cotton yield plant ⁻¹ (g)	-0.4835**	0.6917**	0.4712**	0.7804**	0.8693**	0.4136**	0.5070**	0.3129**

Table 4.23 (cont.)

Table 4.23 (cont.)

Character	Ginning out-turn (%)	2.5% span length (mm)	Uniformity ratio	Micronaire value (10 ⁻⁶ g/inch)	Bundle strength (g/tex)	Fibre elongation (%)	Lint yield plant ⁻¹ (g)
Days to 50% Flowering	-0.0043	0.0060	-0.0055	-0.0023	0.0064	0.0054	-0.0093
Plant height (cm)	-0.0060	0.0152	-0.0125	-0.0176	0.0147	0.0031	0.0127
No. of monopodia plant ⁻¹	0.0067	-0.0100	0.0078	0.0091	-0.0089	-0.0011	-0.0057
No. of sympodia plant ⁻¹	0.0059	-0.0170	0.0127	0.0186	-0.0168	-0.0036	-0.0192
No. of bolls plant ⁻¹	-0.0711	0.2679	-0.1903	-0.3152	0.2922	0.1210	0.4038
Boll weight (g)	0.1385	-0.1594	0.1501	0.1202	-0.1588	-0.0507	0.1532
Lint index (g)	-0.0521	-0.0342	0.0232	0.0273	-0.0382	-0.0323	-0.0638
Seed index (g)	-0.0668	0.0889	-0.0741	-0.0885	0.0841	0.0056	0.0125
Ginning out-turn (%)	0.0038	-0.0019	0.0018	0.0021	-0.0016	0.0008	0.0016
2.5% span length (mm)	-0.0275	0.0565	-0.0487	-0.0459	0.0530	0.0092	0.0048
Uniformity ratio	0.0122	-0.0229	0.0265	0.0205	-0.0182	0.0046	0.0010
Micronaire value (10 ⁻⁶ g/inch)	0.0085	-0.0128	0.0122	0.0157	-0.0119	0.0013	-0.0025
Bundle strength (g/tex)	-0.0049	0.0111	-0.0081	-0.0090	0.0119	0.0046	0.0018
Fibre elongation (%)	0.0001	0.0001	0.0001	0.0000	0.0002	0.0006	0.0001
Lint yield plant ⁻¹ (g)	0.1901	0.0392	0.0171	-0.0745	0.0700	0.0978	0.4657
Seed cotton yield plant ⁻¹ (g)	0.1330**	0.2269**	-0.0878*	-0.3394**	0.2781**	0.1664**	0.9566**

Residual effect = 0.021

* Significant at 5% level

**Significant at 1% level

Note: Bold and diagonal values indicate direct effects

Table 4.51. Estimates of $\mu G'$ in the donor parents for 2.5% span length and bundle strength combined over environments, when the hybrid NDLH 1938 $\times$ MCU 5 was designated as the hybrid to be improved

Parent	$\mu G'$							
	RARS, Lam Farm		ARS, J M Puram		Agricultural College Farm, Bapatla		Pooled	
	2.5% span length (mm)	Bundle strength (g/tex)	2.5% span length (mm)	Bundle strength (g/tex)	2.5% span length (mm)	Bundle strength (g/tex)	2.5% span length (mm)	Bundle strength (g/tex)
GSB 40	2.342 ^{a*}	1.940 ^{a*}	N	N	3.530 ^{c*}	5.305 ^{c*}	3.097 ^{c*}	3.552 ^{c*}
DB 16	2.365 ^{a*}	1.015 ^{b*}	N	N	2.470 ^{c*}	2.045 ^{c*}	2.757 ^{c*}	2.000 ^{b*}
DB 11	1.550 ^{c*}	0.355 ^b	N	N	N	N	1.748 ^{c*}	1.545 ^{b*}
GSB 41	2.557 ^{a*}	1.370 ^{b*}	N	N	2.240 ^{c*}	N	2.267 ^{c*}	1.767 ^{b*}
TCB 37	2.622 ^{a*}	1.315 ^{a*}	N	N	3.075 ^{c*}	N	2.852 ^{c*}	1.887 ^{b*}
SUVIN	3.437 ^{a*}	2.022 ^{a*}	4.072 ^{c*}	N	N	N	3.467 ^{c*}	2.587 ^{c*}
SE a	0.247	0.224	-	-	-	-	-	-
SE b	-	0.224	-	-	-	-	-	0.238
SE c	0.294	-	0.266	-	0.339	0.316	0.301	0.297
SE d	-	-	-	-	-	-	-	-

* Larger than $2 \times SE$; N = $\mu G'$ values could not obtained

a = q_{j0} , q_{kl}

b = q_{j1} , q_{k0}

c = q_{j0} , q_{j1}

d = q_{k0} , q_{k1}

Table 4.52. Estimates of $\mu B'$ $\mu G'$ for 2.5% span length in six donor parents when NDLH 1938 $\times$ MCU 5 is the hybrid to be improved

Class of loci											
Parents	$\mu B'$	$\mu C'$	$\mu D'$	$\mu E'$	$\mu F'$	$\mu G'$	$\mu C+F'$	$\mu D+E'$	Genetic affinity with	Mean <i>per se</i> of NDLH 1938 $\times$ donor	Mean <i>per se</i> of MCU 5 $\times$ donor
GSB 40	0.477	-0.062	-0.062	-0.097	1.417*	3.097*	1.355*	-0.160	NDLH 1938	32.98	37.79
DB 16	0.252	-0.062	-0.062	-0.152	1.472*	2.757*	1.410*	-0.215	NDLH 1938	33.69	35.67
DB 11	0.132	-0.062	-0.062	0.682	0.638	1.748*	0.575	0.620	MCU 5	32.82	33.69
GSB 41	-0.782	-0.062	-0.062	0.408	0.912*	2.267*	0.850	0.345	NDLH 1938	32.76	34.91
TCB 37	-0.608	-0.062	-0.062	0.387	0.933*	2.852*	0.870*	0.325	NDLH 1938	34.93	37.02
SUVIN	0.112	-0.062	-0.062	0.023	1.298*	3.467*	1.235*	-0.040	NDLH 1938	35.92	38.10

@ Mean *per se* of the cross NDLH 1938 $\times$ MCU 5 is: 28.63

* Larger than 2 $\times$ S.E.

Table 4.53. Estimates of $\mu B'$ $\mu G'$ for bundle strength in six donor parents when NDLH 1938 $\times$ MCU 5 is the hybrid to be improved

Class of loci											
Parents	$\mu B'$	$\mu C'$	$\mu D'$	$\mu E'$	$\mu F'$	$\mu G'$	$\mu C+F'$	$\mu D+E'$	Genetic affinity with	Mean <i>per se</i> of NDLH 1938 $\times$ donor	Mean <i>per se</i> of MCU 5 $\times$ donor
GSB 40	0.108	0.283	0.283	-1.108	1.807*	3.552*	2.090*	-0.825	NDLH 1938	26.75	30.67
DB 16	-0.535	0.090	0.475	0.610	0.090	2.000*	0.180	1.085*	MCU 5	27.90	27.20
DB 11	-0.415	0.210	0.355	0.490	0.210	1.545*	0.420	0.845*	MCU 5	25.76	25.88
GSB 41	-1.223	0.043	0.523*	0.657*	0.043	1.767*	0.085	1.180*	MCU 5	26.84	26.12
TCB 37	-1.628	0.198	0.368	0.502	0.198	1.887*	0.395	0.870*	MCU 5	27.79	27.12
SUVIN	-0.653	0.283	0.283	0.318	0.382	2.587*	0.665	0.600	NDLH 1938	28.61	28.85

@ Mean *per se* of the cross NDLH 1938 $\times$ MCU 5 is: 22.89

* Larger than $2 \times$ S.E.

Table 4.30. Good general combiners of lines and testers for different characters from the pooled analysis in cotton during *kharif*, 2014-15

Parents	Days to 50 % flowering	Plant height (cm)	No. of monopodia plant ⁻¹	No. of sympodia plant ⁻¹	No. of bolls plant ⁻¹	Boll weight (g)	Lint index (g)	Seed index (g)
Lines								
NDLH 1938	+	+		+	+	+		
H 1442	+			+	+	+	+	
ADB 542		+	+		+	+		
ADB 532			+			+	+	+
WGCV 48			+					
MR 786		+		+	+	+	+	+
TSH 0250								
BS 37			+		+	+		
SCS 793				+	+			+
MCU 5								+
L 1058			+				+	+
L 762	+				+		+	
Testers								
GSB 40			+	+		+	+	+
DB 16	+			+	+	+	+	
DB 11					+	+		
GSB 41	+		+	+	+		+	
TCB 37		+						+
SUVIN		+	+					

Table 4.30 (cont.)

Table 4.30 (cont.)

Parents	Ginning out-turn (%)	2.5% span length (mm)	Uniformity ratio	Micronaire value (10 ⁻⁶ g/inch)	Bundle strength (g/tex)	Fibre elongation (%)	Seed cotton yield plant ⁻¹ (g)	Lint yield plant ⁻¹ (g)
Lines								
NDLH 1938	+		+	+		+	+	+
H 1442	+			+			+	+
ADB 542	+			+		+	+	+
ADB 532		+			+		+	
WGCV 48				+				
MR 786	+		+				+	+
TSH 0250		+						
BS 37		+			+	+	+	
SCS 793			+		+			
MCU 5		+			+			
L 1058	+	+						
L 762	+			+		+	+	+
Testers								
GSB 40			+	+			+	+
DB 16	+			+		+	+	+
DB 11			+				+	
GSB 41	+		+	+		+	+	+
TCB 37		+						
SUVIN		+						

+ indicates good general combiners

Table 4.49. Stable inter-specific cotton hybrids for different characters as per Eberhart and Russell and AMMI models during *kharif*, 2014-15

Character	Eberhart & Russell model	AMMI model
Days to 50% flowering	MR 786 × DB 11, L 762 × TCB 37	H 1442 × DB 16, H 1442 × GSB 41, ADB 542 × DB 16, ADB 532 × DB 11, TSH 0250 × GSB 40, L 762 × TCB 37
Plant height (cm)	NDLH 1938 × DB 16, BS 37 × DB 16, SCS 793 × DB 16, L 762 × SUVIN	NDLH 1938 × TCB 37, H 1442 × DB 11, ADB 542 × TCB 37, BS 37 × DB 16, SCS 793 × DB 16, L 762 × SUVIN
No. of monopodia plant ⁻¹	---	H 1442 × DB 11, ADB 542 × GSB 41, ADB 542 × SUVIN, WGCV 48 × SUVIN, TSH 0250 × GSB 40, BS 37 × DB 16, BS 37 × TCB 37, BS 37 × SUVIN, SCS 793 × SUVIN, MCU 5 × GSB 40
No. of sympodia plant ⁻¹	NDLH 1938 × SUVIN, L 1058 × DB 11	NDLH 1938 × SUVIN, H 1442 × GSB 40, ADB 532 × DB 16, MR 786 × DB 11
No. of bolls plant ⁻¹	H 1442 × DB 11, L 762 × TCB 37	NDLH 1938 × DB 11, NDLH 1938 × GSB 41, H 1442 × DB 11, ADB 532 × DB 11, TSH 0250 × GSB 41, L 762 × TCB 37
Boll weight (g)	---	NDLH 1938 × GSB 40, NDLH 1938 × DB 16, NDLH 1938 × GSB 41, H 1442 × DB 16, H 1442 × GSB 41, ADB 542 × DB 16, ADB 542 × DB 11, ADB 532 × GSB 40, ADB 532 × DB 16, ADB 532 × DB 11, ADB 532 × GSB 41, MR 786 × DB 11, MR 786 × GSB 41, MR 786 × TCB 37, MR 786 × SUVIN, BS 37 × DB 16, BS 37 × GSB 41, MCU 5 × DB 16, L 1058 × DB 11, L 1058 × GSB 41
Lint index (g)	---	NDLH 1938 × DB 16, NDLH 1938 × DB 11, H 1442 × TCB 37, ADB 532 × GSB 41, ADB 532 × SUVIN, WGCV 48 × DB 16, WGCV 48 × DB 11, MR 786 × TCB 37, L 1058 × DB 11, L 1058 × SUVIN, L 762 × DB 11, L 762 × GSB 41
Seed index (g)	WGCV 48 × TCB 37, MR 786 × DB 11	MR 786 × DB 11, BS 37 × GSB 41, BS 37 × TCB 37, SCS 793 × DB 16, SCS 793 × GSB 41, MCU 5 × DB 16, L 1058 × GSB 40
Ginning out-turn (%)	NDLH 1938 × GSB 41	NDLH 1938 × GSB 41, ADB 542 × GSB 41, WGCV 48 × SUVIN, L 1058 × SUVIN, L 762 × GSB 40, L 762 × GSB 41
2.5% span length (mm)	SCS 793 × GSB 40, ADB 532 × TCB 37	NDLH 1938 × SUVIN, H 1442 × TCB 37, ADB 542 × TCB 37, SCS 793 × GSB 40, MCU 5 × GSB 40
Uniformity ratio	---	NDLH 1938 × DB 11, ADB 542 × DB 11, ADB 542 × GSB 41, ADB 532 × GSB 40, ADB 532 × DB 11

Table 4.49 (cont.)

Table 4.49 (cont.)

Bundle strength (g/tex)	ADB 542 × SUVIN, ADB 532 × GSB 41, WGCV 48 × DB 16, TSH 0250 × DB 16, SCS 793 × GSB 40	NDLH 1938 × GSB 41, ADB 542 × SUVIN, ADB 532 × GSB 41, ADB 532 × SUVIN, WGCV 48 × GSB 40, WGCV 48 × DB 16, WGCV 48 × TCB 37, BS 37 × TCB 37, SCS 793 × GSB 40, MCU 5 × GSB 40, L 1058 × DB 11, L 1058 × GSB 41
Fibre elongation (%)	NDLH 1938 × GSB 41, H 1442 × GSB 41, ADB 542 × GSB 41, MR 786 × TCB 37	NDLH 1938 × DB 16, NDLH 1938 × GSB 41, WGCV 48 × DB 11, BS 37 × GSB 41, L 1058 × DB 11
Micronaire value (10 ⁻⁶ g/inch)	ADB 532 × TCB 37, L 1058 × GSB 41	ADB 542 × GSB 41, ADB 532 × TCB 37, SCS 793 × GSB 40, L 762 × GSB 41
Seed cotton yield plant ⁻¹ (g)	ADB 542 × GSB 41	NDLH 1938 × GSB 41, ADB 542 × GSB 41, ADB 532 × DB 16, WGCV 48 × DB 16, MR 786 × DB 16, MR 786 × SUVIN, TSH 0250 × GSB 40, SCS 793 × DB 11
Lint yield plant ⁻¹ (g)	NDLH 1938 × GSB 41, ADB 542 × GSB 41	NDLH 1938 × GSB 41, ADB 542 × GSB 41, WGCV 48 × DB 16, MR 786 × DB 16, BS 37 × GSB 41, SCS 793 × DB 11, L 762 × DB 11

Table 4.37. The best heterotic inter-specific cotton hybrids identified for different characters based on overall performance over three locations during *kharif*, 2014-15

Character	hybrids	<i>Per se</i> performance	SCA effect	Standard heterosis	
				DCH 32	Mahalakshmi
Days to 50% flowering	H 1442 × GSB 41	55.67	-5.72**	-7.22**	-7.73**
	L 762 × DB 16	58.11	-1.65**	-3.15*	-3.68*
Plant height (cm)	NDLH 1938 × GSB 40	194.54	7.70*	21.36**	8.70**
	NDLH 1938 × GSB 41	190.59	8.21*	18.90**	6.50*
	H 1442 × DB 11	189.85	16.57**	18.44**	6.08*
No. of monopodia plant ⁻¹	ADB 532 × GSB 41	3.20	0.55*	87.94**	16.86**
	BS 37 × GSB 40	3.18	0.18*	86.96**	16.25**
	WGCV 48 × TCB 37	3.03	0.26**	78.23**	10.82**
No. of sympodia plant ⁻¹	MR 786 × GSB 41	31.43	5.60**	36.96**	22.97**
	ADB 542 × DB 16	28.02	3.55**	22.12**	9.64**
	H 1442 × DB 16	27.29	2.03**	18.96**	6.81**
No. of bolls plant ⁻¹	BS 37 × SUVIN	79.98	14.26**	30.09**	10.43**
	H 1442 × DB 16	78.91	4.27**	28.34**	8.95**
	BS 37 × GSB 41	77.89	6.86**	26.69**	7.54**
Boll weight (g)	TSH 0250 × GSB 40	4.21	0.86**	23.29**	11.63**
	H 1442 × GSB 41	3.97	0.54**	16.14**	5.15**
	ADB 532 × GSB 40	3.84	0.13**	12.39**	1.77
Lint index (g)	ADB 532 × DB 16	6.02	0.36**	18.69**	2.71
	TSH 0250 × GSB 40	5.93	0.92**	17.06**	1.31
Seed index (g)	ADB 532 × GSB 40	14.34	0.53**	24.59**	3.73*
	ADB 532 × DB 16	14.22	0.62**	23.57**	2.88
	MR 786 × TCB 37	14.19.	1.18**	23.33**	2.68

Table 4.37 (cont.)

Table 4.37 (cont.)

Character	hybrids	Per se performance	SCA effect	Standard heterosis	
				DCH 32	Mahalakshmi
Ginning out-turn (%)	TSH 0250 × GSB 40	33.49	5.17**	9.43**	11.92**
	L 1058 × DB 16	33.24	1.40**	8.61**	11.07**
	MR 786 × GSB 41	33.13.	2.29**	8.27**	10.73**
2.5% span length (mm)	MCU 5 × SUVIN	37.97	0.90*	12.30**	10.36**
	MCU 5 × GSB 40	37.29	0.75*	10.29**	8.39**
	L 1058 × SUVIN	37.02	0.76*	9.51**	7.62**
Uniformity ratio	MR 786 × TCB 37	47.50	1.26**	4.41**	1.36
	WGCV 48 × DB 11	47.42	1.20**	4.22**	1.18
	BS 37 × GSB 40	47.22	1.16**	3.79**	0.77
Micronaire value (10 ⁻⁶ g/inch)	ADB 542 × DB 16	3.40	0.33**	34.06**	10.94**
	H 1442 × GSB 41	3.32	0.28**	30.65**	8.12**
	NDLH 1938 × DB 16	3.26	0.22**	28.28**	6.16**
Bundle strength (g/tex)	MCU 5 × GSB 40	30.17	2.61**	17.50**	13.80**
	H 1442 × DB 16	29.66	2.36**	15.51**	11.87**
	BS 37 × GSB 40	29.26	1.78**	10.35**	2.18
Fibre elongation (%)	NDLH 1938 × DB 16	5.25	0.14**	13.26**	6.66**
	BS 37 × GSB 40	5.19	0.19**	12.09**	5.56**
	MR 786 × GSB 41	5.15	0.20**	11.20**	4.72**
Seed cotton yield plant ⁻¹ (g)	H 1442 × GSB 41	253.36	34.97**	45.61**	27.18**
	H 1442 × DB 16	251.38	25.28**	44.47**	26.18**
	TSH 0250 × GSB 40	248.02	75.56**	42.54**	24.50**
Lint yield plant ⁻¹ (g)	H 1442 × GSB 41	83.71	15.37**	57.03**	40.36**
	TSH 0250 × GSB 40	83.08	33.18**	55.85**	39.31**
	ADB 542 × DB 16	79.60	14.28**	49.32**	33.47*8

*Significant at 5% level

**Significant at 1% level

Table 4.50. List of superior and stable inter-specific hybrids for different characters during *kharif*, 2014-15

Character	Hybrid (s)
Plant height (cm)	BS 37 × DB 16, SCS 793 × DB 16, L 762 × SUVIN
No. of sympodia plant ⁻¹	L 762 × SUVIN
No. of bolls plant ⁻¹	H 1442 × DB 11
Seed index (g)	MR 786 × DB 11
2.5% span length (mm)	SCS 793 × GSB 40
Bundle strength (g/tex)	ADB 542 × SUVIN, ADB 532 × GSB 41, WGCV 48 × DB 16
Micronaire value (10 ⁻⁶ g/inch)	ADB 532 × TCB 37
Lint yield plant ⁻¹ (g)	NDLH 1938 × GSB 41

Table 4.31. Percentage of heterosis over mid parent, better parent and standard checks for days to 50% flowering, plant height and number of monopodia plant⁻¹ in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) over three locations (pooled) during kharif, 2014-15

Hybrid	Days to 50% flowering				Plant height (cm)				No. of monopodia plant ⁻¹			
	Mid	Better	Standard checks		Mid	Better	Standard checks		Mid	Better	Standard checks	
			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi
NDLH 1938 × GSB 40	-4.03**	-13.50**	7.96**	7.37**	39.44**	32.01**	21.36**	8.70**	44.78**	25.97**	36.90**	-14.88**
NDLH 1938 × DB 16	-5.30**	-13.12**	4.26**	3.68*	27.89**	22.25**	10.13**	-1.36	52.35**	31.47**	45.70**	-9.40*
NDLH 1938 × DB 11	-10.84**	-19.79**	0.56	0.00	19.78**	16.20**	1.53	-9.06**	23.79**	3.54	23.79**	-23.02**
NDLH 1938 × GSB 41	-3.23**	-10.52**	5.56**	4.97**	35.86**	28.00**	18.90**	6.50*	20.65**	14.78*	2.28	-36.40**
NDLH 1938 × TCB 37	-1.57	-10.81**	10.00**	9.39**	44.12**	40.55**	15.45**	3.40	59.46**	48.54**	19.49**	-25.70**
NDLH 1938 × SUVIN	-6.34**	-13.71**	2.59	2.03	32.17**	30.85**	9.67**	-1.77	36.75**	28.64**	17.41**	-27.00**
H 1442 × GSB 40	-0.61	-14.69**	6.48**	5.89**	39.45**	25.23**	15.14**	3.13	44.90**	41.99**	54.30**	-4.05
H 1442 × DB 16	-6.28**	-18.21**	-1.85	-2.39	17.70**	6.66	-3.91	-13.94**	-2.91	-5.76	4.43	-35.06**
H 1442 × DB 11	-1.72	-15.81**	5.56**	4.97**	47.53**	35.55**	18.44**	6.08*	29.82**	21.54**	45.31**	-9.65*
H 1442 × GSB 41	-10.54**	-21.35**	-7.22**	-7.73**	29.40**	15.67**	7.45*	-3.76	41.35**	31.06**	36.70**	-15.00**
H 1442 × TCB 37	0.09	-13.66**	6.48**	5.89**	38.11**	33.79**	4.45	-6.45*	57.60**	31.25**	36.90**	-14.88**
H 1442 × SUVIN	4.53**	-8.41**	8.89**	8.29**	26.83**	18.79**	-0.44	-10.82**	2.27	-4.12	0.00	-37.82**
ADB 542 × GSB 40	-6.38**	-12.91**	8.70**	8.10**	35.30**	18.66**	9.10**	-2.29	5.45	-1.92	6.58	-33.73**
ADB 542 × DB 16	-9.61**	-14.35**	2.78	2.21	43.41**	26.89**	14.31**	2.38	55.46**	43.29**	58.80**	-1.26
ADB 542 × DB 11	-7.88**	-14.48**	7.22**	6.63**	43.29**	28.49**	12.27**	0.56	59.18**	41.82**	69.56**	5.43
ADB 542 × GSB 41	-2.88*	-7.22**	9.44**	8.84**	35.79**	18.57**	10.15**	-1.34	66.58**	62.69**	52.09**	-5.43
ADB 542 × TCB 37	-5.94**	-12.01**	8.52**	7.92**	47.72**	39.45**	8.87**	-2.49	94.72**	69.67**	58.60**	-1.38
ADB 542 × SUVIN	-2.62*	-7.32**	10.19**	9.58**	30.46**	19.19**	-0.10	-10.52**	57.66**	55.79**	45.63**	-9.44*
ADB 532 × GSB 40	-8.20**	-17.80**	2.59	2.03	26.30**	16.57**	7.18*	-4.00	36.03**	35.99**	47.78**	-8.11*
ADB 532 × DB 16	-5.67**	-14.04**	3.15*	2.58	39.68**	30.14**	17.24**	5.01	-0.89	-1.88	8.74	-32.39*
ADB 532 × DB 11	-7.27**	-17.13**	3.89**	3.31*	29.77**	22.65**	7.16*	-4.02	33.31**	27.21**	52.09**	-5.43
ADB 532 × GSB 41	-1.03	-9.11**	7.22**	6.63**	18.45**	8.82*	1.09	-9.46**	90.11**	73.05**	87.94**	16.86**
ADB 532 × TCB 37	1.42	-8.71**	12.59**	11.97**	19.91**	19.69**	-6.56*	-16.31**	85.57**	52.10**	65.19**	2.72
ADB 532 × SUVIN	-1.96	-10.28**	6.67**	6.08**	19.50**	15.20**	-3.44	-13.51**	58.84**	46.16**	58.74**	-1.30

Table 4.31 (cont.)

Table 4.31 (cont.)

Hybrid	Days to 50% flowering				Plant height (cm)				No. of monopodia plant ⁻¹			
	Mid	Better	Standard checks		Mid	Better	Standard checks		Mid	Better	Standard checks	
			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi
WGCV 48 × GSB 40	-7.47**	-15.43**	5.56**	4.97**	23.48**	14.34**	5.12	-5.85*	21.85**	16.30**	39.05**	-13.54**
WGCV 48 × DB 16	-7.96**	-14.35**	2.78	2.21	29.57**	21.11**	9.11**	-2.28	52.86**	47.27**	76.08**	9.49*
WGCV 48 × DB 11	-7.85**	-15.95**	5.37**	4.79**	24.41**	17.97**	3.07	-7.68**	40.02**	40.02**	67.41**	4.09
WGCV 48 × GSB 41	-1.42	-7.54**	9.07**	8.47**	19.06**	9.73**	1.93	-8.70**	58.26**	38.11**	65.12**	2.68
WGCV 48 × TCB 37	-4.25**	-12.01**	8.52**	7.92**	24.07**	23.86**	-2.98	-13.10**	88.62**	49.07**	78.23**	10.82**
WGCV 48 × SUVIN	-3.50**	-9.81**	7.22**	6.63**	20.06**	16.13**	-2.67	-12.82**	48.48**	30.92**	56.52**	-2.68
MR 786 × GSB 40	-4.71**	-14.39**	6.85**	6.26**	38.30**	28.96**	18.57**	6.20*	20.36**	17.94**	28.16**	-20.31**
MR 786 × DB 16	-5.15**	-13.27**	4.07**	3.50*	29.90**	22.29**	10.17**	-1.32	17.21**	13.76*	26.08**	-21.61**
MR 786 × DB 11	-5.44**	-15.21**	6.30**	5.71**	34.25**	28.23**	12.04**	0.35	22.36**	14.56**	36.96**	-14.84**
MR 786 × GSB 41	-6.64**	-13.97**	1.48	0.92	28.82**	19.55**	11.06**	-0.53	34.75**	24.94**	30.31**	-18.97**
MR 786 × TCB 37	-6.23**	-15.32**	4.44**	3.87**	37.86**	36.59**	8.63**	-2.70	50.09**	25.00**	30.38**	-18.93**
MR 786 × SUVIN	1.95	-6.39**	11.30**	10.68**	33.70**	30.28**	9.20**	-2.19	55.47**	45.75**	52.02**	-5.47
TSH 0250 × GSB 40	-11.50**	-20.62**	-0.93	-1.47	35.04**	27.90**	17.59**	5.32	86.14**	61.97**	76.01**	9.44*
TSH 0250 × DB 16	-4.48**	-12.81**	4.63**	4.05**	28.47**	22.85**	10.68**	-0.87	56.78**	35.29**	49.93**	-6.77
TSH 0250 × DB 11	-4.13**	-14.18**	7.59**	7.00**	25.87**	22.14**	6.73*	-4.41	-2.28	-18.27**	-2.28	-39.24**
TSH 0250 × GSB 41	-0.17	-8.16**	8.33**	7.73**	19.07**	12.23**	4.25	-6.62*	51.33**	43.96**	28.29**	-20.23**
TSH 0250 × TCB 37	-0.92	-10.66**	10.19**	9.58**	23.26**	20.15**	-1.22	-11.53**	13.18	5.43	-15.19*	-47.26**
TSH 0250 × SUVIN	-3.82**	-11.84**	4.81**	4.24**	26.24**	25.03**	4.80	-6.14*	55.73**	46.50**	33.70**	-16.86**
BS 37 × GSB 40	-1.21	-8.90**	13.70**	13.08**	19.24**	15.54**	6.23	-4.85	59.29**	48.29**	86.96**	16.25**
BS 37 × DB 16	-5.51**	-11.27**	6.48**	5.89**	23.14**	20.51**	8.56**	-2.76	39.46**	31.02**	65.19**	2.72
BS 37 × DB 11	-4.82**	-12.41**	9.81**	9.21**	23.00**	22.20**	6.77*	-4.37	28.24**	24.92**	57.50**	-2.07
BS 37 × GSB 41	-4.64**	-9.73**	6.48**	5.89**	21.84**	17.47**	9.13**	-2.26	57.59**	34.49**	69.56**	5.43
BS 37 × TCB 37	-2.51*	-9.61**	11.48**	10.87**	24.75**	18.85**	2.49	-8.21**	77.86**	37.90**	73.86**	8.11*
BS 37 × SUVIN	-1.40	-7.01**	10.56**	9.94**	26.31**	24.54**	7.40*	-3.81	65.93**	43.02**	80.31**	12.12**

Table 4.31 (cont.)

Table 4.31 (cont.)

Hybrid	Days to 50% flowering				Plant height (cm)				No. of monopodia plant ⁻¹			
	Mid	Better	Standard checks		Mid	Better	Standard checks		Mid	Better	Standard checks	
			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi
SCS 793 × GSB 40	0.59	-11.28**	10.74**	10.13**	28.50**	16.93**	7.50*	-3.72	44.70**	24.00**	34.75**	-16.21**
SCS 793 × DB 16	-0.60	-10.80**	7.04**	6.45**	33.91**	22.97**	10.78**	-0.78	26.78**	7.76	19.43**	-25.74**
SCS 793 × DB 11	-6.38**	-17.58**	3.33*	2.76	34.52**	25.28**	9.46**	-1.96	56.55**	29.06**	54.30**	-4.05
SCS 793 × GSB 41	-4.51**	-13.66**	1.85	1.29	28.84**	16.69**	8.40**	-2.91	74.58**	63.28**	45.50**	-9.53*
SCS 793 × TCB 37	-3.13**	-14.11**	5.93**	5.34**	35.27**	32.94**	3.78	-7.05*	92.28**	82.18**	41.33**	-12.12**
SCS 793 × SUVIN	-0.09	-9.97**	7.04**	6.45**	25.29**	18.98**	-0.27	-10.68**	100.69**	85.64**	69.43**	5.35
MCU 5 × GSB 40	-5.50**	-10.83**	11.30**	10.68**	24.04**	12.16**	3.12	-7.64**	107.87**	60.05**	73.92**	8.15*
MCU 5 × DB 16	-8.35**	-11.88**	5.74**	5.16**	26.45**	15.39**	3.95	-6.89*	56.46**	19.65**	32.59**	-17.55**
MCU 5 × DB 11	-6.51**	-11.96**	10.37**	9.76**	25.87**	16.47**	1.77	-8.85**	12.00*	-16.52**	-0.20	-37.94**
MCU 5 × GSB 41	-3.81**	-6.75**	10.00**	9.39**	26.44**	13.81**	5.72	-5.31	23.51**	2.41	-8.74	-43.25**
MCU 5 × TCB 37	-10.28**	-14.86**	5.00**	4.42**	29.33**	26.23**	-1.45	-11.73**	164.73**	144.23**	69.56**	5.43
MCU 5 × SUVIN	-6.61**	-9.81**	7.22**	6.63**	22.67**	15.73**	-3.00	-13.12**	97.04**	61.86**	47.72**	-8.15*
L 1058 × GSB 40	-6.94**	-15.43**	5.56**	4.97**	28.48**	18.04**	8.53**	-2.79	70.07**	47.93**	60.76**	-0.04
L 1058 × DB 16	5.25**	-2.62*	16.85**	16.21**	21.22**	12.41**	1.27	-9.29**	54.59**	33.35**	47.78**	-8.11*
L 1058 × DB 11	-7.17**	-15.81**	5.56**	4.97**	33.57**	25.64**	9.78**	-1.68	17.38**	-1.85	17.34**	-27.04**
L 1058 × GSB 41	-1.35	-8.01**	8.52**	7.92**	25.01**	14.31**	6.19	-4.88	102.46**	92.54**	71.58**	6.69
L 1058 × TCB 37	-1.07	-9.61**	11.48**	10.87**	40.56**	39.59**	8.98**	-2.39	82.85**	70.40**	36.96**	-14.84**
L 1058 × SUVIN	-3.10**	-9.97**	7.04**	6.45**	36.97**	31.40**	10.13**	-1.36	69.54**	59.43**	45.50**	-9.53*
L 762 × GSB 40	-15.35**	-18.99**	1.11	0.55	29.38**	19.13**	9.52**	-1.90	24.63**	5.94	15.12*	-28.42**
L 762 × DB 16	-17.25**	-19.29**	-3.15*	-3.68*	26.33**	17.42**	5.78	-5.26	20.96**	2.00	13.04*	-29.71**
L 762 × DB 11	-14.62**	-18.46**	2.22	1.66	33.90**	26.23**	10.30**	-1.21	35.55**	10.91*	32.59**	-17.55**
L 762 × GSB 41	-9.66**	-11.15**	4.81**	4.24**	30.72**	19.80**	11.29**	-0.32	94.71**	80.47**	60.82**	0.00
L 762 × TCB 37	-13.26**	-16.52**	2.96*	2.39	35.24**	34.64**	5.11	-5.86*	49.37**	42.84**	8.67	-32.43**
L 762 × SUVIN	-13.67**	-15.42**	0.56	0.00	33.07**	27.95**	7.25*	-3.94	81.85**	66.71**	52.15**	-5.39

*Significant at 5% level

**Significant at 1% level

Table 4.32. Percentage of heterosis over mid parent, better parent and standard checks for number of sympodia plant⁻¹, number of bolls plant⁻¹ and boll weight in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) over three locations (pooled) during *kharif*, 2014-15

Hybrid	No. of sympodia plant ⁻¹				No. of bolls plant ⁻¹				Boll weight (g)			
	Mid	Better	Standard checks		Mid	Better	Standard checks		Mid	Better	Standard checks	
			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi
NDLH 1938 × GSB 40	29.18**	25.02**	1.60	-8.78**	62.88**	44.32**	15.54**	-1.92	9.81**	-6.87**	8.91**	-1.38
NDLH 1938 × DB 16	45.36**	40.03**	6.47*	-4.41	58.10**	34.13**	18.98**	1.00	10.40**	-8.34**	7.19**	-2.95
NDLH 1938 × DB 11	26.05**	24.55**	-2.99	-12.90**	73.98**	60.94**	17.01**	-0.67	3.42*	-10.90**	4.20*	-5.66**
NDLH 1938 × GSB 41	47.53**	47.44**	12.11**	0.65	81.16**	63.93**	25.12**	6.21**	4.00*	-12.88**	1.89	-7.75**
NDLH 1938 × TCB 37	40.25**	31.31**	-0.16	-10.36**	83.89**	74.16**	20.39**	2.20	-2.14	-21.61**	-8.33**	-17.00**
NDLH 1938 × SUVIN	41.73**	38.95**	5.65*	-5.15*	57.48**	45.23**	6.30*	-9.76**	-3.24	-22.45**	-9.30**	-17.88**
H 1442 × GSB 40	39.63**	32.49**	7.68**	-3.33	64.55**	49.81**	19.94**	1.82	-0.58	-15.45**	-1.76	-11.05**
H 1442 × DB 16	65.89**	63.05**	18.96**	6.81**	66.22**	44.69**	28.34**	8.95**	13.35**	-5.66**	9.63**	-0.74
H 1442 × DB 11	34.93**	30.66**	1.77	-8.63**	76.86**	68.36**	22.41**	3.91	-8.86**	-21.28**	-8.52**	-17.17**
H 1442 × GSB 41	47.32**	44.42**	9.69**	-1.52	72.18**	60.22**	22.29**	3.81	19.00**	-0.06	16.14**	5.15**
H 1442 × TCB 37	39.52**	33.19**	-2.82	-12.75**	50.77**	47.06**	1.66	-13.70**	3.28	-17.08**	-3.64*	-12.75**
H 1442 × SUVIN	37.97**	37.89**	0.72	-9.57**	57.97**	49.91**	9.73**	-6.85**	-4.43**	-23.21**	-10.77**	-19.20**
ADB 542 × GSB 40	28.43**	17.79**	-4.27	-14.05**	65.93**	46.77**	17.50**	-0.25	-1.03	-15.18**	-3.29	-12.43**
ADB 542 × DB 16	76.65**	73.32**	22.12**	9.64**	65.64**	40.31**	24.46**	5.65*	13.28**	-4.99**	8.33**	-1.91
ADB 542 × DB 11	39.48**	30.45**	1.61	-8.77**	69.72**	56.72**	13.94**	-3.27	11.53**	-2.88	10.74**	0.27
ADB 542 × GSB 41	45.98**	38.15**	4.92	-5.80*	42.42**	28.65**	-1.81	-16.65**	9.49**	-7.33**	5.66**	-4.33**
ADB 542 × TCB 37	47.17**	45.58**	-1.29	-11.38**	74.00**	64.49**	13.70**	-3.48	0.34	-18.86**	-7.48**	-16.23**
ADB 542 × SUVIN	30.65**	25.96**	-7.99**	-17.39**	24.81**	14.89**	-15.90**	-28.61**	-3.90*	-22.23**	-11.32**	-19.71**
ADB 532 × GSB 40	38.10**	31.59**	6.94*	-3.99	56.84**	36.04**	8.91**	-7.54**	13.00**	-4.35**	12.39**	1.77
ADB 532 × DB 16	52.38**	49.13**	9.76**	-1.45	29.60**	7.78*	-4.40	-18.84**	14.67**	-4.98**	11.65**	1.09
ADB 532 × DB 11	32.33**	28.69**	0.24	-10.00**	63.07**	47.50**	7.24**	-8.96**	0.69	-13.43**	1.72	-7.89**
ADB 532 × GSB 41	18.63**	16.80**	-11.30**	-20.36**	51.82**	34.41**	2.59	-12.91**	2.12	-14.62**	0.33	-9.16**
ADB 532 × TCB 37	25.15**	18.97**	-12.43**	-21.38**	60.40**	48.45**	2.62	-12.89**	0.45	-19.68**	-5.63**	-14.55**
ADB 532 × SUVIN	27.02**	26.53**	-6.87*	-16.38**	50.49**	35.72**	-0.66	-15.67**	2.53	-17.97**	-3.61*	-12.72**

Table 4.32 (cont.)

Table 4.32 (cont.)

Hybrid	No. of sympodia plant ⁻¹				No. of bolls plant ⁻¹				Boll weight (g)			
	Mid	Better	Standard checks		Mid	Better	Standard checks		Mid	Better	Standard checks	
			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi
WGCV 48 × GSB 40	38.07**	32.58**	7.75**	-3.26	31.52**	27.39**	1.99	-13.42**	3.16*	-12.53**	2.37	-7.30**
WGCV 48 × DB 16	48.56**	44.24**	7.91**	-3.12	33.15**	22.89**	9.01**	-7.47**	1.64	-15.65**	-1.27	-10.60**
WGCV 48 × DB 11	41.45**	38.65**	8.00**	-3.04	63.23**	60.70**	20.57**	2.35	-6.73**	-19.68**	-5.99**	-14.87**
WGCV 48 × GSB 41	19.81**	18.91**	-9.69**	-18.92**	45.91**	44.68**	10.42**	-6.26**	-5.44**	-20.82**	-7.32**	-16.08**
WGCV 48 × TCB 37	36.31**	28.59**	-3.80	-13.63**	40.02**	34.52**	0.93	-14.32**	-2.67	-22.07**	-8.78**	-17.41**
WGCV 48 × SUVIN	21.08**	19.65**	-10.49**	-19.63**	16.54**	15.12**	-13.63**	-26.68**	-2.57	-21.93**	-8.62**	-17.26**
MR 786 × GSB 40	45.01**	30.10**	5.73*	-5.07*	44.35**	25.21**	0.24	-14.91**	7.97**	-8.72**	7.58**	-2.59
MR 786 × DB 16	50.87**	44.56**	1.85	-8.55**	48.26**	23.29**	9.37**	-7.16**	10.39**	-8.64**	7.68**	-2.50
MR 786 × DB 11	48.67**	35.95**	5.89*	-4.93	68.72**	52.62**	10.96**	-5.81*	-0.42	-14.49**	0.78	-8.75**
MR 786 × GSB 41	94.95**	80.34**	36.96**	22.97**	74.95**	54.89**	18.22**	0.36	7.95**	-9.85**	6.25**	-3.80*
MR 786 × TCB 37	59.45**	57.31**	4.36	-6.30*	75.47**	62.40**	12.26**	-4.70*	5.24**	-15.95**	-0.94	-10.31**
MR 786 × SUVIN	48.63**	40.00**	2.26	-8.19**	59.29**	43.66**	5.15	-10.74**	5.40**	-15.76**	-0.72	-10.10**
TSH 0250 × GSB 40	52.15**	32.28**	7.51**	-3.48	64.41**	40.78**	12.71**	-4.32	26.67**	8.88**	23.29**	11.63**
TSH 0250 × DB 16	46.32**	35.51**	-4.52	-14.28**	40.65**	15.55**	2.50	-12.99**	-5.79**	-20.77**	-10.28**	-18.76**
TSH 0250 × DB 11	47.56**	30.66**	1.77	-8.63**	65.97**	48.10**	7.68**	-8.59**	-12.99**	-24.02**	-13.96**	-22.09**
TSH 0250 × GSB 41	46.94**	31.56**	-0.08	-10.29**	63.01**	42.42**	8.71**	-7.72**	-11.46**	-24.85**	-14.90**	-22.95**
TSH 0250 × TCB 37	40.24**	33.59**	-11.38**	-20.43**	14.20**	4.22	-27.95**	-38.84**	-3.14	-21.46**	-11.06**	-19.47**
TSH 0250 × SUVIN	38.88**	26.52**	-7.58**	-17.02**	43.84**	27.98**	-6.33*	-20.48**	-11.70**	-28.35**	-18.87**	-26.54**
BS 37 × GSB 40	35.45**	29.60**	5.33	-5.43*	46.18**	37.85**	10.36**	-6.32**	10.90**	-4.86**	8.23**	-2.00
BS 37 × DB 16	44.79**	41.09**	4.77	-5.94*	34.94**	21.42**	7.71**	-8.57**	3.53*	-13.10**	-1.14	-10.49**
BS 37 × DB 11	22.65**	19.79**	-6.70*	-16.23**	33.03**	31.41**	-4.46	-18.90**	7.61**	-6.21**	6.70**	-3.39*
BS 37 × GSB 41	49.81**	48.14**	12.51**	1.01	72.06**	65.98**	26.69**	7.54**	2.04	-13.55**	-1.66	-10.96**
BS 37 × TCB 37	41.92**	34.36**	-0.24	-10.43**	37.51**	35.76**	-3.70	-18.25**	2.70	-16.87**	-5.43**	-14.37**
BS 37 × SUVIN	36.11**	35.00**	0.24	-10.00**	80.52**	77.73**	30.09**	10.43**	-5.77**	-23.68**	-13.18**	-21.38**

Table 4.32 (cont.)

Table 4.32 (cont.)

Hybrid	No. of sympodia plant ⁻¹				No. of bolls plant ⁻¹				Boll weight (g)			
	Mid	Better	Standard checks		Mid	Better	Standard checks		Mid	Better	Standard checks	
			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi
SCS 793 × GSB 40	36.84**	32.09**	7.35**	-3.62	11.01**	3.44	-4.10	-18.59**	-5.12**	-16.37**	-10.74**	-19.18**
SCS 793 × DB 16	39.01**	34.26**	1.54	-8.84**	30.56**	27.74**	18.43**	0.54	5.57**	-9.02**	-2.90	-12.08**
SCS 793 × DB 11	36.90**	34.92**	5.08	-5.65*	44.61**	29.01**	19.61**	1.53	-1.87	-12.07**	-6.15**	-15.02**
SCS 793 × GSB 41	38.22**	37.93**	4.76	-5.95*	45.76**	32.88**	23.20**	4.58*	-1.28	-14.11**	-8.33**	-17.00**
SCS 793 × TCB 37	45.65**	36.71**	3.39	-7.17**	24.85**	8.96**	1.02	-14.24**	-13.46**	-28.19**	-23.36**	-30.60**
SCS 793 × SUVIN	58.52**	55.82**	17.84**	5.80*	42.59**	27.58**	18.28**	0.41	-11.65**	-26.64**	-21.70**	-29.10**
MCU 5 × GSB 40	30.55**	19.27**	-3.07	-12.97**	11.33**	-5.91	-24.67**	-36.05**	-8.57**	-22.69**	-8.91**	-17.53**
MCU 5 × DB 16	43.02**	39.75**	-1.54	-11.60**	23.39**	0.13	-11.18**	-24.60**	-0.50	-17.64**	-2.96	-12.14**
MCU 5 × DB 11	32.14**	23.10**	-4.12	-13.92**	15.93**	2.03	-25.82**	-37.03**	-18.08**	-29.65**	-17.11**	-24.95**
MCU 5 × GSB 41	27.95**	20.61**	-8.40**	-17.76**	31.89**	13.70**	-13.22**	-26.33**	-13.02**	-27.36**	-14.41**	-22.50**
MCU 5 × TCB 37	30.99**	30.12**	-12.52**	-21.46**	39.52**	25.53**	-13.22**	-26.34**	-6.22**	-25.10**	-11.74**	-20.09**
MCU 5 × SUVIN	31.07**	25.86**	-8.07**	-17.46**	34.11**	17.69**	-13.86**	-26.87**	-17.37**	-33.96**	-22.19**	-29.54**
L 1058 × GSB 40	19.88**	17.98**	-4.12	-13.91**	38.69**	20.51**	-3.52	-18.10**	-1.93	-15.39**	-5.04**	-14.02**
L 1058 × DB 16	41.02**	33.64**	5.17	-5.58*	40.36**	16.91**	3.70	-11.97**	-0.96	-16.41**	-6.18**	-15.05**
L 1058 × DB 11	31.75**	31.08**	3.15	-7.39**	56.13**	41.48**	2.86	-12.68**	4.68**	-8.23**	2.99	-6.75**
L 1058 × GSB 41	39.34**	36.91**	7.74**	-3.27	52.08**	34.89**	2.95	-12.60**	4.22*	-11.22**	-0.36	-9.78**
L 1058 × TCB 37	36.79**	26.06**	-0.80	-10.94**	51.27**	40.26**	-3.04	-17.69**	2.96	-16.23**	-5.99**	-14.87**
L 1058 × SUVIN	38.08**	33.13**	4.76	-5.94*	51.86**	37.20**	0.42	-14.75**	-0.36	-18.87**	-8.95**	-17.56**
L 762 × GSB 40	29.51**	26.62**	2.91	-7.61**	43.03**	32.13**	5.78*	-10.20**	2.21	-10.03**	-3.68*	-12.78**
L 762 × DB 16	36.90**	30.56**	1.38	-8.98**	56.25**	37.89**	22.32**	3.84	4.11*	-10.39**	-4.07*	-13.14**
L 762 × DB 11	37.62**	37.40**	7.02*	-3.91	66.24**	60.70**	16.84**	-0.82	-0.98	-11.39**	-5.14**	-14.11**
L 762 × GSB 41	32.00**	30.55**	1.37	-8.99**	51.08**	42.70**	8.92**	-7.54**	-14.64**	-25.83**	-20.59**	-28.10**
L 762 × TCB 37	34.75**	24.94**	-2.99	-12.90**	73.48**	71.90**	18.83**	0.87	21.58**	0.76	7.87**	-2.33
L 762 × SUVIN	31.86**	27.95**	-0.65	-10.80**	57.25**	51.52**	10.91**	-5.85*	5.81**	-12.25**	-6.05**	-14.93**

*Significant at 5% level

* *Significant at 1% level

Table 4.33. Percentage of heterosis over mid parent, better parent and standard checks for lint index, seed index and ginning out-turn in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) over three locations (pooled) during *kharif*, 2014-15

Hybrid	Lint index (g)				Seed index (g)				Ginning out-turn (%)			
	Mid	Better	Standard checks		Mid	Better	Standard checks		Mid	Better	Standard checks	
			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi
NDLH 1938 × GSB 40	0.97	-7.32**	0.61	-12.93**	12.08**	-1.32	4.22*	-13.23**	-7.64**	-10.45**	-2.60	-0.39
NDLH 1938 × DB 16	2.90*	-4.51**	1.20	-12.42**	20.84**	9.91**	7.85**	-10.21**	-10.25**	-11.47**	-3.71*	-1.52
NDLH 1938 × DB 11	14.31**	14.05**	3.48*	-10.45**	9.02**	-2.44	-0.72	-17.35**	3.03*	-4.67**	3.68*	6.03**
NDLH 1938 × GSB 41	6.40**	-2.51	6.27**	-8.04**	12.29**	0.09	2.78	-14.43**	-4.01**	-5.84**	2.41	4.74
NDLH 1938 × TCB 37	8.89**	3.60*	4.12*	-9.90**	26.22**	19.39**	7.61**	-10.41**	-8.74**	-9.04**	-1.07	1.17
NDLH 1938 × SUVIN	-0.04	-4.44*	-13.30**	-24.97**	25.23**	13.62**	12.09**	-6.68**	-16.19**	-23.38**	-16.67**	-14.78**
H 1442 × GSB 40	1.39	-4.16**	4.05*	-9.95**	18.21**	7.35**	13.37**	-5.61**	-9.00**	-11.57**	-4.27**	-2.10
H 1442 × DB 16	4.00**	-0.56	5.39**	-8.80**	11.71**	4.93*	2.96	-14.28**	-5.09**	-6.16**	1.58	3.88*
H 1442 × DB 11	4.32**	0.88	-2.45	-15.58**	10.14**	1.73	3.51	-13.82**	-3.78**	-10.78**	-3.42*	-1.23
H 1442 × GSB 41	9.69**	3.50*	12.81**	-2.37	6.89**	-1.68	0.96	-15.95**	1.34	-0.36	7.86**	10.31**
H 1442 × TCB 37	4.00**	2.03	2.54	-11.26**	20.46**	17.84**	6.21**	-11.58**	-9.58**	-9.67**	-2.22	0.00
H 1442 × SUVIN	7.56**	-0.20	-3.50*	-16.49**	15.36**	8.08**	6.62**	-11.23**	-5.65**	-13.56**	-6.43**	-4.31**
ADB 542 × GSB 40	4.41**	-6.21**	1.82	-11.89**	15.64**	6.18**	12.14**	-6.64**	-6.35**	-7.66**	-5.69**	-3.55*
ADB 542 × DB 16	17.47**	6.66**	13.03**	-2.18	8.07**	2.68	0.75	-16.12**	5.45**	2.19	8.13**	10.58**
ADB 542 × DB 11	7.91**	5.60**	-4.62**	-17.46**	16.55**	8.86**	10.78**	-7.77**	-4.62**	-7.87**	-8.54**	-6.46**
ADB 542 × GSB 41	13.19**	1.49	10.62**	-4.27**	16.58**	8.43**	11.34**	-7.30**	-1.81	-4.32**	0.10	2.37
ADB 542 × TCB 37	0.55	-6.47**	-6.00**	-18.65**	21.19**	19.98**	8.14**	-9.97**	-11.80**	-15.37**	-8.58**	-6.50**
ADB 542 × SUVIN	13.02**	10.59**	-4.38**	-17.25**	11.33**	5.51**	4.08*	-13.34**	0.53	-4.13**	-4.81**	-2.65
ADB 532 × GSB 40	10.24**	2.97*	11.79**	-3.26*	29.18**	17.97**	24.59**	3.73*	-10.61**	-12.32**	-6.88**	-4.77**
ADB 532 × DB 16	18.56**	11.99**	18.69**	2.71	33.28**	25.93**	23.57**	2.88	-8.13**	-8.30**	-2.62	-0.41
ADB 532 × DB 11	1.44	-0.67	-6.40**	-19.00**	18.41**	9.99**	11.92**	-6.82**	-10.71**	-16.47**	-11.29**	-9.28**
ADB 532 × GSB 41	5.48**	-1.67	7.19**	-7.24**	16.47**	7.74**	10.63**	-7.89**	-6.99**	-7.68**	-1.96	0.26
ADB 532 × TCB 37	-3.85**	-6.84**	-6.37**	-18.98**	32.24**	30.16**	17.31**	-2.33	-19.30**	-19.98**	-13.56**	-11.60**
ADB 532 × SUVIN	12.51**	5.65**	-0.44	-13.84**	26.38**	19.11**	17.50**	-2.18	-8.32**	-15.27**	-10.02**	-7.98**

Table 4.33 (cont.)

Table 4.33 (cont.)

Hybrid	Lint index (g)				Seed index (g)				Ginning out-turn (%)			
	Mid	Better	Standard checks		Mid	Better	Standard checks		Mid	Better	Standard checks	
			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi
WGCV 48 × GSB 40	-2.81*	-8.86**	-1.05	-14.37**	16.34**	8.11**	14.17**	-4.94**	-10.70**	-11.34**	-8.12**	-6.03**
WGCV 48 × DB 16	3.13*	-2.19	3.66*	-10.29**	17.63**	13.16**	11.04**	-7.56**	-8.24**	-9.18**	-3.90*	-1.72
WGCV 48 × DB 11	10.80**	8.04**	2.69	-11.13**	8.96**	3.02	4.83*	-12.73**	2.16	-3.33*	0.19	2.46
WGCV 48 × GSB 41	-5.27**	-11.33**	-3.35*	-16.36**	7.30**	1.02	3.73	-13.64**	-7.73**	-8.17**	-3.92*	-1.75
WGCV 48 × TCB 37	2.16	-0.61	-0.11	-13.55**	22.85**	22.49**	11.06**	-7.54**	-11.79**	-13.59**	-6.65**	-4.53**
WGCV 48 × SUVIN	22.03**	14.13**	8.48**	-6.12**	23.18**	18.20**	16.60**	-2.93	-0.64	-7.13**	-3.76*	-1.57
MR 786 × GSB 40	9.84**	-1.27	7.19**	-7.24**	21.90**	9.44**	15.58**	-3.77*	-6.89**	-6.94**	-4.95**	-2.80
MR 786 × DB 16	20.51**	9.49**	16.04**	0.42	24.82**	15.85**	13.68**	-5.35**	-1.89	-3.64*	1.96	4.27**
MR 786 × DB 11	3.02	0.90	-8.87**	-21.14**	19.71**	9.28**	11.20**	-7.42**	-10.58**	-14.76**	-13.03**	-11.06**
MR 786 × GSB 41	15.31**	3.46*	12.77**	-2.41	7.46**	-2.30	0.32	-16.48**	4.79**	3.49*	8.27**	10.73**
MR 786 × TCB 37	13.43**	5.58**	6.11**	-8.17**	41.62**	36.83**	23.33**	2.68	-13.83**	-16.22**	-9.49**	-7.44**
MR 786 × SUVIN	27.06**	24.23**	7.58**	-6.90**	16.89**	8.23**	6.77**	-11.11**	4.94**	-1.20	0.81	3.09
TSH 0250 × GSB 40	23.73**	7.83**	17.06**	1.31	15.42**	-2.98	2.46	-14.69**	3.98**	1.01	9.43**	11.92**
TSH 0250 × DB 16	13.90**	0.29	6.29**	-8.02**	29.44**	12.16**	10.06**	-8.37**	-8.18**	-9.26**	-1.69	0.54
TSH 0250 × DB 11	15.08**	8.93**	-1.62	-14.86**	32.89**	13.42**	15.41**	-3.91*	-9.96**	-16.54**	-9.58**	-7.53**
TSH 0250 × GSB 41	2.22	-11.07**	-3.07	-16.11**	20.31**	2.29	5.04**	-12.55**	-10.79**	-12.32**	-5.01**	-2.86
TSH 0250 × TCB 37	-4.33**	-13.78**	-13.34**	-25.00**	33.57**	20.09**	8.24**	-9.89**	-20.50**	-20.61**	-13.99**	-12.04**
TSH 0250 × SUVIN	-1.84	-3.07	-19.80**	-30.60**	30.38**	12.72**	11.20**	-7.42**	-20.19**	-26.91**	-20.82**	-19.02**
BS 37 × GSB 40	4.19**	-5.89**	2.17	-11.58**	16.28**	3.91*	9.74**	-8.63**	-6.35**	-7.37**	-3.28*	-1.09
BS 37 × DB 16	0.94	-7.83**	-2.32	-15.47**	23.81**	14.37**	12.22**	-6.57**	-13.68**	-14.25**	-9.27**	-7.21**
BS 37 × DB 11	-3.20*	-4.68**	-13.91**	-25.50**	18.51**	7.68**	9.57**	-8.78**	-14.33**	-19.21**	-15.65**	-13.74**
BS 37 × GSB 41	2.73	-7.38**	0.96	-12.63**	21.64**	10.07**	13.03**	-5.90**	-10.98**	-11.07**	-6.96**	-4.85**
BS 37 × TCB 37	-12.08**	-17.74**	-17.33**	-28.45**	36.25**	30.97**	18.05**	-1.72	-26.77**	-28.00**	-22.21**	-20.45**
BS 37 × SUVIN	-1.34	-4.05*	-15.99**	-27.30**	6.06**	-2.27	-3.59	-19.73**	-6.74**	-13.13**	-9.30**	-7.24**

Table 4.33 (cont.)

Table 4.33 (cont.)

Hybrid	Lint index (g)				Seed index (g)				Ginning out-turn (%)			
	Mid	Better	Standard checks		Mid	Better	Standard checks		Mid	Better	Standard checks	
			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi
SCS 793 × GSB 40	-7.56**	-20.90**	-14.13**	-25.69**	19.27**	3.40	9.20**	-9.08**	-14.29**	-15.13**	-13.31**	-11.35**
SCS 793 × DB 16	18.45**	2.38	8.50**	-6.10**	29.23**	15.65**	13.49**	-5.51**	-5.43**	-7.97**	-2.62	-0.41
SCS 793 × DB 11	20.42**	11.69**	0.88	-12.70**	29.09**	13.71**	15.71**	-3.67*	-4.91**	-8.54**	-8.41**	-6.33**
SCS 793 × GSB 41	-4.34**	-18.29**	-10.93**	-22.92**	26.42**	10.93**	13.90**	-5.17**	-16.71**	-18.50**	-14.73**	-12.80**
SCS 793 × TCB 37	9.36**	-3.31*	-2.83	-15.91**	32.22**	22.97**	10.83**	-7.73**	-11.81**	-15.03**	-8.21**	-6.12**
SCS 793 × SUVIN	1.84	-1.56	-18.55**	-29.52**	21.50**	8.49**	7.02**	-10.90**	-12.98**	-17.34**	-17.23**	-15.35**
MCU 5 × GSB 40	-13.27**	-20.98**	-14.22**	-25.76**	16.75**	8.85**	14.96**	-4.29**	-20.11**	-21.42**	-19.74**	-17.92**
MCU 5 × DB 16	8.28**	-0.27	5.70**	-8.53**	30.03**	25.51**	23.16**	2.54	-12.38**	-15.29**	-10.37**	-8.33**
MCU 5 × DB 11	4.62**	4.00*	-6.07**	-18.71**	10.71**	5.03**	6.87**	-11.02**	-3.83**	-6.88**	-8.02**	-5.93**
MCU 5 × GSB 41	-1.50	-10.43**	-2.37	-15.51**	14.14**	7.82**	10.72**	-7.82**	-9.89**	-12.40**	-8.35**	-6.28**
MCU 5 × TCB 37	-4.20**	-9.57**	-9.11**	-21.35**	22.06**	21.28**	10.74**	-7.81**	-15.23**	-18.86**	-12.34**	-10.35**
MCU 5 × SUVIN	11.07**	7.02**	-4.49**	-17.35**	25.11**	20.46**	18.83**	-1.07	-8.84**	-12.85**	-13.91**	-11.96**
L 1058 × GSB 40	10.37**	3.87*	12.77**	-2.41	26.57**	14.74**	21.17**	0.88	-9.37**	-11.86**	-4.74**	-2.58
L 1058 × DB 16	18.77**	13.06**	19.82**	3.70**	16.16**	8.90**	6.86**	-11.03**	1.55	0.48	8.61**	11.07**
L 1058 × DB 11	17.56**	14.20**	9.40**	-5.33**	20.36**	10.96**	12.91**	-6.00**	-2.36	-9.40**	-2.08	0.14
L 1058 × GSB 41	3.71**	-2.57	6.20**	-8.09**	13.67**	4.36*	7.16**	-10.78**	-6.28**	-7.78**	-0.33	1.93
L 1058 × TCB 37	13.87**	11.20**	11.76**	-3.28*	28.98**	25.92**	13.50**	-5.51**	-8.31**	-8.34**	-0.93	1.32
L 1058 × SUVIN	18.43**	10.36**	5.72**	-8.51**	21.64**	13.76**	12.22**	-6.57**	-1.84	-10.01**	-2.73	-0.53
L 762 × GSB 40	2.73	-7.87**	0.02	-13.44**	10.64**	0.02	5.63**	-12.06**	-5.04**	-5.58**	-3.56*	-1.37
L 762 × DB 16	11.37**	0.95	6.99**	-7.41**	8.57**	1.50	-0.41	-17.08**	1.92	-0.42	5.37**	7.76**
L 762 × DB 11	21.85**	19.04**	7.51**	-6.96**	15.26**	5.96**	7.82**	-10.23**	3.23*	-1.10	-0.14	2.12
L 762 × GSB 41	7.49**	-3.78*	4.88**	-9.23**	6.01**	-2.94	-0.34	-17.03**	0.98	-0.78	3.80*	6.15**
L 762 × TCB 37	12.87**	4.82**	5.35**	-8.83**	12.47**	9.48**	-1.32	-17.85**	0.48	-2.81	5.00**	7.38**
L 762 × SUVIN	29.99**	27.41**	9.77**	-5.00**	15.78**	7.97**	6.51**	-11.33**	7.22**	1.45	2.43	4.75**

*Significant at 5% level

**Significant at 1% level

Table 4.34. Percentage of heterosis over mid parent, better parent and standard checks for 2.5% span length, uniformity ratio and micronaire value in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) over three locations (pooled) during *kharif*, 2014-15

Hybrid	2.5% span length (mm)				Uniformity ratio				Micronaire value (10 ⁻⁶ g/inch)			
	Mid	Better	Standard checks		Mid	Better	Standard checks		Mid	Better	Standard checks	
			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi
NDLH 1938 × GSB 40	10.41**	1.74	0.50	-1.24	-2.27*	-3.63**	2.68*	-0.32	-18.70**	-20.08**	19.53**	-1.09
NDLH 1938 × DB 16	9.27**	1.05	-0.94	-2.65	-2.07*	-3.56**	2.75*	-0.25	-2.09	-11.21**	28.28**	6.16**
NDLH 1938 × DB 11	7.96**	0.13	-2.48	-4.17**	-2.40*	-4.47**	1.78	-1.19	-9.55**	-14.79**	23.12**	1.88
NDLH 1938 × GSB 41	5.45**	-5.22**	-1.05	-2.76	-2.83**	-4.17**	2.10	-0.88	-21.39**	-25.48**	7.66**	-10.91**
NDLH 1938 × TCB 37	7.96**	-4.03**	2.73	0.96	-2.75**	-5.48**	0.71	-2.23	-24.40**	-27.61**	4.60*	-13.44**
NDLH 1938 × SUVIN	11.53**	0.39	4.47**	2.66	-3.52**	-6.28**	-0.15	-3.06*	-20.26**	-20.88**	16.11**	-3.91*
H 1442 × GSB 40	14.37**	2.68	1.43	-0.32	-3.97**	-6.18**	1.86	-1.11	-24.71**	-29.33**	20.49**	-0.29
H 1442 × DB 16	22.89**	10.70**	8.52**	6.65**	-4.09**	-6.42**	1.60	-1.36	-23.27**	-35.18**	10.51**	-8.55**
H 1442 × DB 11	11.71**	0.92	-1.71	-3.41*	-3.86**	-6.76**	1.23	-1.72	-24.84**	-34.26**	12.08**	-7.25**
H 1442 × GSB 41	9.78**	-3.79**	0.44	-1.29	-3.80**	-5.99**	2.06	-0.92	-12.88**	-23.37**	30.65**	8.12**
H 1442 × TCB 37	11.38**	-3.43*	3.38*	1.59	-3.58**	-7.13**	0.83	-2.11	-22.07**	-30.82**	17.95**	-2.39
H 1442 × SUVIN	13.12**	-0.73	3.31*	1.52	-4.69**	-8.26**	-0.39	-3.30**	-25.37**	-30.56**	18.39**	-2.03
ADB 542 × GSB 40	13.05**	2.02	0.77	-0.97	-5.34**	-7.86**	0.82	-2.12	-23.07**	-25.70**	19.26**	-1.30
ADB 542 × DB 16	16.57**	5.55**	3.47*	1.68	-5.03**	-7.68**	1.01	-1.93	-3.57**	-16.48**	34.06**	10.94**
ADB 542 × DB 11	16.46**	5.76**	3.00*	1.22	-3.74**	-6.99**	1.77	-1.20	-25.61**	-33.20**	7.22**	-11.27**
ADB 542 × GSB 41	12.19**	-1.19	3.16*	1.38	-4.97**	-7.49**	1.22	-1.73	-22.62**	-30.11**	12.17**	-7.17**
ADB 542 × TCB 37	11.19**	-3.11*	3.71*	1.92	-4.27**	-8.14**	0.51	-2.42*	-23.27**	-30.03**	12.30**	-7.07**
ADB 542 × SUVIN	18.17**	4.22**	8.46**	6.58**	-5.69**	-9.55**	-1.03	-3.92**	-20.09**	-23.51**	22.77**	1.59
ADB 532 × GSB 40	14.00**	4.09**	2.81	1.04	-4.75**	-7.16**	1.30	-1.65	-32.81**	-33.35**	1.31	-16.16**
ADB 532 × DB 16	17.27**	7.45**	5.33**	3.51*	-6.78**	-9.27**	-0.99	-3.88**	-17.36**	-26.73**	11.38**	-7.83**
ADB 532 × DB 11	12.15**	3.06*	0.37	-1.36	-3.57**	-6.71**	1.80	-1.17	-24.19**	-30.24**	6.04**	-12.25**
ADB 532 × GSB 41	12.88**	0.55	4.98**	3.17*	-5.45**	-7.83**	0.57	-2.36	-23.99**	-29.64**	6.96**	-11.49**
ADB 532 × TCB 37	12.62**	-0.76	6.23**	4.39**	-5.96**	-9.64**	-1.40	-4.28**	-19.38**	-24.63**	14.58**	-5.18**
ADB 532 × SUVIN	16.70**	4.11**	8.34**	6.47**	-6.25**	-9.98**	-1.77	-4.63**	-30.92**	-32.11**	3.20	-14.60**

Table 4.34 (cont.)

Table 4.34 (cont.)

Hybrid	2.5% span length (mm)				Uniformity ratio				Micronaire value (10 ⁻⁶ g/inch)			
	Mid	Better	Standard checks		Mid	Better	Standard checks		Mid	Better	Standard checks	
			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi
WGCV 48 × GSB 40	16.90**	7.05**	5.74**	3.91**	-5.69**	-7.50**	-0.35	-3.26**	-27.76**	-32.80**	16.81**	-3.33*
WGCV 48 × DB 16	13.90**	4.66**	2.60	0.83	-5.75**	-7.69**	-0.56	-3.46**	-21.26**	-34.01**	14.71**	-5.07**
WGCV 48 × DB 11	13.17**	4.30**	1.58	-0.17	-0.62	-3.25**	4.22**	1.18	-21.43**	-31.84**	18.48**	-1.96
WGCV 48 × GSB 41	7.32**	-4.13**	0.10	-1.63	-4.57**	-6.39**	0.85	-2.10	-20.39**	-30.55**	20.71**	-0.11
WGCV 48 × TCB 37	12.96**	-0.19	6.85**	5.00**	-5.98**	-9.10**	-2.08	-4.93**	-25.15**	-34.11**	14.54**	-5.22**
WGCV 48 × SUVIN	10.46**	-1.18	2.83	1.06	-3.47**	-6.73**	0.48	-2.45*	-26.60**	-32.32**	17.64**	-2.64
MR 786 × GSB 40	8.74**	-2.26	-3.45*	-5.12**	-2.74**	-5.60**	3.89**	0.86	-29.20**	-31.89**	10.25**	-8.77**
MR 786 × DB 16	10.65**	-0.20	-2.17	-3.86**	-4.45**	-7.39**	1.93	-1.05	-17.17**	-28.51**	15.72**	-4.24**
MR 786 × DB 11	9.85**	-0.64	-3.23*	-4.90**	-3.74**	-7.26**	2.07	-0.91	-26.74**	-34.46**	6.09**	-12.21**
MR 786 × GSB 41	9.23**	-4.17**	0.05	-1.68	-2.34*	-5.20**	4.33**	1.29	-18.29**	-26.48**	19.00**	-1.52
MR 786 × TCB 37	8.89**	-5.48**	1.18	-0.57	-0.86	-5.13**	4.41**	1.36	-21.66**	-28.83**	15.19**	-4.67**
MR 786 × SUVIN	9.26**	-4.01**	-0.11	-1.83	-6.30**	-10.38**	-1.37	-4.25**	-34.03**	-37.11**	1.80	-15.76**
TSH 0250 × GSB 40	20.19**	10.15**	8.80**	6.92**	-5.12**	-5.31**	-1.53	-4.40**	-16.10**	-20.81**	18.43**	-1.99
TSH 0250 × DB 16	16.31**	6.96**	4.85**	3.04*	-3.91**	-4.23**	-0.41	-3.31**	-11.74**	-16.79**	10.46**	-8.59**
TSH 0250 × DB 11	13.67**	4.85**	2.12	0.35	-2.23*	-3.15**	0.71	-2.22	-19.53**	-21.04**	4.82*	-13.26**
TSH 0250 × GSB 41	5.48**	-5.69**	-1.54	-3.24*	-4.69**	-4.86**	-1.06	-3.95**	-23.91**	-24.87**	-0.26	-17.46**
TSH 0250 × TCB 37	14.27**	1.05	8.17**	6.30**	-4.49**	-6.06**	-2.31	-5.16**	-18.84**	-19.00**	7.53**	-11.01**
TSH 0250 × SUVIN	12.27**	0.51	4.60**	2.79	-4.96**	-6.58**	-2.85*	-5.68**	-26.54**	-30.04**	2.67	-15.04**
BS 37 × GSB 40	15.57**	9.66**	8.32**	6.45**	-0.16	-0.53	3.79**	0.77	-23.38**	-25.12**	12.00**	-7.32**
BS 37 × DB 16	12.28**	6.93**	4.82**	3.01*	-5.08**	-5.55**	-1.45	-4.33**	-10.43**	-18.34**	16.59**	-3.51*
BS 37 × DB 11	13.23**	8.16**	5.34**	3.52*	-1.19	-2.29	1.95	-1.02	-21.77**	-25.88**	5.82**	-12.43**
BS 37 × GSB 41	7.67**	-0.44	3.94**	2.14	-3.12**	-3.46**	0.73	-2.21	-16.74**	-20.64**	13.31**	-6.23**
BS 37 × TCB 37	11.51**	1.94	9.12**	7.23**	-3.78**	-5.52**	-1.42	-4.29**	-23.20**	-26.03**	5.60**	-12.61**
BS 37 × SUVIN	7.83**	-0.14	3.92**	2.12	-3.26**	-5.06**	-0.94	-3.82**	-21.64**	-22.70**	13.44**	-6.12**

Table 4.34 (cont.)

Table 4.34 (cont.)

Hybrid	2.5% span length (mm)				Uniformity ratio				Micronaire value (10^{-6} g/inch)			
	Mid	Better	Standard checks		Mid	Better	Standard checks		Mid	Better	Standard checks	
			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi
SCS 793 × GSB 40	19.19**	6.86**	5.56**	3.73*	-5.46**	-8.21**	0.96	-1.98	-25.37**	-26.44**	13.27**	-6.27**
SCS 793 × DB 16	13.00**	1.66	-0.35	-2.07	-4.43**	-7.34**	1.92	-1.06	-19.61**	-29.12**	9.15**	-9.67**
SCS 793 × DB 11	13.90**	2.77	0.09	-1.64	-2.32*	-5.86**	3.54**	0.52	-25.72**	-32.04**	4.64*	-13.41**
SCS 793 × GSB 41	7.84**	-5.62**	-1.46	-3.16*	-2.77**	-5.59**	3.85**	0.82	-21.74**	-27.98**	10.90**	-8.22**
SCS 793 × TCB 37	14.50**	-0.85	6.14**	4.30**	-3.67**	-7.80**	1.41	-1.54	-24.25**	-29.60**	8.41**	-10.29**
SCS 793 × SUVIN	9.61**	-3.93**	-0.03	-1.75	-5.59**	-9.68**	-0.66	-3.56**	-30.91**	-32.53**	3.90*	-14.02**
MCU 5 × GSB 40	15.85**	11.66**	10.29**	8.39**	0.24	-2.16	1.34	-1.61	-23.39**	-29.57**	5.34**	-12.83**
MCU 5 × DB 16	14.06**	10.34**	8.16**	6.29**	-4.48**	-6.64**	-3.56**	-6.37**	-14.02**	-16.72**	4.47*	-13.55**
MCU 5 × DB 11	7.94**	4.75**	2.02	0.26	0.08	-1.59	0.40	-2.53*	-18.31**	-19.05**	3.42	-14.42**
MCU 5 × GSB 41	7.44**	0.87	5.31**	3.49*	-1.80	-4.16**	-0.70	-3.59**	-14.83**	-16.14**	8.54**	-10.18**
MCU 5 × TCB 37	9.92**	2.01	9.20**	7.31**	-2.98**	-3.92**	-3.38**	-6.19**	-14.63**	-16.82**	9.98**	-8.99**
MCU 5 × SUVIN	14.77**	7.91**	12.30**	10.36**	-0.93	-1.83	-1.38	-4.26**	-23.05**	-28.64**	4.73*	-13.33**
L 1058 × GSB 40	12.64**	4.02**	2.74	0.97	-3.57**	-3.82**	0.14	-2.78*	-25.41**	-25.61**	11.25**	-7.93**
L 1058 × DB 16	12.68**	4.41**	2.36	0.59	-4.81**	-5.18**	-1.28	-4.16**	-17.95**	-26.55**	9.24**	-9.60**
L 1058 × DB 11	17.14**	8.87**	6.03**	4.20**	-2.11*	-3.09**	0.89	-2.05	-20.54**	-26.14**	9.85**	-9.09**
L 1058 × GSB 41	12.80**	1.58	6.06**	4.22**	-5.42**	-5.64**	-1.76	-4.63**	-18.53**	-23.82**	13.31**	-6.23**
L 1058 × TCB 37	11.49**	-0.69	6.31**	4.47**	-4.30**	-5.93**	-2.06	-4.92**	-23.61**	-27.85**	7.31**	-11.20**
L 1058 × SUVIN	16.68**	5.23**	9.51**	7.62**	-2.45*	-4.16**	-0.22	-3.13**	-27.10**	-27.58**	7.71**	-10.87**
L 762 × GSB 40	10.61**	-0.73	-1.94	-3.64*	-3.54**	-4.15**	0.56	-2.37*	-29.34**	-34.83**	15.41**	-4.49**
L 762 × DB 16	13.52**	2.22	0.21	-1.52	-1.82	-2.58*	2.21	-0.77	-17.00**	-30.95**	22.29**	1.20
L 762 × DB 11	13.47**	2.47	-0.20	-1.92	-3.84**	-5.17**	-0.51	-3.41**	-22.36**	-33.18**	18.35**	-2.07
L 762 × GSB 41	9.31**	-4.24**	-0.02	-1.75	-3.84**	-4.44**	0.26	-2.67*	-22.21**	-32.68**	19.22**	-1.34
L 762 × TCB 37	7.85**	-6.52**	0.06	-1.67	-2.69*	-4.71**	-0.02	-2.94*	-23.82**	-33.47**	17.82**	-2.50
L 762 × SUVIN	12.29**	-1.49	2.51	0.74	-2.74**	-4.81**	-0.13	-3.04*	-32.51**	-38.29**	9.28**	-9.57**

*Significant at 5% level

* *Significant at 1% level

Table 4.35. Percentage of heterosis over mid parent, better parent and standard checks for bundle strength, fibre elongation and seed cotton yield plant⁻¹ in inter- specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) over three locations (pooled) during *kharif*, 2014-15

Hybrid	Bundle strength (g/tex)				Fibre elongation (%)				Seed cotton yield plant ⁻¹ (g)			
	Mid	Better	Standard checks		Mid	Better	Standard checks		Mid	Better	Standard checks	
			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi
NDLH 1938 × GSB 40	11.77**	2.77	6.11**	2.77	-0.57	-2.80	9.16**	2.80	81.64**	72.38**	28.26**	12.02**
NDLH 1938 × DB 16	9.55**	-1.37	6.69**	3.34*	2.69*	-0.06	13.26**	6.66**	80.63**	74.96**	30.18**	13.70**
NDLH 1938 × DB 11	7.31**	-1.35	1.90	-1.31	-2.89*	-5.89**	7.60**	1.33	81.10**	65.31**	23.00**	7.42*
NDLH 1938 × GSB 41	6.77**	-4.82**	5.30**	1.99	-1.94	-3.67*	7.10**	0.86	90.08**	73.97**	29.44**	13.05**
NDLH 1938 × TCB 37	4.95**	-8.05**	5.87**	2.54	-5.98**	-8.31**	3.48*	-2.55	78.71**	50.72**	12.14**	-2.06
NDLH 1938 × SUVIN	10.38**	-2.04	9.48**	6.03**	0.20	-1.32	9.16**	2.80	54.89**	32.76**	-1.22	-13.72**
H 1442 × GSB 40	15.48**	-0.13	3.12*	-0.12	-0.34	-5.34**	6.31**	0.11	62.84**	50.22**	18.78**	3.75
H 1442 × DB 16	25.89**	6.78**	15.51**	11.87**	0.08	-5.35**	7.27**	1.02	94.17**	82.70**	44.47**	26.18**
H 1442 × DB 11	13.91**	-1.50	1.74	-1.46	-0.32	-6.13**	7.34**	1.08	61.66**	43.63**	13.57**	-0.81
H 1442 × GSB 41	12.76**	-5.23**	4.86**	1.55	0.51	-4.08**	6.64**	0.43	106.74**	84.14**	45.61**	27.18**
H 1442 × TCB 37	9.56**	-9.38**	4.35**	1.06	-4.43**	-9.44**	2.21	-3.75*	53.00**	25.93**	-0.42	-13.03**
H 1442 × SUVIN	12.45**	-5.87**	5.20**	1.89	1.31	-3.08*	7.22**	0.97	51.79**	26.90**	0.35	-12.36**
ADB 542 × GSB 40	9.19**	-3.50*	-0.35	-3.49*	-1.31	-4.74**	6.98**	0.75	67.59**	61.57**	16.31**	1.59
ADB 542 × DB 16	13.22**	-1.90	6.11**	2.77	2.06	-1.93	11.15**	4.68**	95.04**	91.98**	38.21**	20.71**
ADB 542 × DB 11	14.62**	1.29	4.63**	1.33	-3.69**	-7.85**	5.37**	-0.77	93.37**	79.19**	29.00**	12.67**
ADB 542 × GSB 41	14.01**	-2.16	8.25**	4.84**	1.12	-1.92	9.04**	2.69	59.01**	47.74**	6.36	-7.11*
ADB 542 × TCB 37	4.22**	-12.02**	1.31	-1.88	-3.68**	-7.25**	4.68**	-1.42	75.30**	49.86**	7.89	-5.77
ADB 542 × SUVIN	10.98**	-5.15**	6.01**	2.67	1.65	-1.17	9.33**	2.96	20.96**	5.12	-24.32**	-33.90**
ADB 532 × GSB 40	16.96**	6.32**	9.77**	6.32**	-2.70*	-6.17**	5.37**	-0.77	78.99**	70.08**	26.20**	10.22**
ADB 532 × DB 16	14.54**	1.98	10.32**	6.84**	1.69	-2.37	10.65**	4.20**	51.50**	46.94**	9.03*	-4.78
ADB 532 × DB 11	8.47**	-1.42	1.83	-1.38	-2.01	-6.31**	7.12**	0.88	65.73**	51.48**	12.39**	-1.84
ADB 532 × GSB 41	13.77**	0.31	10.98**	7.49**	0.97	-2.16	8.78**	2.44	54.77**	41.83**	5.24	-8.09*
ADB 532 × TCB 37	11.04**	-3.76**	10.82**	7.33**	-2.75*	-6.44**	5.59**	-0.56	58.17**	33.54**	-0.91	-13.46**
ADB 532 × SUVIN	8.95**	-4.36**	6.89**	3.52*	-1.99	-4.79**	5.33**	-0.81	52.96**	31.26**	-2.61	-14.94**

Table 4.35 (cont.)

Table 4.35 (cont.)

Hybrid	Bundle strength (g/tex)				Fibre elongation (%)				Seed cotton yield plant ⁻¹ (g)			
	Mid	Better	Standard checks		Mid	Better	Standard checks		Mid	Better	Standard checks	
			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi
WGCV 48 × GSB 40	14.31**	2.44	5.78**	2.45	-2.04	-5.98**	5.59**	-0.56	32.42**	15.38**	3.81	-9.33**
WGCV 48 × DB 16	12.20**	-1.47	6.58**	3.23*	-1.35	-5.74**	6.84**	0.61	38.21**	22.67**	10.37*	-3.61
WGCV 48 × DB 11	10.96**	-0.58	2.70	-0.54	-1.59	-6.36**	7.08**	0.84	53.57**	29.22**	16.26**	1.54
WGCV 48 × GSB 41	5.74**	-8.03**	1.75	-1.45	2.33	-1.32	9.71**	3.32*	37.30**	15.80**	4.19	-9.00*
WGCV 48 × TCB 37	8.83**	-6.92**	7.17**	3.80*	-4.44**	-8.50**	3.26*	-2.76	32.90**	4.19	-6.26	-18.13**
WGCV 48 × SUVIN	9.56**	-5.11**	6.05**	2.71	-1.22	-4.51**	5.64**	-0.52	14.08**	-9.26*	-18.36**	-28.70**
MR 786 × GSB 40	6.48**	-4.94**	-1.84	-4.93**	-6.00**	-7.39**	4.01*	-2.06	54.58**	47.50**	8.48*	-5.25
MR 786 × DB 16	8.24**	-5.30**	2.44	-0.78	-1.00	-2.90*	10.05**	3.64*	68.81**	64.44**	20.94**	5.63
MR 786 × DB 11	5.58**	-5.75**	-2.65	-5.71**	-9.38**	-11.50**	1.20	-4.70**	69.43**	55.47**	14.35**	-0.13
MR 786 × GSB 41	7.59**	-6.76**	3.15*	-0.09	1.01	0.02	11.20**	4.72**	90.45**	75.22**	28.87**	12.56**
MR 786 × TCB 37	7.79**	-8.14**	5.78**	2.45	-2.19	-3.87**	8.49**	2.17	80.65**	53.08**	12.58**	-1.67
MR 786 × SUVIN	1.23	-12.65**	-2.37	-5.44**	-6.99**	-7.68**	2.13	-3.82*	69.39**	45.89**	7.30	-6.28
TSH 0250 × GSB 40	16.70**	4.35**	7.75**	4.35**	-2.13	-7.13**	4.29**	-1.78	104.52**	96.40**	42.54**	24.50**
TSH 0250 × DB 16	13.02**	-0.96	7.13**	3.76*	1.59	-4.02**	8.78**	2.44	34.14**	31.51**	-4.55	-16.64**
TSH 0250 × DB 11	13.23**	1.23	4.57**	1.27	-2.47	-8.24**	4.92**	-1.20	41.21**	30.37**	-5.38	-17.36**
TSH 0250 × GSB 41	7.19**	-6.98**	2.92	-0.32	-1.27	-5.87**	4.65**	-1.45	41.51**	31.00**	-4.93	-16.96**
TSH 0250 × TCB 37	7.36**	-8.38**	5.50**	2.18	-5.97**	-10.99**	0.46	-5.40**	-0.27	-15.03**	-38.33**	-46.14**
TSH 0250 × SUVIN	8.41**	-6.31**	4.71**	1.41	-7.14**	-11.25**	-1.82	-7.54**	20.51**	4.38	-24.24**	-33.83**
BS 37 × GSB 40	17.93**	10.35**	13.94**	10.35**	2.18	-0.19	12.09**	5.56**	64.57**	48.90**	22.89**	7.33*
BS 37 × DB 16	3.82**	-4.92**	2.86	-0.38	-4.81**	-7.43**	4.92**	-1.20	42.43**	31.38**	8.43*	-5.29
BS 37 × DB 11	10.30**	3.19*	6.59**	3.23*	-3.18*	-6.25**	7.20**	0.95	40.52**	22.56**	1.15	-11.66**
BS 37 × GSB 41	7.61**	-2.44	7.94**	4.54**	-0.90	-2.72	8.16**	1.85	77.17**	54.90**	27.85**	11.66**
BS 37 × TCB 37	5.45**	-6.07**	8.15**	4.75**	-1.55	-4.06**	8.28**	1.97	42.87**	15.66**	-4.54	-16.63**
BS 37 × SUVIN	-1.10	-10.74**	-0.24	-3.38*	-3.40**	-4.94**	5.16**	-0.97	69.85**	39.61**	15.22**	0.64

Table 4.35 (cont.)

Table 4.35 (cont.)

Hybrid	Bundle strength (g/tex)				Fibre elongation (%)				Seed cotton yield plant ⁻¹ (g)			
	Mid	Better	Standard checks		Mid	Better	Standard checks		Mid	Better	Standard checks	
			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi			DCH 32	Mahalakshmi
SCS 793 × GSB 40	14.02**	3.11*	6.46**	3.11*	-1.04	-3.23*	8.68**	2.35	5.17	-12.79**	-11.52**	-22.72**
SCS 793 × DB 16	9.25**	-3.22*	4.69**	1.40	-1.96	-4.55**	8.18**	1.87	37.74**	16.21**	17.90**	2.97
SCS 793 × DB 11	18.49**	7.13**	10.66**	7.18**	-2.81*	-5.79**	7.72**	1.45	39.66**	12.12**	13.74**	-0.66
SCS 793 × GSB 41	7.30**	-5.86**	4.15**	0.87	-1.19	-2.89*	7.96**	1.67	42.62**	14.74**	16.40**	1.67
SCS 793 × TCB 37	8.13**	-6.73**	7.40**	4.01**	-3.97**	-6.31**	5.73**	-0.43	3.82	-21.95**	-20.82**	-30.84**
SCS 793 × SUVIN	8.63**	-5.11**	6.05**	2.71	-5.21**	-6.61**	3.31*	-2.71	22.43**	-6.72	-5.36	-17.34**
MCU 5 × GSB 40	23.06**	13.80**	17.50**	13.80**	0.97	-4.68**	7.05**	0.81	1.74	1.63	-31.94**	-40.56**
MCU 5 × DB 16	6.17**	-3.87**	3.99*	0.72	-3.52**	-9.31**	2.78	-3.21*	28.65**	26.09**	-12.07**	-23.20**
MCU 5 × DB 11	7.57**	-0.54	2.73	-0.50	-3.69**	-9.84**	3.09	-2.91	-2.11	-6.16	-37.16**	-45.11**
MCU 5 × GSB 41	3.36*	-7.35**	2.51	-0.72	-2.79*	-7.79**	2.52	-3.46*	18.87**	14.27*	-23.48**	-33.17**
MCU 5 × TCB 37	3.02*	-9.25**	4.49**	1.20	-1.32	-7.06**	4.89**	-1.22	33.57**	17.74**	-21.15**	-31.13**
MCU 5 × SUVIN	10.29**	-1.58	10.00**	6.54**	-0.89	-5.77**	4.25**	-1.83	14.68*	2.85	-31.13**	-39.85**
L 1058 × GSB 40	10.23**	-2.20	0.98	-2.20	-1.73	-5.45**	6.19**	0.00	39.28**	37.97**	-6.05	-17.94**
L 1058 × DB 16	8.30**	-5.82**	1.88	-1.33	-2.53*	-6.62**	5.83**	-0.34	47.22**	45.49**	1.46	-11.38**
L 1058 × DB 11	18.02**	4.70**	8.14**	4.74**	-0.08	-4.68**	8.99**	2.64	69.69**	61.39**	9.90*	-4.01
L 1058 × GSB 41	13.22**	-2.47	7.91**	4.51**	-3.51**	-6.71**	3.72*	-2.33	61.69**	54.20**	5.01	-8.29*
L 1058 × TCB 37	8.28**	-8.26**	5.63**	2.31	-3.22*	-7.10**	4.85**	-1.26	58.80**	38.97**	-5.36	-17.34**
L 1058 × SUVIN	15.99**	-0.51	11.20**	7.70**	-0.45	-3.51*	6.74**	0.52	52.68**	35.92**	-7.45	-19.16**
L 762 × GSB 40	9.69**	-4.16**	-1.04	-4.16**	-2.85*	-6.36**	5.16**	-0.97	47.18**	39.50**	4.07	-9.10*
L 762 × DB 16	8.98**	-6.64**	1.00	-2.18	1.57	-2.54	10.46**	4.02**	66.02**	60.61**	19.82**	4.65
L 762 × DB 11	11.99**	-2.17	1.06	-2.12	1.21	-3.29*	10.58**	4.13**	64.75**	50.20**	12.06**	-2.13
L 762 × GSB 41	5.90**	-10.11**	-0.55	-3.68*	-0.58	-3.71*	7.05**	0.81	32.56**	21.18**	-9.60*	-21.04**
L 762 × TCB 37	5.47**	-11.92**	1.42	-1.77	-1.86	-5.63**	6.50**	0.29	106.68**	74.11**	29.90**	13.45**
L 762 × SUVIN	11.51**	-5.75**	5.34**	2.03	-1.04	-3.92**	6.28**	0.09	63.75**	40.20**	4.59	-8.65*

*Significant at 5% level

* *Significant at 1% level

Table 4.36. Percentage of heterosis over mid parent, better parent and standard checks for lint yield plant⁻¹ in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) over three locations (pooled) during *kharif*, 2014-15

Hybrid	Lint yield plant ⁻¹ (g)			
	Mid	Better	Standard checks	
			DCH 32	Mahalakshmi
NDLH 1938 × GSB 40	66.57**	53.32**	23.86**	10.72**
NDLH 1938 × DB 16	65.05**	58.26**	27.86**	14.29**
NDLH 1938 × DB 11	91.04**	63.06**	31.74**	17.76**
NDLH 1938 × GSB 41	81.84**	63.25**	31.89**	17.89**
NDLH 1938 × TCB 37	63.91**	36.65**	10.39*	-1.32
NDLH 1938 × SUVIN	27.74**	1.34	-18.13**	-26.82**
H 1442 × GSB 40	48.01**	33.38**	12.95**	0.96
H 1442 × DB 16	85.09**	73.57**	46.99**	31.39**
H 1442 × DB 11	55.07**	29.84**	9.95*	-1.72
H 1442 × GSB 41	110.84**	85.43**	57.03**	40.36**
H 1442 × TCB 37	41.21**	15.55**	-2.14	-12.53**
H 1442 × SUVIN	40.72**	9.74*	-7.07	-16.93**
ADB 542 × GSB 40	56.46**	51.59**	9.82*	-1.83
ADB 542 × DB 16	103.71**	101.38**	49.32**	33.47**
ADB 542 × DB 11	84.58**	65.06**	19.59**	6.90
ADB 542 × GSB 41	54.22**	45.51**	5.42	-5.77
ADB 542 × TCB 37	53.75**	34.08**	-2.86	-13.17**
ADB 542 × SUVIN	20.45**	-0.38	-27.82**	-35.48**
ADB 532 × GSB 40	62.80**	51.17**	19.83**	7.11
ADB 532 × DB 16	38.03**	33.57**	5.88	-5.36
ADB 532 × DB 11	47.15**	26.60**	0.35	-10.30**
ADB 532 × GSB 41	43.32**	29.76**	2.86	-8.06*
ADB 532 × TCB 37	26.39**	6.18	-15.84**	-24.77**
ADB 532 × SUVIN	39.32**	11.31*	-11.77**	-21.13**
WGCV 48 × GSB 40	20.00**	3.87	-3.49	-13.73**
WGCV 48 × DB 16	26.06**	13.33**	5.30	-5.87
WGCV 48 × DB 11	56.44**	26.31**	17.36**	4.91
WGCV 48 × GSB 41	28.34**	8.55	0.86	-9.84**
WGCV 48 × TCB 37	20.64**	-4.68	-11.43**	-20.83**
WGCV 48 × SUVIN	13.36**	-14.41**	-20.47**	-28.91**
MR 786 × GSB 40	42.86**	36.02**	2.19	-8.66*
MR 786 × DB 16	65.27**	64.20**	23.36**	10.27**
MR 786 × DB 11	51.48**	33.34**	0.17	-10.46**
MR 786 × GSB 41	101.21**	86.67**	40.24**	25.36
MR 786 × TCB 37	58.94**	36.50**	2.55	-8.33*
MR 786 × SUVIN	73.89**	41.79**	6.52	-4.78

Table 4.36 (cont.)

Table 4.36 (cont.)

Hybrid	Lint yield plant ⁻¹ (g)			
	Mid	Better	Standard checks	
			DCH 32	Mahalakshmi
TSH 0250 × GSB 40	112.76**	98.37**	55.85**	39.31**
TSH 0250 × DB 16	22.14**	18.70**	-6.74	-16.64**
TSH 0250 × DB 11	25.62**	8.48	-14.77**	-23.82**
TSH 0250 × GSB 41	26.88**	15.34**	-9.39*	-19.00**
TSH 0250 × TCB 37	-20.39**	-32.88**	-47.27**	-52.87**
TSH 0250 × SUVIN	-4.57	-23.50**	-39.90**	-46.28**
BS 37 × GSB 40	54.70**	38.18**	19.36**	6.70
BS 37 × DB 16	22.13**	13.48**	-1.97	-12.38**
BS 37 × DB 11	18.07**	-1.93	-15.28**	-24.27**
BS 37 × GSB 41	58.90**	38.56**	19.69**	6.99
BS 37 × TCB 37	8.20	-12.13*	-24.10**	-32.15**
BS 37 × SUVIN	56.32**	21.04**	4.56	-6.54
SCS 793 × GSB 40	-9.66*	-24.67**	-23.35**	-31.48**
SCS 793 × DB 16	29.40**	11.85**	13.81**	1.73
SCS 793 × DB 11	30.44**	1.84	3.62	-7.37*
SCS 793 × GSB 41	18.43**	-3.38	-1.69	-12.12**
SCS 793 × TCB 37	-8.93	-30.34**	-29.12**	-36.64**
SCS 793 × SUVIN	5.42	-22.74**	-21.38**	-29.73**
MCU 5 × GSB 40	-19.19**	-20.01**	-45.66**	-51.42**
MCU 5 × DB 16	11.66*	5.95	-21.44**	-29.78**
MCU 5 × DB 11	-7.02	-13.61*	-42.50**	-48.60**
MCU 5 × GSB 41	7.96	6.10	-29.38**	-36.87**
MCU 5 × TCB 37	13.88*	3.06	-31.40**	-38.68**
MCU 5 × SUVIN	3.04	-11.80	-41.29**	-47.52**
L 1058 × GSB 40	26.12**	21.09**	-10.60*	-20.09**
L 1058 × DB 16	48.11**	47.79**	9.58*	-2.05
L 1058 × DB 11	65.53**	46.81**	8.39*	-3.11
L 1058 × GSB 41	52.26**	42.40**	5.13	-6.03
L 1058 × TCB 37	44.06**	24.63**	-7.98	-17.75**
L 1058 × SUVIN	49.92**	23.08**	-9.13*	-18.78**
L 762 × GSB 40	40.00**	33.28**	0.16	-10.47**
L 762 × DB 16	67.21**	66.09**	24.82**	11.57**
L 762 × DB 11	68.68**	48.45**	11.56**	-0.28
L 762 × GSB 41	34.34**	24.61**	-6.35	-16.29**
L 762 × TCB 37	105.70**	76.63**	32.74**	18.65**
L 762 × SUVIN	75.87**	43.39**	7.76	-3.68

*Significant at 5% level

**Significant at 1% level

Table 4.1. Analysis of variance for different characters in American cotton (*Gossypium hirsutum* L.)

Source of variation	d.f	Days to 50% flowering	Plant height (cm)	No. of monopodia plant ⁻¹	No. of sympodia plant ⁻¹	No. of bolls plant ⁻¹	Boll weight (g)	Lint index (g)	Seed index (g)
		Mean squares							
Replications	2	1.60	0.10	0.01	0.78	2.64	0.03	0.05	0.02
Treatments	69	50.78**	209.11**	0.61**	7.79**	126.58**	0.51**	1.69**	4.18**
Error	138	0.94	42.49	0.01	0.85	4.16	0.03	0.02	0.09

Source of variation	d.f	Ginning out-turn (%)	2.5% span length (mm)	Uniformity ratio	Micronaire value (10 ⁻⁶ g/inch)	Bundle strength (g/tex)	Fibre elongation (%)	Seed cotton yield plant ⁻¹ (g)	Lint yield plant ⁻¹ (g)
		Mean squares							
Replications	2	1.57	0.31	2.83	0.02	0.24	0.02	48.62	12.62
Treatments	62	33.04**	11.92**	14.32**	0.93**	4.54**	0.15**	1036.02**	181.14**
Error	124	1.50	0.54	2.27	0.01	0.36	0.02	97.04	14.44

** Significant at 1% level,

Table 4.3. Mean, genetic variability, heritability (broad sense) and genetic advance as per cent of mean for different characters in American cotton (*Gossypium hirsutum* L.)

S.No.	Character	Mean	Range		Co-efficient of variation		Heritability (%) (broad sense)	Genetic advance as per cent of mean
			Minimum	Maximum	PCV (%)	GCV (%)		
1	Days to 50 % flowering	60.22	52.00	71.00	6.95	6.76	94.60	13.56
2	Plant height (cm)	127.77	104.22	140.99	7.74	5.83	56.70	9.04
3	No. of monopodia plant ⁻¹	1.33	0.67	2.33	34.37	33.37	94.30	66.75
4	No. of sympodia plant ⁻¹	14.96	10.44	18.22	11.88	10.16	73.10	17.90
5	No. of bolls plant ⁻¹	37.25	20.90	54.20	18.00	17.14	90.70	33.64
6	Boll weight (g)	4.20	3.45	5.36	10.28	9.53	86.00	18.22
7	Lint index (g)	4.37	2.36	6.27	17.42	17.06	95.90	34.42
8	Seed index (g)	8.51	5.80	11.35	14.16	13.70	93.70	27.34
9	Ginning out turn (%)	33.87	27.41	41.06	10.23	10.00	87.50	18.44
10	2.5% span length (mm)	26.93	20.84	33.05	7.73	7.23	87.50	13.93
11	Uniformity ratio	48.44	43.22	51.63	5.17	4.13	63.90	6.81
12	Micronaire value (10 ⁻⁶ g/inch)	3.62	2.55	5.64	15.55	15.20	95.50	30.61
13	Bundle strength (g/tex)	20.39	17.00	24.16	6.49	5.78	79.40	10.63
14	Fibre elongation (%)	5.03	4.30	5.55	5.11	4.16	66.20	6.97
15	Seed cotton yield plant ⁻¹ (g)	130.79	89.32	184.22	15.48	13.52	76.30	24.34
16	Lint yield plant ⁻¹ (g)	44.33	30.38	60.64	18.87	16.81	79.40	30.86

PCV: Phenotypic co-efficient of variation

GCV: Genotypic co-efficient of variation

Table 4.5. Contribution of different characters towards genetic divergence in 70 genotypes of American cotton (*Gossypium hirsutum* L.)

S.No.	Source	Times Ranked first	Contribution %
1	Days to 50% flowering	396	16.40
2	Plant height (cm)	0	0.00
3	No. of monopodia plant ⁻¹	336	13.94
4	No. of sympodia plant ⁻¹	13	0.54
5	No. of bolls plant ⁻¹	142	5.88
6	Boll weight (g)	83	3.44
7	Lint index (g)	466	19.30
8	Seed index (g)	321	13.29
9	Ginning out-turn (%)	9	0.37
10	2.5% span length (mm)	82	3.40
11	Uniformity ratio	1	0.04
12	Micronaire value (10 ⁻⁶ g/inch)	515	21.33
13	Bundle strength (g/tex)	9	0.37
14	Fibre elongation (%)	14	0.58
15	Seed cotton yield plant ⁻¹ (g)	20	0.80
16	Lint yield plant ⁻¹ (g)	8	0.33

Table 4.6. Clustering of 70 genotypes of American cotton (*Gossypium hirsutum* L.) by Tocher's method

Cluster No.	No. of genotypes	Name of genotype(s)
I	33	RS 266, H 1442, F 2310, SCS 1002, LH 2296, BGDS 1063, ADB 532, SCS 1001, RS2669, CCH 12-2, CCH 11-1, GJHV 514, LH 2232, P 5430, L 1060, MR 786, TSH 0499, L 804, Su-Flum, ARBH 701, TSH 0250, NDLH 1938, RS 2718, L 1058, ADB 542, CA 105, CNH 44, HS 289, RAH 1066, LH 2256, LH 2306, L 808, L 389
II	1	RAH 1004
III	6	WGCV 48, SCS 793, BS 37, PUSA 5760, L 1801, L 761
IV	11	TCH 1705, GISV 103, CPD 867, GISV 272, CNH 40, BS 51, GSHV 162, LH 2220, ARBH 702, L 1569, TCH 1741
V	1	CCH 11-2
VI	1	L 762
VII	7	KH 1101, L 799, MCU 5, RHC 0811, HYPS 152, L 1008, GJHV 44
VIII	1	P 72-9-37
IX	1	SHS 2-4
X	5	RAH 1065, GSHV 167, CCH 12-6, GISV 267, SCS 1062
XI	1	GJHV 08/70
XII	1	L 604
XIII	1	GTHV 04/13

Table 4.7. Average intra and inter-cluster D² values among thirteen clusters in 70 American cotton (*Gossypium hirsutum* L.) genotypes

Cluster No.	I	II	III	IV	V	VI	VII	VIII	IX	X	XI	XII	XIII
I	48.38	71.68	95.53	84.43	72.11	72.38	100.22	90.42	106.69	180.17	146.47	113.55	113.76
II		0.00	109.33	59.91	96.51	124.71	102.80	116.49	132.64	107.25	155.92	141.21	120.86
III			67.03	153.31	110.20	92.43	120.80	87.59	226.62	165.79	297.04	250.85	162.61
IV				110.20	141.70	116.61	142.46	155.86	110.17	185.31	130.33	126.03	149.78
V					0.00	126.20	83.14	85.62	197.35	196.46	260.37	129.11	101.08
VI						0.00	99.21	111.77	130.50	235.53	215.52	198.98	166.59
VII							92.49	128.74	176.58	225.14	273.72	169.86	156.19
VIII								0.00	212.74	143.64	266.12	217.22	57.85
IX									0.00	315.66	41.00	112.31	236.30
X										124.02	315.32	317.26	164.71
XI											0.00	134.68	254.97
XII												0.00	139.23
XIII													0.00

Note: Bold and diagonal values indicate intra-cluster D² distance

Table 4.8. The nearest and the farthest cluster from each cluster based on D^2 values using Tocher's method in 70 American cotton (*Gossypium hirsutum* L.) genotypes

Cluster No.	Nearest cluster with D^2 values	Farthest cluster with D^2 values
I	II (71.68)	X (180.17)
II	IV (59.91)	XI (155.92)
III	VIII (87.59)	XI (297.04)
IV	II (59.91)	X (185.31)
V	I (72.11)	XI (260.37)
VI	I (72.38)	X (235.53)
VII	V (83.14)	XI (273.72)
VIII	XIII (57.85)	XI (266.12)
IX	XI (41.00)	X (315.66)
X	II (107.25)	XII (317.26)
XI	IX (41.00)	X (315.32)
XII	IX (112.31)	X (317.26)
XIII	VIII (57.85)	XI (254.97)

Note: Values in parentheses indicate D^2 values

Table 4.9. Mean values of thirteen clusters estimated by Tocher's method from 70 American cotton (*Gossypium hirsutum* L.) genotypes

Cluster No.	Days to 50 % flowering	Plant height (cm)	No. of monopodia plant ⁻¹	No. of sympodia plant ⁻¹	No. of bolls plant ⁻¹	Boll weight (g)	Lint index (g)	Seed index (g)	Ginning out turn (%)	2.5% span length (mm)	Uniformity ratio	Micronaire value (10 ⁻⁶ g/inch)	Bundle strength (g/tex)	Fibre elongation (%)	Seed cotton yield plant ⁻¹ (g)	Lint yield plant ⁻¹ (g)
I	59.41	128.13	1.12	15.06	38.07	4.11	4.27	8.51	33.36	26.87	48.24	3.42	20.34	5.01	131.74	44.01
II	61.33	135.55	2.00	17.11	35.78	4.64	4.34	7.95	35.31	25.84	49.14	4.09	19.93	5.27	140.87	49.72
III	62.00	130.99	1.09	16.23	45.32	4.18	5.17	9.86	34.39	27.35	48.60	3.84	21.32	5.05	159.83	54.79
IV	61.39	127.90	1.66	14.99	38.49	4.07	3.93	7.15	35.36	26.02	49.37	3.77	19.76	5.08	128.68	45.50
V	56.00	129.00	1.33	15.33	32.17	4.65	4.70	10.77	30.39	27.67	49.79	3.07	21.59	5.25	128.17	38.99
VI	68.33	124.33	1.00	12.67	42.89	3.45	4.31	8.97	32.47	26.00	47.03	3.36	19.01	5.05	135.93	44.17
VII	64.57	127.59	1.60	14.81	31.13	4.74	4.46	9.87	31.02	28.97	47.35	3.50	21.29	4.89	124.02	38.27
VIII	58.00	122.78	1.00	14.22	28.99	4.43	5.86	8.85	39.85	25.99	51.03	3.59	20.40	5.12	108.95	43.42
IX	63.00	107.11	1.00	14.22	28.11	4.60	2.60	6.67	28.07	26.92	50.72	3.39	21.16	5.04	109.79	30.86
X	57.07	129.07	1.91	14.13	35.38	4.30	5.29	8.83	37.54	25.21	48.21	4.89	19.39	5.29	124.75	47.34
XI	57.00	131.22	1.00	15.67	32.45	3.84	2.37	5.80	28.95	26.27	50.04	3.75	20.29	5.25	105.95	30.76
XII	54.00	116.55	1.67	12.67	30.45	4.35	3.60	6.59	35.35	33.06	46.22	3.03	22.99	4.77	112.34	39.71
XIII	53.00	117.77	2.00	12.07	30.67	3.83	5.53	8.39	39.75	27.82	48.05	3.42	19.51	4.53	99.59	39.57

Note: Bold figures are minimum and maximum values

Table 4.17. PCA scores of 70 American cotton (*Gossypium hirsutum* L.) genotypes

S.No.	GENOTYPE	PCA I X VECTOR	PCA II Y VECTOR	PCA III Z VECTOR
1	BGDS 1063	35.01	51.89	-21.08
2	GISV 267	34.31	54.98	-28.01
3	SCS 1062	33.69	55.22	-24.64
4	RAH 1065	26.73	52.18	-24.22
5	CCH 12-2	34.61	52.45	-16.83
6	TSH 0499	35.43	51.31	-16.75
7	LH 2306	34.65	52.69	-20.57
8	GJHV 514	34.67	49.46	-17.29
9	P 5430	32.35	52.91	-18.52
10	L 1801	37.55	55.95	-21.46
11	RAH 1066	37.93	51.31	-15.64
12	LH 2232	32.33	52.63	-17.42
13	RS 266	33.39	51.23	-17.48
14	LH 2298	34.55	52.19	-20.77
15	TCH 1705	30.72	49.74	-17.61
16	GTHV 04/13	35.84	50.90	-22.69
17	RS 2718	33.10	52.86	-17.64
18	CCH 12-6	26.62	53.12	-21.41
19	GSHV 167	24.34	51.90	-24.16
20	ARBH 702	32.59	52.32	-14.49
21	ARBH 701	34.10	53.49	-18.78
22	Su-Flum	35.27	52.23	-17.39
23	MCU 5	41.14	55.69	-17.19
24	L 1060	32.57	53.46	-17.07
25	L 1058	35.37	53.78	-15.38
26	L 761	35.34	57.27	-23.58
27	L 1008	36.77	55.56	-23.91
28	P 72-9-37	35.81	52.87	-23.12
29	L 1569	33.73	50.12	-15.57
30	L 604	36.96	49.47	-14.55
31	GISV 103	30.21	51.15	-17.84
32	L 389	38.57	51.13	-19.03
33	HYPS 152	39.45	52.24	-17.54

Table 4.17 (cont.)

Table 4.17 (cont.)

S.No.	GENOTYPE	PCA I X VECTOR	PCA II Y VECTOR	PCA III Z VECTOR
34	RHC 0811	37.21	55.38	-15.74
35	HS 289	32.38	49.61	-18.21
36	H 1442	33.71	52.14	-19.84
37	F 2310	33.96	53.56	-17.53
38	CPD 867	29.76	52.33	-20.43
39	GISV 272	31.78	49.68	-15.44
40	RS 2669	32.93	52.37	-16.97
41	SCS 1002	33.88	53.81	-19.12
42	GJHV 44	33.25	56.84	-24.09
43	SHS 2-4	35.19	47.50	-13.15
44	GSHV 162	33.41	51.54	-14.87
45	CCH 11-2	36.07	55.14	-21.05
46	CCH 11-1	36.29	53.01	-19.27
47	CA 105	33.09	50.48	-14.51
48	CNH 50	30.17	48.62	-16.78
49	CNH 44	32.27	52.62	-16.69
50	RAH 1004	30.17	53.10	-19.38
51	GJHV 08/70	30.91	45.44	-12.87
52	KH 1101	36.32	55.23	-18.23
53	TCH 1741	36.54	51.28	-15.32
54	LH 2256	35.88	50.83	-14.08
55	PUSA 5760	34.18	55.40	-19.50
56	L 799	35.98	54.17	-19.69
57	L 804	35.76	54.48	-15.85
58	L 762	37.65	53.10	-17.48
59	L 808	38.82	53.95	-17.02
60	MR 786	33.19	52.01	-15.94
61	NDLH 1938	32.74	54.63	-19.15
62	BS 51	33.60	51.59	-22.02
63	LH 2220	32.12	51.81	-14.35
64	SCS 1001	34.71	53.56	-17.90
65	ADB 542	36.86	54.77	-15.89
66	ADB 532	35.91	53.49	-16.26
67	WGCV 48	32.05	57.96	-17.52
68	TSH 0250	35.19	56.86	-15.97
69	BS 37	36.17	59.69	-17.05
70	SCS 793	31.27	57.15	-17.67

Table 4.15. Eigen values, proportion of the total variance represented by first six principal components, cumulative per cent variance and component loading of different characters in American cotton (*Gossypium hirsutum* L.)

	PC₁	PC₂	PC₃	PC₄	PC₅	PC₆
Eigene Value (Root)	3.17	2.21	2.11	1.74	1.52	1.19
% Var. Exp.	19.83	13.79	13.17	10.91	9.49	7.43
Cum. Var. Exp.	19.83	33.62	46.79	57.69	67.19	74.62
Days to 50% flowering	0.15	0.12	0.13	0.15	0.53	0.41
Plant height (cm)	-0.34	0.24	0.08	-0.02	0.01	-0.11
No. of monopodia plant ⁻¹	-0.24	0.03	-0.18	-0.19	0.36	-0.27
No. of sympodia plant ⁻¹	-0.32	0.20	0.23	0.05	0.27	0.39
No. of bolls plant ⁻¹	-0.14	0.29	0.36	0.24	-0.33	0.02
Boll weight (g)	-0.12	0.40	0.02	0.10	0.43	-0.25
Lint index (g)	0.04	0.26	-0.40	0.38	-0.19	-0.12
Seed index (g)	0.23	0.41	-0.38	0.14	-0.04	0.11
Ginning out-turn (%)	0.10	0.05	-0.01	-0.56	0.11	-0.15
2.5% span length (mm)	0.43	0.21	0.14	0.01	0.21	-0.25
Uniformity ratio	0.22	-0.31	0.09	0.22	0.08	0.23
Micronaire value (10 ⁻⁶ g/inch)	-0.34	0.05	-0.38	0.13	-0.06	0.18
Bundle strength (g/tex)	-0.04	0.33	0.13	-0.33	-0.26	-0.08
Fibre elongation (%)	-0.25	-0.21	-0.44	-0.18	0.14	0.12
Seed cotton yield plant ⁻¹ (g)	0.07	0.28	-0.03	-0.42	-0.20	0.56
Lint yield plant ⁻¹ (g)	-0.43	-0.12	0.26	0.11	-0.04	-0.08

PC= Principal component

Appendix I. Mean performance for 16 characters of 70 American cotton (*Gossypium hirsutum* L.) genotypes

S.No.	Genotype	Days to 50% flowering	Plant height (cm)	Number of monopodia plant ⁻¹	Number of sympodia plant ⁻¹	Number of bolls plant ⁻¹	Boll weight (g)	Lint index (g)	Seed index (g)
1	BGDS 1063	58.00	113.44	1.00	12.67	33.51	4.23	4.96	8.45
2	GISV 267	61.00	123.83	2.00	10.44	20.90	5.04	5.43	10.52
3	SCS 1062	56.33	120.78	1.22	12.22	40.76	3.97	6.27	9.87
4	RAH 1065	59.00	135.00	2.00	16.45	30.33	4.57	4.33	8.33
5	CCH 12-2	62.33	129.90	1.33	15.00	39.22	3.92	4.48	7.73
6	TSH 0499	58.33	135.44	1.33	13.22	32.33	4.08	3.90	7.89
7	LH 2306	61.00	116.70	0.67	13.33	34.33	4.25	4.29	9.40
8	GJHV 514	59.00	126.11	1.22	14.00	33.94	3.71	4.00	7.23
9	P 5430	58.00	132.89	1.67	16.11	35.44	4.43	4.30	8.26
10	L 1801	60.00	117.22	1.00	14.89	40.22	3.77	5.60	10.50
11	RAH 1066	63.00	129.78	0.67	14.34	36.78	3.53	4.23	7.97
12	LH 2232	62.00	139.67	1.56	18.22	39.00	3.94	4.30	8.07
13	RS 266	56.00	121.05	1.00	15.67	40.31	3.66	4.03	8.34
14	LH 2298	59.00	132.44	1.00	13.89	32.67	3.98	4.55	9.31
15	TCH 1705	57.00	121.45	1.33	15.00	38.78	3.74	4.057	6.24
16	GTHV 04/13	53.00	117.80	2.00	12.07	30.67	3.83	5.53	8.39
17	RS 2718	65.00	138.44	1.00	17.45	39.33	4.11	3.98	8.57
18	CCH 12-6	52.00	135.11	2.33	15.33	43.22	4.08	5.14	7.90
19	GSHV 167	57.00	130.70	2.00	16.22	41.67	3.86	5.25	7.53
20	ARBH 702	62.00	129.22	1.60	15.22	53.50	3.59	4.58	7.52
21	ARBH 701	57.00	126.00	1.33	16.89	37.31	4.37	5.29	8.57
22	Su-Flum	65.00	129.30	1.22	16.33	39.28	3.57	4.53	8.18
23	MCU 5	66.00	117.44	1.11	13.78	33.97	4.43	4.31	9.87
24	L 1060	57.67	134.55	1.60	15.67	45.67	3.80	4.60	8.32
25	L 1058	61.67	133.55	1.00	14.89	46.11	3.81	4.95	7.75
26	L 761	65.00	128.90	1.00	15.67	37.78	4.35	5.64	10.75
27	L 1008	58.00	124.45	1.22	13.56	31.22	4.39	5.39	11.35
28	P 72-9-37	58.00	122.80	1.00	14.22	28.98	4.43	5.86	8.85
29	L 1569	59.33	118.90	2.33	13.56	42.11	3.58	4.12	6.77
30	L 604	54.00	116.55	1.67	12.67	30.45	4.35	3.60	6.59
31	GISV 103	56.00	121.11	1.33	15.44	44.11	3.68	4.67	6.97
32	L 389	55.00	104.22	1.00	13.44	26.04	4.43	4.45	9.17
33	HYPS 152	60.00	112.89	1.00	12.11	23.89	5.36	4.24	8.55
34	RHC 0811	63.33	127.22	2.00	14.00	37.67	4.33	3.54	9.37
35	HS 289	57.00	118.11	1.00	14.44	36.11	3.79	3.47	8.63
36	H 1442	53.00	113.00	1.00	14.45	38.44	3.97	4.49	8.90
37	F 2310	56.00	132.22	0.89	16.00	41.62	4.12	3.74	9.60
38	CPD 867	54.00	131.33	1.44	16.11	36.67	4.28	4.21	8.55
39	GISV 272	59.00	127.89	1.00	15.89	37.43	4.18	3.17	6.85

Appendix I (cont.)

Appendix I (cont.)

S.No.	Genotype	Days to 50% flowering	Plant height (cm)	Number of mono-podia plant ⁻¹	Number of sympodia plant ⁻¹	Number of bolls plant ⁻¹	Boll weight (g)	Lint index (g)	Seed index (g)
40	RS 2669	57.00	136.44	0.67	15.67	41.11	4.03	4.20	8.25
41	SCS 1002	58.00	128.33	1.11	15.33	37.89	4.36	4.57	9.03
42	GJHV 44	63.00	136.11	2.33	17.00	35.28	4.45	5.29	11.13
43	SHS 2-4	63.00	107.11	1.00	14.22	28.11	4.60	2.60	6.67
44	GSHV 162	68.00	134.78	1.44	18.22	36.67	4.20	3.43	7.62
45	CCH 11-2	56.00	129.00	1.33	15.33	32.17	4.65	4.70	10.77
46	CCH 11-1	59.00	115.00	1.00	14.44	30.67	4.81	4.17	9.57
47	CA 105	58.00	133.55	1.00	16.33	39.56	3.88	3.20	8.02
48	CNH 50	64.00	128.00	2.11	14.78	34.67	3.99	3.03	6.78
49	CNH 44	61.00	132.22	2.00	15.44	39.56	4.37	3.71	7.98
50	RAH 1004	61.33	135.55	2.00	17.11	35.78	4.64	4.34	7.95
51	GJHV 08/70	57.00	131.22	1.00	15.67	32.45	3.84	2.37	5.80
52	KH 1101	71.00	135.44	1.78	16.45	31.67	4.93	3.83	9.63
53	TCH 1741	66.00	131.11	2.00	13.67	35.89	3.74	4.00	6.94
54	LH 2256	59.00	129.45	0.78	16.22	33.56	4.13	3.30	8.03
55	PUSA 5760	64.00	141.00	0.67	16.56	39.00	4.68	5.61	9.06
56	L 799	70.67	139.55	1.78	16.78	24.23	5.25	4.58	9.18
57	L 804	56.67	140.44	1.00	15.22	41.56	4.24	4.46	8.78
58	L 762	68.33	124.33	1.00	12.67	42.89	3.45	4.31	8.97
59	L 808	60.33	136.22	1.00	13.11	36.00	4.21	4.48	9.51
60	MR 786	59.00	130.56	1.44	15.33	40.44	4.53	3.91	7.92
61	NDLH 1938	60.67	131.44	1.67	13.89	42.33	4.32	5.14	8.36
62	BS 51	63.33	125.80	2.00	11.50	25.79	4.93	4.62	7.76
63	LH 2220	66.67	137.33	1.67	15.55	37.78	4.87	3.32	6.65
64	SCS 1001	62.67	132.22	1.11	13.33	40.99	4.37	4.13	8.73
65	ADB 542	65.67	119.00	0.780	16.36	38.30	4.30	4.10	8.67
66	ADB 532	60.67	118.60	0.78	15.33	40.43	4.17	4.37	8.50
67	WGCV 48	62.67	131.60	1.44	16.53	49.47	4.20	4.80	9.20
68	TSH 0250	59.00	138.03	1.22	14.80	46.40	4.33	4.47	9.23
69	BS 37	63.33	135.03	1.10	15.90	51.23	4.10	4.87	10.20
70	SCS 793	57.00	132.23	1.33	17.83	54.20	4.00	4.50	9.43
	Mean	60.22	127.77	1.34	14.96	37.25	4.20	4.37	8.51
	C.V.	1.61	5.10	8.23	6.16	5.48	3.84	3.52	3.55
	S.E.	0.57	3.76	0.06	0.53	1.18	0.09	0.09	0.17
	C.D. 5%	1.57	10.52	0.18	1.49	3.29	0.26	0.25	0.49
	C.D. 1%	2.07	13.90	0.23	1.97	4.35	0.34	0.33	0.65
	Range Lowest	52.00	104.22	0.67	10.44	20.90	3.45	2.37	5.80
	Range Highest	71.00	140.99	2.33	18.22	54.20	5.36	6.27	11.35

Appendix I (cont.)

Appendix I (cont.)

S.No.	Genotype	Ginning out-turn (%)	2.5% span length (mm)	Uniformity ratio	Micro naire value (10^{-6} g/inch)	Bundle strength (g/tex)	Fibre elongation (%)	Seed cotton yield plant ⁻¹ (g)	Lint yield plant ⁻¹ (g)
1	BGDS 1063	37.02	26.26	50.49	3.95	19.84	5.08	120.25	44.49
2	GISV 267	34.05	28.29	43.22	4.85	20.82	5.24	89.32	30.38
3	SCS 1062	38.90	27.47	48.47	4.28	20.65	5.19	137.23	53.44
4	RAH 1065	34.25	23.96	51.63	5.64	19.19	5.55	117.53	40.21
5	CCH 12-2	36.67	26.19	50.84	3.35	21.06	5.04	127.12	46.52
6	TSH 0499	33.07	28.51	43.46	3.14	21.18	4.90	112.08	36.98
7	LH 2306	31.35	23.99	48.28	4.00	18.63	5.12	124.09	38.92
8	GJHV 514	35.64	26.83	50.45	3.66	19.95	5.03	106.51	38.01
9	P 5430	34.24	27.05	45.50	3.46	20.44	5.15	133.44	45.72
10	L 1801	34.78	29.30	46.03	3.61	20.82	4.99	128.70	44.83
11	RAH 1066	34.71	27.59	45.81	3.00	19.89	4.81	110.03	38.17
12	LH 2232	34.79	26.50	49.22	3.73	19.77	5.09	130.15	45.28
13	RS 266	32.59	26.06	50.67	3.66	20.09	5.13	125.45	40.89
14	LH 2298	32.84	25.16	50.44	3.75	19.89	5.21	110.48	36.26
15	TCH 1705	39.43	25.32	50.70	4.21	19.62	5.34	123.08	48.57
16	GTHV 04/13	39.75	27.82	48.05	3.42	19.51	4.53	99.59	39.58
17	RS 2718	31.73	25.74	50.70	4.10	19.22	5.26	134.91	42.81
18	CCH 12-6	39.43	25.48	46.47	4.36	19.27	4.98	142.93	56.51
19	GSHV 167	41.06	20.84	51.27	5.33	17.00	5.48	136.75	56.18
20	ARBH 702	37.89	25.09	50.69	2.97	18.82	4.85	146.27	55.39
21	ARBH 701	38.18	27.36	47.57	3.24	19.33	4.63	138.29	52.81
22	Su-Flum	35.65	25.54	50.04	3.30	19.92	5.18	118.94	42.41
23	MCU 5	30.43	32.23	44.96	3.16	22.81	4.87	132.19	40.25
24	L 1060	35.61	27.29	48.63	3.72	19.69	4.57	147.46	52.47
25	L 1058	38.98	29.34	45.06	3.12	20.57	4.90	149.17	58.16
26	L 761	34.44	28.17	47.74	4.66	19.81	5.13	139.17	48.01
27	L 1008	32.21	26.42	50.18	3.53	20.52	5.05	116.35	37.45
28	P 72-9-37	39.85	25.99	51.03	3.59	20.39	5.12	108.95	43.42
29	L 1569	37.75	26.87	48.87	2.89	19.98	4.85	127.81	48.25
30	L 604	35.35	33.05	46.22	3.03	22.99	4.77	112.34	39.71
31	GISV 103	40.12	24.40	50.31	4.05	18.44	4.88	137.84	55.33
32	L 389	32.68	29.41	45.45	2.96	20.30	4.68	98.05	32.12
33	HYPS 152	33.14	31.33	45.90	3.04	22.01	4.75	108.89	36.04
34	RHC 0811	27.41	31.18	44.77	3.60	22.98	4.30	136.38	37.39
35	HS 289	28.66	23.40	48.04	3.75	17.75	5.05	116.31	33.43
36	H 1442	33.53	25.81	50.92	3.55	20.34	5.30	139.80	46.85
37	F 2310	28.04	25.97	47.81	3.34	20.07	5.14	142.39	39.90
38	CPD 867	33.010	24.89	50.74	4.19	20.29	5.40	134.16	44.35
39	GISV 272	31.61	26.64	50.72	4.19	20.02	5.22	136.40	43.05

Appendix I (cont.)

Appendix I (cont.)

S.No.	Genotype	Ginning out-turn (%)	2.5% span length (mm)	Uniformity ratio	Micron aire value (10^{-6} g/inch)	Bundle strength (g/tex)	Fibre elongation (%)	Seed cotton yield plant ⁻¹ (g)	Lint yield plant ⁻¹ (g)
40	RS 2669	33.75	24.99	50.49	3.49	20.04	5.13	140.72	47.49
41	SCS 1002	33.61	27.84	47.55	3.80	20.64	5.08	130.14	43.81
42	GJHV 44	32.23	26.25	49.03	3.93	19.62	5.15	133.50	43.00
43	SHS 2-4	28.07	26.92	50.72	3.39	21.16	5.04	109.79	30.86
44	GSHV 162	31.09	25.56	50.98	3.75	19.42	4.93	131.06	40.89
45	CCH 11-2	30.39	27.67	49.79	3.07	21.59	5.25	128.17	39.00
46	CCH 11-1	30.34	26.90	48.67	3.23	20.49	5.19	125.45	38.06
47	CA 105	28.59	26.24	46.19	3.16	20.00	5.09	122.32	34.97
48	CNH 50	30.92	24.22	48.20	4.08	18.72	5.22	117.75	36.46
49	CNH 44	31.74	27.26	48.33	3.62	20.98	5.07	139.95	44.41
50	RAH 1004	35.31	25.84	49.14	4.09	19.92	5.27	140.88	49.72
51	GJHV 08/70	28.95	26.27	50.04	3.75	20.29	5.25	105.95	30.76
52	KH 1101	28.47	28.35	50.68	3.82	21.60	5.19	132.69	37.73
53	TCH 1741	36.58	29.36	45.25	3.12	21.22	4.87	113.71	41.61
54	LH 2256	29.12	28.11	49.33	3.00	22.25	5.12	118.02	34.35
55	PUSA 5760	38.25	26.05	51.60	3.58	20.18	5.22	151.83	58.11
56	L 799	33.29	27.06	45.92	3.41	19.52	4.93	108.15	36.01
57	L 804	33.69	29.39	44.87	2.89	21.30	4.70	149.72	50.43
58	L 762	32.47	26.00	47.03	3.36	19.01	5.05	135.93	44.17
59	L 808	32.02	29.38	44.89	2.55	21.20	4.82	128.48	41.26
60	MR 786	33.06	26.59	48.59	3.17	19.58	4.96	145.74	48.09
61	NDLH 1938	38.07	27.80	47.76	3.68	21.07	5.15	155.64	59.22
62	BS 51	37.31	26.54	48.81	4.27	19.94	5.09	107.95	40.30
63	LH 2220	33.26	27.37	47.81	3.77	20.85	5.21	139.45	46.30
64	SCS 1001	32.12	26.53	49.84	3.69	20.16	5.17	152.30	48.92
65	ADB 542	32.11	28.00	48.40	3.53	22.27	5.07	139.85	45.03
66	ADB 532	33.94	25.63	50.30	3.07	20.90	4.93	143.37	48.49
67	WGCV 48	34.28	25.50	46.57	3.83	21.43	4.75	176.56	60.65
68	TSH 0250	32.59	27.87	47.40	3.10	22.53	4.65	170.88	55.71
69	BS 37	32.30	28.10	48.93	3.27	24.16	5.12	178.53	57.65
70	SCS 793	32.29	27.00	50.71	4.07	21.50	5.10	184.22	59.49
	Mean	33.87	26.93	48.44	3.63	20.39	5.04	130.79	44.33
	C.V.	3.63	2.73	3.11	3.28	2.95	2.98	7.53	8.57
	S.E.	0.71	0.43	0.87	0.07	0.35	0.09	5.69	2.19
	C.D. 5%	1.98	1.18	2.43	0.19	0.98	0.24	15.90	6.14
	C.D. 1%	2.62	1.58	3.22	0.25	1.28	0.32	21.00	8.10
	Range Lowest	27.41	20.84	43.22	2.55	17.00	4.30	89.41	30.38
	Range Highest	41.06	33.05	51.63	5.64	24.16	5.55	184.22	60.65

Appendix II. Mean performance for 16 characters of 20 Egyptian cotton (*Gossypium barbadense* L.) genotypes

S.No.	Genotype	Days to 50% flowering	Plant height (cm)	Number of mono-podia plant ⁻¹	Number of sympo-dia plant ⁻¹	Number of bolls plant ⁻¹	Boll weight (g)	Lint index (g)	Seed index (g)
1	GSB 43	75.00	129.45	1.67	16.45	47.00	2.64	4.53	9.83
2	ARBD 27	72.00	125.00	1.44	15.89	46.78	2.90	4.70	9.53
3	DB 40	74.00	130.08	1.00	13.67	49.22	2.77	4.20	8.53
4	CCB 30	75.33	139.56	1.00	13.32	37.89	2.31	3.70	8.10
5	SUVIN	71.33	131.33	1.22	16.11	46.78	2.10	3.77	8.17
6	CCB 33	74.67	128.00	1.67	17.00	36.11	2.60	4.07	10.07
7	DB 39	77.00	128.30	1.11	16.56	32.80	2.40	3.36	7.40
8	GSB 21	70.67	145.33	1.67	17.23	45.44	2.85	5.13	9.87
9	DB 16	71.00	156.83	1.00	16.33	55.89	2.36	4.23	8.53
10	CCB 11	70.00	132.00	1.00	17.22	37.39	2.63	4.17	8.33
11	GSB 40	74.00	146.44	1.33	17.78	43.55	2.67	5.07	10.23
12	TCB 37	72.00	130.44	1.67	18.00	40.67	2.47	5.66	11.20
13	DB 11	74.00	141.00	1.33	18.22	41.78	2.80	4.77	9.77
14	RAB 8	75.33	148.11	1.00	19.56	42.39	3.10	4.90	9.20
15	GSB 41	68.00	155.78	1.11	20.11	44.00	2.79	5.10	10.23
16	RhCB 011	71.33	149.34	0.67	16.55	57.22	2.75	4.43	9.77
17	DB 14	69.00	132.67	1.67	17.67	41.40	2.41	4.03	9.83
18	GSB 39	73.00	130.29	1.22	12.21	48.90	2.37	3.53	8.67
19	TCB 51	70.00	146.63	2.00	15.83	35.77	2.55	4.57	10.17
20	TCB 26	72.33	140.03	1.67	14.10	52.77	2.87	3.87	8.90
	Mean	72.50	138.33	1.32	16.50	44.19	2.62	4.39	9.32
	C.V.	1.51	6.05	7.39	6.83	6.59	4.38	3.84	2.91
	S.E.	0.63	4.83	0.06	0.65	1.68	0.07	0.09	0.16
	C.D. 5%	1.81	13.83	0.16	1.87	4.82	0.19	0.28	0.45
	C.D. 1%	2.42	18.52	0.22	2.49	6.45	0.25	0.37	0.60
	Range Lowest	68.00	125.00	0.67	12.21	32.80	2.10	3.36	7.40
	Range Highest	77.00	156.83	2.00	20.11	57.22	3.10	5.66	11.20

Appendix II (cont.)

Appendix II (cont.)

S.No.	Genotype	Ginning out-turn (%)	2.5% span length (mm)	Uniformity ratio	Micronaire value (10^{-6} g/inch)	Bundle strength (g/tex)	Fibre elongation (%)	Seed cotton yield plant ⁻¹ (g)	Lint yield plant ⁻¹ (g)
1	GSB 43	31.56	31.04	45.20	2.87	25.78	5.45	105.21	33.19
2	ARBD 27	33.03	29.91	50.05	2.90	23.67	5.27	115.34	38.15
3	DB 40	32.98	31.48	48.35	2.93	24.68	5.34	115.46	38.09
4	CCB 30	31.36	34.93	47.60	2.96	25.92	5.18	74.60	23.33
5	SUVIN	31.55	36.39	44.69	2.40	26.93	5.07	85.13	26.85
6	CCB 33	28.77	33.64	46.85	2.72	25.26	5.07	79.82	22.95
7	DB 39	31.27	32.92	48.21	2.81	27.56	5.38	66.88	20.86
8	GSB 21	34.22	33.74	44.18	2.66	24.64	5.00	110.01	37.65
9	DB 16	33.17	35.49	46.98	2.67	25.18	5.11	112.00	37.17
10	CCB 11	33.35	33.15	44.90	2.78	25.39	5.30	83.48	27.85
11	GSB 40	33.13	34.55	46.57	2.89	25.64	5.19	99.18	32.94
12	TCB 37	33.61	37.82	45.56	3.09	29.49	5.53	85.61	28.81
13	DB 11	32.81	34.44	48.62	2.94	26.21	5.46	99.39	32.59
14	RAB 8	34.75	30.61	46.90	3.11	25.83	5.45	111.55	38.78
15	GSB 41	33.26	33.34	45.79	2.71	26.01	5.29	104.23	34.70
16	RhCB 011	31.22	29.18	48.03	3.20	24.42	5.52	133.20	41.59
17	DB 14	29.07	29.17	47.88	2.74	24.26	5.30	85.00	24.68
18	GSB 39	28.96	30.57	45.80	2.83	23.16	5.21	98.48	28.65
19	TCB 51	30.98	28.27	48.31	2.67	21.73	4.90	77.37	23.96
20	TCB 26	30.31	31.00	44.73	3.00	22.03	5.04	128.60	39.04
	Mean	31.97	32.58	46.76	2.85	25.19	5.25	98.53	31.59
	C.V.	3.67	2.85	2.84	3.87	3.36	2.38	7.63	8.16
	S.E.	0.68	0.54	0.77	0.06	0.49	0.07	4.34	1.49
	C.D. 5%	1.94	1.53	2.19	0.19	1.39	0.21	12.43	4.26
	C.D. 1%	2.59	2.05	2.94	0.24	1.87	0.28	16.65	5.70
	Range Lowest	28.77	28.27	44.18	2.40	21.73	4.90	66.88	20.86
	Range Highest	34.75	37.82	50.05	3.20	29.49	5.53	133.20	41.59

Appendix III. Mean performance for 16 characters of 72 inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) over three locations (pooled) during *kharif*, 2014-15

S.No.	Parent /Cross	Days to 50% flowering	Plant height (cm)	Number of mono-podia plant ⁻¹	Number of sympo-dia plant ⁻¹	Number of bolls plant ⁻¹	Boll weight (g)	Lint index (g)	Seed index (g)
LINES									
1	NDLH 1938	60.11	131.67	1.37	17.45	38.00	4.00	4.60	9.25
2	H 1442	53.66	117.31	1.78	16.74	40.41	3.97	4.90	9.92
3	ADB 542	64.44	111.13	1.59	15.56	37.85	3.89	4.39	10.16
4	ADB 532	59.22	124.68	1.85	16.89	36.17	4.01	4.78	10.05
5	WGCV 48	62.00	125.56	2.04	17.17	46.13	4.00	4.82	10.43
6	MR 786	59.67	127.48	1.78	14.81	36.17	4.03	4.39	9.67
7	TSH 0250	59.44	131.78	1.37	13.77	35.07	3.87	4.09	8.27
8	BS 37	63.22	138.22	2.15	17.04	43.61	3.89	4.44	9.57
9	SCS 793	57.22	120.82	1.32	17.35	57.00	3.65	3.91	8.92
10	MCU 5	66.44	119.15	1.00	15.43	33.98	4.02	4.53	10.51
11	L 1058	61.22	123.43	1.37	18.06	36.31	3.83	4.86	9.89
12	L 762	68.44	124.02	1.29	17.82	41.72	3.66	4.37	9.82
TESTERS									
1	GSB 40	74.89	147.37	1.85	18.65	49.22	2.78	5.51	12.15
2	DB 16	72.00	144.41	1.89	16.17	54.54	2.64	5.38	11.29
3	DB 11	75.22	140.06	2.04	17.87	44.70	2.89	4.58	11.71
4	GSB 41	70.78	148.91	1.52	17.43	46.93	2.70	5.53	11.82
5	TCB 37	74.00	125.14	1.18	15.22	42.50	2.40	5.10	10.37
6	SUVIN	71.33	134.35	1.55	16.76	45.00	2.41	4.20	11.35
CROSSES									
1	NDLH 1938 × GSB 40	64.78	194.53	2.33	23.31	71.04	3.72	5.10	11.99
2	NDLH 1938 × DB 16	62.56	176.54	2.48	24.43	73.15	3.67	5.13	12.41
3	NDLH 1938 × DB 11	60.34	162.74	2.11	22.26	71.94	3.56	5.25	11.42
4	NDLH 1938 × GSB 41	63.33	190.59	1.74	25.72	76.93	3.48	5.39	11.83
5	NDLH 1938 × TCB 37	66.00	185.05	2.04	22.91	74.02	3.13	5.28	12.38
6	NDLH 1938 × SUVIN	61.56	175.80	2.00	24.24	65.35	3.09	4.39	12.89
7	H 1442 × GSB 40	63.89	184.56	2.63	24.71	73.74	3.36	5.27	13.04
8	H 1442 × DB 16	58.89	154.02	1.78	27.29	78.91	3.74	5.35	11.85
9	H 1442 × DB 11	63.33	189.85	2.47	23.35	75.26	3.12	4.95	11.91
10	H 1442 × GSB 41	55.67	172.24	2.33	25.17	75.18	3.97	5.72	11.62
11	H 1442 × TCB 37	63.89	167.43	2.33	22.29	62.50	3.29	5.20	12.22
12	H 1442 × SUVIN	65.33	159.59	1.70	23.11	67.46	3.05	4.89	12.27
13	ADB 542 × GSB 40	65.22	174.87	1.82	21.96	72.24	3.30	5.16	12.90
14	ADB 542 × DB 16	61.67	183.23	2.71	28.02	76.52	3.70	5.73	11.59
15	ADB 542 × DB 11	64.33	179.96	2.89	23.31	70.054	3.78	4.83	12.75

Appendix III (cont.)

Appendix III (cont.)

S.No.	Hybrid	Days to 50% flowering	Plant height (cm)	Number of mono-podia plant ⁻¹	Number of sympodia plant ⁻¹	Number of bolls plant ⁻¹	Boll weight (g)	Lint index (g)	Seed index (g)
16	ADB 542 × GSB 41	65.67	176.56	2.59	24.07	60.370	3.61	5.61	12.81
17	ADB 542 × TCB 37	65.11	174.51	2.70	22.65	69.91	3.16	4.77	12.44
18	ADB 542 × SUVIN	66.11	160.13	2.48	21.11	51.70	3.03	4.85	11.97
19	ADB 532 × GSB 40	61.56	171.87	2.52	24.54	66.96	3.84	5.67	14.33
20	ADB 532 × DB 16	61.89	187.93	1.85	25.18	58.78	3.81	6.02	14.22
21	ADB 532 × DB 11	62.33	171.78	2.59	22.99	65.94	3.47	4.75	12.88
22	ADB 532 × GSB 41	64.33	162.04	3.20	20.35	63.07	3.43	5.44	12.73
23	ADB 532 × TCB 37	67.56	149.78	2.82	20.09	63.09	3.22	4.75	13.50
24	ADB 532 × SUVIN	64.00	154.78	2.71	21.36	61.07	3.29	5.05	13.52
25	WGCV 48 × GSB 40	63.33	168.50	2.37	24.72	62.70	3.49	5.02	13.14
26	WGCV 48 × DB 16	61.67	174.90	3.00	24.76	67.02	3.37	5.25	12.78
27	WGCV 48 × DB 11	63.22	165.22	2.85	24.78	74.13	3.21	5.21	12.06
28	WGCV 48 × GSB 41	65.44	163.40	2.81	20.72	67.89	3.16	4.90	11.94
29	WGCV 48 × TCB 37	65.11	155.52	3.03	22.07	62.05	3.11	5.06	12.78
30	WGCV 48 × SUVIN	64.33	156.02	2.67	20.54	53.10	3.12	5.50	13.42
31	MR 786 × GSB 40	64.11	190.06	2.18	24.26	61.63	3.67	5.44	13.30
32	MR 786 × DB 16	62.44	176.60	2.15	23.37	67.24	3.67	5.89	13.08
33	MR 786 × DB 11	63.78	179.59	2.33	24.29	68.22	3.44	4.62	12.79
34	MR 786 × GSB 41	60.89	178.02	2.22	31.42	72.68	3.63	5.72	11.54
35	MR 786 × TCB 37	62.67	174.13	2.22	23.94	69.02	3.38	5.38	14.19
36	MR 786 × SUVIN	66.78	175.04	2.59	23.46	64.65	3.39	5.46	12.29
37	TSH 0250 × GSB 40	59.44	188.48	3.00	24.67	69.29	4.21	5.93	11.79
38	TSH 0250 × DB 16	62.78	177.41	2.56	21.91	63.02	3.06	5.39	12.67
39	TSH 0250 × DB 11	64.56	171.07	1.67	23.35	66.20	2.94	4.99	13.28
40	TSH 0250 × GSB 41	65.00	167.11	2.18	22.93	66.83	2.91	4.92	12.09
41	TSH 0250 × TCB 37	66.11	158.33	1.45	20.33	44.29	3.04	4.39	12.45
42	TSH 0250 × SUVIN	62.89	167.98	2.28	21.21	57.59	2.77	4.07	12.79
43	BS 37 × GSB 40	68.22	170.28	3.18	24.16	67.85	3.69	5.18	12.63
44	BS 37 × DB 16	63.89	174.01	2.82	24.03	66.22	3.37	4.95	12.91
45	BS 37 × DB 11	65.89	171.15	2.69	21.41	58.74	3.64	4.37	12.61
46	BS 37 × GSB 41	63.89	174.93	2.89	25.82	77.89	3.36	5.12	13.00
47	BS 37 × TCB 37	66.89	164.28	2.96	22.89	59.20	3.23	4.19	13.58
48	BS 37 × SUVIN	66.33	172.15	3.07	23.00	79.98	2.96	4.26	11.09
49	SCS 793 × GSB 40	66.44	172.31	2.29	24.63	58.96	3.05	4.36	12.57
50	SCS 793 × DB 16	64.22	177.57	2.03	23.29	72.81	3.32	5.50	13.06
51	SCS 793 × DB 11	62.00	175.46	2.63	24.11	73.54	3.21	5.12	13.32

Appendix III (cont.)

Appendix III (cont.)

S.No.	Hybrid	Days to 50% flowering	Plant height (cm)	Number of mono-podia plant ⁻¹	Number of sympo-dia plant ⁻¹	Number of bolls plant ⁻¹	Boll weight (g)	Lint index (g)	Seed index (g)
52	SCS 793 × GSB 41	61.11	173.76	2.48	24.04	75.74	3.13	4.52	13.12
53	SCS 793 × TCB 37	63.56	166.35	2.41	23.72	62.11	2.62	4.93	12.75
54	SCS 793 × SUVIN	64.22	159.85	2.88	27.04	72.72	2.67	4.13	12.32
55	MCU 5 × GSB 40	66.78	165.29	2.96	22.24	46.31	3.11	4.35	13.23
56	MCU 5 × DB 16	63.44	166.63	2.26	22.59	54.61	3.31	5.36	14.17
57	MCU 5 × DB 11	66.22	163.12	1.70	21.99	45.61	2.83	4.76	12.29
58	MCU 5 × GSB 41	66.00	169.46	1.56	21.02	53.35	2.92	4.95	12.74
59	MCU 5 × TCB 37	63.00	157.96	2.89	20.07	53.35	3.01	4.61	12.74
60	MCU 5 × SUVIN	64.33	155.48	2.52	21.09	52.96	2.66	4.84	13.67
61	L 1058 × GSB 40	63.33	173.96	2.74	22.00	59.32	3.24	5.72	13.94
62	L 1058 × DB 16	70.11	162.33	2.52	24.13	63.76	3.20	6.07	12.29
63	L 1058 × DB 11	63.33	175.96	2.00	23.67	63.24	3.52	5.55	12.99
64	L 1058 × GSB 41	65.11	170.22	2.93	24.72	63.29	3.40	5.39	12.33
65	L 1058 × TCB 37	66.89	174.68	2.33	22.76	59.61	3.21	5.67	13.06
66	L 1058 × SUVIN	64.22	176.54	2.48	24.04	61.74	3.11	5.36	12.91
67	L 762 × GSB 40	60.67	175.56	1.96	23.61	65.04	3.29	5.07	12.15
68	L 762 × DB 16	58.11	169.56	1.93	23.26	75.20	3.27	5.43	11.46
69	L 762 × DB 11	61.33	176.79	2.26	24.56	71.83	3.24	5.45	12.41
70	L 762 × GSB 41	62.89	178.39	2.74	23.26	66.96	2.71	5.32	11.47
71	L 762 × TCB 37	61.78	168.48	1.85	22.26	73.05	3.68	5.34	11.36
72	L 762 × SUVIN	60.33	171.91	2.59	22.79	68.18	3.21	5.57	12.26
	Mean	64.02	163.20	2.27	22.06	61.01	3.34	5.04	12.17
	C.V.	4.04	9.41	25.61	11.96	16.51	8.92	8.12	9.41
	S.E.	0.86	5.12	0.19	0.88	3.36	0.10	0.14	0.38
	C.D. 5%	2.40	14.21	0.54	2.44	9.32	0.27	0.38	1.06
	C.D. 1%	3.15	18.69	0.71	3.21	12.26	0.36	0.50	1.39
	Range Lowest	53.66	111.13	1.00	13.77	33.98	2.40	3.91	8.27
	Range Highest	75.22	194.53	3.20	31.42	79.98	4.21	6.07	14.33

Appendix III (cont.)

Appendix III (cont.)

S.No.	Hybrid	Ginning out-turn (%)	2.5% span length (mm)	Unifor mity ratio	Micron aire value (10 ⁻⁶ g/inch)	Bundle strength (g/tex)	Fibre elonga tion (%)	Seed cotton yield plant ⁻¹ (g)	Lint yield plant ⁻¹ (g)
LINES									
1	NDLH 1938	33.28	28.15	48.47	3.67	22.24	4.97	129.46	43.07
2	H 1442	33.13	26.57	49.39	4.33	19.34	4.68	137.60	45.14
3	ADB 542	30.38	26.88	49.78	4.07	20.35	4.84	125.26	38.62
4	ADB 532	32.50	27.59	49.64	3.86	21.68	4.83	129.11	42.26
5	WGCV 48	31.71	27.77	49.01	4.41	21.00	4.78	156.55	49.53
6	MR 786	31.22	26.64	50.07	4.11	20.83	5.05	127.97	40.05
7	TSH 0250	33.15	27.82	47.31	3.37	20.90	4.67	126.28	41.88
8	BS 37	31.95	29.98	47.47	3.62	23.10	4.96	143.61	46.05
9	SCS 793	30.64	26.48	50.04	3.91	21.44	4.97	176.52	54.25
10	MCU 5	30.23	30.98	44.87	3.18	22.52	4.62	116.52	35.49
11	L 1058	33.08	28.28	47.37	3.77	20.54	4.81	118.49	39.36
12	L 762	30.89	26.55	47.73	4.49	19.82	4.83	129.81	40.06
TESTERS									
1	GSB 40	31.26	33.40	47.13	3.80	26.51	5.20	116.26	36.22
2	DB 16	32.38	33.14	47.00	2.98	27.78	5.25	121.34	39.53
3	DB 11	28.31	32.93	46.41	3.24	26.52	5.29	106.89	30.45
4	GSB 41	32.02	35.29	47.14	3.28	28.41	5.15	107.51	34.26
5	TCB 37	33.06	36.19	45.75	3.36	29.57	5.23	88.90	28.74
6	SUVIN	27.57	35.18	45.70	3.72	28.70	5.12	92.47	25.26
CROSSES									
1	NDLH 1938 × GSB 40	29.81	33.98	46.71	3.03	27.25	5.06	223.16	66.03
2	NDLH 1938 × DB 16	29.47	33.49	46.75	3.26	27.39	5.25	226.51	68.16
3	NDLH 1938 × DB 11	31.73	32.97	46.31	3.12	26.16	4.98	214.01	70.23
4	NDLH 1938 × GSB 41	31.34	33.45	46.45	2.73	27.04	4.96	225.23	70.1
5	NDLH 1938 × TCB 37	30.27	34.73	45.82	2.65	27.18	4.79	195.12	58.85
6	NDLH 1938 × SUVIN	25.50	35.32	45.43	2.95	28.11	5.06	171.88	43.64
7	H 1442 × GSB 40	29.29	34.29	46.34	3.06	26.48	4.92	206.68	60.21
8	H 1442 × DB 16	31.08	36.69	46.22	2.80	29.66	4.97	251.38	78.36
9	H 1442 × DB 11	29.56	33.23	46.06	2.84	26.13	4.97	197.62	58.62
10	H 1442 × GSB 41	33.00	33.96	46.43	3.32	26.92	4.94	253.36	83.71
11	H 1442 × TCB 37	29.92	34.95	45.87	2.99	26.79	4.73	173.27	52.17
12	H 1442 × SUVIN	28.63	34.95	45.32	3.00	27.01	4.97	174.60	49.54
13	ADB 542 × GSB 40	28.86	34.07	45.87	3.03	25.59	4.96	202.38	58.55
14	ADB 542 × DB 16	33.09	34.98	45.96	3.40	27.25	5.15	240.49	79.60
15	ADB 542 × DB 11	27.99	34.82	46.30	2.72	26.86	4.88	224.46	63.75

Appendix III (cont.)

S.No.	Hybrid	Ginn ing out- turn (%)	2.5% span length (mm)	Unifor mity ratio	Micron aire value (10 ⁻⁶ g/inch)	Bundle strength (g/tex)	Fibre elongati on (%)	Seed cotton yield plant ⁻¹ (g)	Lint yield plant ⁻¹ (g)
16	ADB 542 × GSB 41	30.63	34.88	46.05	2.85	27.79	5.05	185.06	56.20
17	ADB 542 × TCB 37	27.98	35.06	45.73	2.85	26.01	4.85	187.72	51.79
18	ADB 542 × SUVIN	29.13	36.67	45.03	3.12	27.22	5.06	131.68	38.48
19	ADB 532 × GSB 40	28.49	34.76	46.09	2.57	28.19	4.88	219.57	63.88
20	ADB 532 × DB 16	29.80	35.61	45.04	2.83	28.32	5.12	189.71	56.45
21	ADB 532 × DB 11	27.15	33.94	46.32	2.69	26.15	4.96	195.56	53.5
22	ADB 532 × GSB 41	30.00	35.49	45.76	2.71	28.49	5.04	183.11	54.83
23	ADB 532 × TCB 37	26.45	35.92	44.86	2.91	28.45	4.89	172.41	44.87
24	ADB 532 × SUVIN	27.53	36.63	44.69	2.62	27.45	4.88	169.46	47.04
25	WGCV 48 × GSB 40	28.12	35.75	45.33	2.96	27.16	4.89	180.63	51.45
26	WGCV 48 × DB 16	29.41	34.69	45.24	2.91	27.37	4.95	192.04	56.14
27	WGCV 48 × DB 11	30.66	34.34	47.42	3.01	26.37	4.96	202.29	62.57
28	WGCV 48 × GSB 41	29.40	33.84	45.88	3.06	26.13	5.08	181.28	53.77
29	WGCV 48 × TCB 37	28.57	36.12	44.55	2.91	27.52	4.78	163.11	47.22
30	WGCV 48 × SUVIN	29.45	34.77	45.71	2.98	27.23	4.89	142.05	42.40
31	MR 786 × GSB 40	29.09	32.64	47.27	2.79	25.20	4.82	188.76	54.48
32	MR 786 × DB 16	31.20	33.08	46.37	2.94	26.31	5.09	210.44	65.76
33	MR 786 × DB 11	26.61	32.72	46.44	2.69	24.99	4.69	198.96	53.40
34	MR 786 × GSB 41	33.13	33.83	47.47	3.02	26.49	5.15	224.24	74.76
35	MR 786 × TCB 37	27.69	34.21	47.50	2.92	27.16	5.03	195.89	54.67
36	MR 786 × SUVIN	30.85	33.77	44.87	2.58	25.07	4.73	186.70	56.79
37	TSH 0250 × GSB 40	33.48	36.78	44.80	3.00	27.67	4.83	248.02	83.08
38	TSH 0250 × DB 16	30.09	35.45	45.31	2.80	27.51	5.04	166.08	49.72
39	TSH 0250 × DB 11	27.67	34.53	45.82	2.66	26.85	4.86	164.63	45.44
40	TSH 0250 × GSB 41	29.07	33.29	45.01	2.53	26.43	4.85	165.43	48.31
41	TSH 0250 × TCB 37	26.32	36.57	44.45	2.73	27.09	4.65	107.31	28.11
42	TSH 0250 × SUVIN	24.23	35.37	44.20	2.61	26.89	4.54	131.82	32.04
43	BS 37 × GSB 40	29.59	36.62	47.22	2.84	29.26	5.19	213.83	63.63
44	BS 37 × DB 16	27.77	35.44	44.83	2.96	26.41	4.86	188.68	52.26
45	BS 37 × DB 11	25.81	35.61	46.38	2.69	27.37	4.97	176.00	45.17
46	BS 37 × GSB 41	28.47	35.14	45.83	2.87	27.72	5.01	222.46	63.81
47	BS 37 × TCB 37	23.80	36.89	44.85	2.68	27.77	5.02	166.09	40.46
48	BS 37 × SUVIN	27.76	35.13	45.07	2.88	25.62	4.87	200.49	55.74
49	SCS 793 × GSB 40	26.53	35.69	45.93	2.87	27.34	5.03	153.95	40.86
50	SCS 793 × DB 16	29.80	33.69	46.37	2.77	26.88	5.01	205.14	60.67
51	SCS 793 × DB 11	28.03	33.84	47.11	2.66	28.42	4.99	197.91	55.24

Appendix III (cont.)

Appendix III (cont.)

S.No.	Hybrid	Ginning out-turn (%)	2.5% span length (mm)	Uniformity ratio	Micro naire value (10 ⁻⁶ g/inch)	Bundle strength (g/tex)	Fibre elongation (%)	Seed cotton yield plant ⁻¹ (g)	Lint yield plant ⁻¹ (g)
52	SCS 793 × GSB 41	26.09	33.32	47.25	2.81	26.74	5.00	202.54	52.41
53	SCS 793 × TCB 37	28.09	35.89	46.14	2.75	27.58	4.89	137.78	37.79
54	SCS 793 × SUVIN	25.33	33.80	45.19	2.64	27.23	4.78	164.67	41.91
55	MCU 5 × GSB 40	24.56	37.29	46.11	2.67	30.17	4.96	118.42	28.97
56	MCU 5 × DB 16	27.43	36.57	43.87	2.65	26.70	4.76	152.99	41.88
57	MCU 5 × DB 11	28.15	34.49	45.68	2.62	26.38	4.78	109.35	30.66
58	MCU 5 × GSB 41	28.05	35.61	45.18	2.75	26.32	4.75	133.15	37.65
59	MCU 5 × TCB 37	26.83	36.92	43.96	2.79	26.83	4.86	137.19	36.57
60	MCU 5 × SUVIN	26.35	37.96	44.87	2.66	28.25	4.83	119.84	31.29
61	L 1058 × GSB 40	29.15	34.74	45.56	2.82	25.93	4.92	163.48	47.66
62	L 1058 × DB 16	33.24	34.61	44.91	2.77	26.16	4.90	176.54	58.42
63	L 1058 × DB 11	29.97	35.85	45.90	2.79	27.77	5.05	191.22	57.78
64	L 1058 × GSB 41	30.50	35.86	44.69	2.87	27.71	4.80	182.71	56.05
65	L 1058 × TCB 37	30.32	35.94	44.56	2.72	27.12	4.86	164.67	49.05
66	L 1058 × SUVIN	29.77	37.02	45.39	2.73	28.55	4.94	161.04	48.44
67	L 762 × GSB 40	29.51	33.15	45.75	2.93	25.41	4.87	181.08	53.39
68	L 762 × DB 16	32.25	33.88	46.50	3.10	25.94	5.12	208.48	66.54
69	L 762 × DB 11	30.56	33.74	45.26	3.00	25.95	5.12	194.98	59.48
70	L 762 × GSB 41	31.76	33.80	45.61	3.03	25.54	4.96	157.30	49.92
71	L 762 × TCB 37	32.13	33.83	45.48	2.99	26.04	4.93	226.02	70.77
72	L 762 × SUVIN	31.34	34.66	45.44	2.77	27.05	4.92	181.99	57.45
	Mean	29.53	33.93	46.14	3.03	26.30	4.94	172.27	51.01
	C.V.	6.46	3.88	2.86	6.86	4.54	3.43	18.33	18.89
	S.E.	0.64	0.44	0.44	0.07	0.40	0.06	10.52	3.21
	C.D. 5%	1.77	1.22	1.22	0.19	1.10	0.16	29.22	8.92
	C.D. 1%	2.32	1.60	1.61	0.25	1.45	0.21	38.44	11.73
	Range Lowest	23.80	26.48	43.88	2.53	19.34	4.54	88.90	25.26
	Range Highest	33.48	37.96	50.07	4.49	30.17	5.29	253.36	83.71

Table 4.20. Mean, genetic variability, heritability (broad sense) and genetic advance as per cent of mean for different characters in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) over three environments (pooled) during *kharif*, 2014-15

S.No.	Character	Mean	Range		Coefficient of variation		Heritability (%) (broad sense)	Genetic advance as per cent of mean
			Minimum	Maximum	PCV (%)	GCV (%)		
1	Days to 50% flowering	64.01	53.66	75.22	6.87	5.56	65.40	9.27
2	Plant height (cm)	163.19	111.13	194.53	14.83	11.47	59.80	18.28
3	No. of monopodia plant ⁻¹	2.26	1.00	3.20	33.36	21.37	41.10	28.22
4	No. of sympodia plant ⁻¹	22.06	13.77	31.42	18.53	14.16	58.40	28.56
5	No. of bolls plant ⁻¹	61.01	33.98	79.98	25.20	19.04	57.10	29.65
6	Boll weight (g)	3.33	2.40	4.21	14.76	11.76	63.50	19.32
7	Lint index (g)	5.03	3.91	6.07	12.49	9.49	57.70	14.85
8	Seed index (g)	12.17	8.27	14.33	13.48	9.64	51.20	14.22
9	Ginning out-turn (%)	29.52	23.80	33.48	9.90	7.50	57.40	11.72
10	2.5% span length (mm)	33.92	26.48	37.96	8.82	7.92	80.60	14.66
11	Uniformity ratio	46.13	43.87	50.07	3.93	2.70	47.10	3.81
12	Micronaire value (10 ⁻⁶ g/inch)	3.02	2.53	4.49	15.71	14.13	80.90	26.20
13	Bundle strength (g/tex)	26.29	19.34	30.17	9.70	8.57	78.10	15.60
14	Fibre elongation (%)	4.93	4.54	5.29	4.43	2.80	40.00	3.65
15	Seed cotton yield plant ⁻¹ (g)	172.27	88.90	253.36	28.43	21.74	58.50	34.24
16	Lint yield plant ⁻¹ (g)	51.01	25.26	83.71	30.91	24.47	62.70	39.91

PCV: Phenotypic co-efficient of variation

GCV: Genotypic co-efficient of variation

Table 4.40. Stability parameters for days to 50% flowering and plant height in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) as per Eberhart and Russell model during *kharif*, 2014-15

Hybrid	Days to 50% flowering			Plant height (cm)		
	Mean	bi	s ² di	Mean	bi	s ² di
NDLH 1938 × GSB 40	64.78	1.41	13.97**	194.54	1.23	-26.16
NDLH 1938 × DB 16	62.56	1.07	31.53**	176.54	0.97	56.22
NDLH 1938 × DB 11	60.34	0.18	3.22	162.74	0.82*	-39.43
NDLH 1938 × GSB 41	63.33	-0.19	1.39	190.59	1.13*	-39.43
NDLH 1938 × TCB 37	66.00	2.12	5.40*	185.05	0.98	137.29*
NDLH 1938 × SUVIN	61.56	1.32	1.68	175.80	-0.16	-32.60
H 1442 × GSB 40	63.89	0.61	-1.13	184.56	1.50	427.16**
H 1442 × DB 16	58.89	0.07*	-1.12	154.02	-0.10*	-36.36
H 1442 × DB 11	63.33	0.88	-0.08	189.85	0.84	351.72**
H 1442 × GSB 41	55.67	-0.06	-0.97	172.24	0.29	-32.29
H 1442 × TCB 37	63.89	1.01	0.44	167.43	0.64	851.09**
H 1442 × SUVIN	65.33	1.65	9.51**	159.59	0.89	65.76
ADB 542 × GSB 40	65.22	1.17	19.22**	174.87	-0.18	-33.84
ADB 542 × DB 16	61.67	0.30*	-1.14	183.231	0.40	-37.62
ADB 542 × DB 11	64.33	0.75	8.14**	179.96	1.78	-24.63
ADB 542 × GSB 41	65.67	0.45	7.71**	176.56	1.96	181.03*
ADB 542 × TCB 37	65.11	1.53	-0.15	174.51	0.87	-1.45
ADB 542 × SUVIN	66.11	1.90	4.46*	160.13	1.13	150.12*
ADB 532 × GSB 40	61.56	1.05	7.18**	171.87	1.21	70.41
ADB 532 × DB 16	61.89	0.69	10.30**	187.93	1.52	304.17**
ADB 532 × DB 11	62.33	0.45*	-1.13	171.78	1.35	-36.84
ADB 532 × GSB 41	64.33	0.82	10.91**	162.04	1.34	122.98*
ADB 532 × TCB 37	67.56	2.07	21.22**	149.78	-0.08	402.49**
ADB 532 × SUVIN	64.00	1.26	3.49*	154.78	0.79	-4.41
WGCV 48 × GSB 40	63.33	1.32	1.84	168.50	1.43	-14.13
WGCV 48 × DB 16	61.67	-0.19	1.39	174.90	0.75	-26.93
WGCV 48 × DB 11	63.22	0.14	-0.81	165.22	0.86	-10.44
WGCV 48 × GSB 41	65.44	1.68	13.50**	163.40	-0.08	522.26**
WGCV 48 × TCB 37	65.11	0.30	9.16**	155.52	0.99	205.51*
WGCV 48 × SUVIN	64.33	0.56	2.00	156.02	1.54	1.50
MR 786 × GSB 40	64.11	1.47	0.87	190.06	1.17	-32.96
MR 786 × DB 16	62.44	0.94	1.84	176.60	1.53	21.36
MR 786 × DB 11	63.78	1.66	7.93**	179.59	0.54	21.33
MR 786 × GSB 41	60.89	0.14	-0.81	178.02	0.20	-27.41
MR 786 × TCB 37	62.67	1.27	32.90**	174.13	1.64	14.98
MR 786 × SUVIN	66.78	2.22	1.50	175.04	1.60	127.65*

Table 4.40 (cont.)

Table 4.40 (cont.)

Hybrid	Days to 50% flowering			Plant height (cm)		
	Mean	bi	s ² di	Mean	bi	s ² di
TSH 0250 × GSB 40	59.44	0.25	-0.34	188.48	0.05	-34.66
TSH 0250 × DB 16	62.78	0.35	3.26	177.41	2.01	181.64*
TSH 0250 × DB 11	64.56	0.31	5.97*	171.073	0.51	118.91*
TSH 0250 × GSB 41	65.00	1.26	3.49*	167.11	1.43	40.97
TSH 0250 × TCB 37	66.11	0.66	12.60**	158.33	1.02	509.78**
TSH 0250 × SUVIN	62.89	1.72	4.22*	167.98	0.44	-28.61
BS 37 × GSB 40	68.22	1.94	13.90**	170.28	1.86	25.62
BS 37 × DB 16	63.89	0.97	5.09*	174.01	0.98	-4.90
BS 37 × DB 11	65.89	0.91	-1.14	171.15	1.64	9.48
BS 37 × GSB 41	63.89	1.18	3.00	174.93	0.74	195.86*
BS 37 × TCB 37	66.89	1.96*	-1.11	164.28	1.75	-33.58
BS 37 × SUVIN	66.33	1.16	2.53	172.15	0.45	-31.44
SCS 793 × GSB 40	66.44	0.98	7.65**	172.31	1.04	334.26**
SCS 793 × DB 16	64.22	1.01	0.44	177.57	1.01	104.42
SCS 793 × DB 11	62.00	0.85	-0.10	175.46	1.47	14.75
SCS 793 × GSB 41	61.11	0.48	0.41	173.76	1.24	-37.56
SCS 793 × TCB 37	63.56	0.30	8.26**	166.35	2.03	-35.73
SCS 793 × SUVIN	64.22	0.54	-0.84	159.85	1.95	12.16
MCU 5 × GSB 40	66.78	2.00	19.73**	165.29	0.28	19.23
MCU 5 × DB 16	63.44	1.12	6.32*	166.63	0.88	288.75**
MCU 5 × DB 11	66.22	0.89	12.01**	163.12	0.85	96.91
MCU 5 × GSB 41	66.00	2.09	4.43*	169.46	0.32	-14.06
MCU 5 × TCB 37	63.00	1.26	3.49*	157.96	-0.83	-28.43
MCU 5 × SUVIN	64.33	1.34	5.32*	155.48	-0.05	238.92**
L 1058 × GSB 40	63.33	1.94	4.61*	173.96	1.64	-5.95
L 1058 × DB 16	70.11	0.36	-0.56	162.33	1.62	24.05
L 1058 × DB 11	63.33	2.79	38.40**	175.96	1.56	-27.51
L 1058 × GSB 41	65.11	2.13	-0.42	170.22	2.11	-21.11
L 1058 × TCB 37	66.89	1.48	54.39**	174.68	1.29	68.75
L 1058 × SUVIN	64.22	1.16	0.35	176.54	0.48	9.72
L 762 × GSB 40	60.67	0.38	8.99**	175.56	1.42	18.48
L 762 × DB 16	58.11	-0.21	13.84**	169.56	0.84	-37.56
L 762 × DB 11	61.33	0.88	-0.08	176.79	1.46	151.17*
L 762 × GSB 41	62.89	0.73	3.45*	178.39	1.26	21.48
L 762 × TCB 37	61.78	0.98	-1.14	168.48	0.84	221.87*
L 762 × SUVIN	60.33	-0.18	3.22	171.91	1.04	-24.60
Population mean	63.72			171.60		

*Significant at 5% level

**Significant at 1% level

Table 4.41. Stability parameters for number of monopodia plant⁻¹ and number of sympodia plant⁻¹ in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) as per Eberhart and Russell model during *kharif*, 2014-15

Hybrid	No. of monopodia plant ⁻¹			No. of sympodia plant ⁻¹		
	Mean	bi	s ² di	Mean	Bi	s ² di
NDLH 1938 × GSB 40	2.33	1.14	0.42**	23.31	0.85	6.11**
NDLH 1938 × DB 16	2.48	-0.61	2.14**	24.43	1.15	-0.06
NDLH 1938 × DB 11	2.11	-0.08	0.27**	22.26	0.91	8.31**
NDLH 1938 × GSB 41	1.74	-0.20	-0.01	25.72	1.73	42.43**
NDLH 1938 × TCB 37	2.04	0.01	-0.01	22.91	0.82	0.00
NDLH 1938 × SUVIN	2.00	0.04	0.06*	24.24	0.97	-0.42
H 1442 × GSB 40	2.63	3.43	0.13**	24.71	0.70	10.33**
H 1442 × DB 16	1.78	0.23	0.00	27.29	-0.05*	-0.41
H 1442 × DB 11	2.47	1.51	0.02	23.35	0.77	4.14**
H 1442 × GSB 41	2.33	0.40*	-0.02	25.17	0.07*	-0.42
H 1442 × TCB 37	2.33	-3.01	0.21**	22.29	0.41*	-0.60
H 1442 × SUVIN	1.70	-1.59	0.43**	23.11	0.99	1.59
ADB 542 × GSB 40	1.82	1.45	1.31**	21.96	1.07	0.56
ADB 542 × DB 16	2.71	-0.21	-0.01	28.02	0.08	-0.23
ADB 542 × DB 11	2.89	3.18	-0.01	23.31	1.04	-0.61
ADB 542 × GSB 41	2.59	-0.68	0.08*	24.07	1.73	3.16*
ADB 542 × TCB 37	2.70	-1.36	0.62**	22.65	1.20	18.25**
ADB 542 × SUVIN	2.48	3.03	0.31**	21.11	-0.02	5.39**
ADB 532 × GSB 40	2.52	2.67	0.87**	24.54	1.21	9.41**
ADB 532 × DB 16	1.85	-0.85	-0.01	25.18	1.35	2.38*
ADB 532 × DB 11	2.59	3.64	0.16**	22.99	0.74	-0.50
ADB 532 × GSB 41	3.20	5.19	0.02	20.35	0.60	0.85
ADB 532 × TCB 37	2.82	-0.06	1.09**	20.09	1.27	8.54**
ADB 532 × SUVIN	2.71	2.33	1.96**	21.36	0.82	-0.52
WGCV 48 × GSB 40	2.37	2.07	0.04	24.72	1.61	9.76**
WGCV 48 × DB 16	3.00	1.21	0.07*	24.76	1.67	2.12*
WGCV 48 × DB 11	2.85	-0.16	0.09*	24.78	1.33	7.20**
WGCV 48 × GSB 41	2.81	3.30	0.26**	20.72	0.69	0.30
WGCV 48 × TCB 37	3.03	0.98	0.78**	22.07	0.94	-0.62
WGCV 48 × SUVIN	2.67	1.95	0.12**	20.54	0.69	5.26**
MR 786 × GSB 40	2.18	0.37	0.12**	24.26	1.23	-0.41
MR 786 × DB 16	2.15	-1.16	0.42**	23.37	0.88	2.68*
MR 786 × DB 11	2.33	-1.17	0.31**	24.29	0.86	3.10*
MR 786 × GSB 41	2.22	0.38	0.06*	31.43	0.01	1.20
MR 786 × TCB 37	2.22	0.80	0.07*	23.94	1.34	-0.44
MR 786 × SUVIN	2.59	0.75	0.56**	23.46	1.16	-0.14

Table 4.41 (cont.)

Table 4.41 (cont.)

Hybrid	No. of monopodia plant ⁻¹			No. of sympodia plant ⁻¹		
	Mean	bi	s ² di	Mean	bi	s ² di
TSH 0250 × GSB 40	3.00	0.42*	-0.02	24.67	0.14	0.21
TSH 0250 × DB 16	2.56	3.32	0.10**	21.91	1.20	-0.48
TSH 0250 × DB 11	1.67	1.79	0.50**	23.35	1.36	5.37**
TSH 0250 × GSB 41	2.18	3.27	0.48**	22.93	0.48	0.66
TSH 0250 × TCB 37	1.45	0.07	0.89**	20.33	1.32	-0.41
TSH 0250 × SUVIN	2.28	2.08	0.02	21.21	0.90	-0.43
BS 37 × GSB 40	3.18	-2.80	0.18**	24.16	1.30	14.12**
BS 37 × DB 16	2.82	0.58	0.09**	24.03	0.93	3.61**
BS 37 × DB 11	2.69	-1.03	0.03	21.41	1.26	-0.32
BS 37 × GSB 41	2.89	-0.19	0.00	25.82	1.23	4.52**
BS 37 × TCB 37	2.96	1.10	0.07*	22.89	1.63	7.57**
BS 37 × SUVIN	3.07	2.13	0.00	23.00	0.50	8.86**
SCS 793 × GSB 40	2.29	-0.12	0.34**	24.63	1.53	-0.29
SCS 793 × DB 16	2.03	-0.77	0.71**	23.29	0.92	0.51
SCS 793 × DB 11	2.63	1.38	4.10**	24.11	0.89	0.70
SCS 793 × GSB 41	2.48	2.03	0.23**	24.04	1.23	3.82**
SCS 793 × TCB 37	2.41	0.70	0.83**	23.72	1.07	2.15*
SCS 793 × SUVIN	2.88	1.77	0.24**	27.04	0.99	2.66*
MCU 5 × GSB 40	2.96	3.94	0.83**	22.24	1.23	8.67**
MCU 5 × DB 16	2.26	2.41	0.58**	22.59	1.04	-0.06
MCU 5 × DB 11	1.70	1.61	0.22**	21.99	0.93	3.37*
MCU 5 × GSB 41	1.56	-0.39	0.06*	21.02	0.90	3.37*
MCU 5 × TCB 37	2.89	1.87	0.01	20.07	0.87	15.10**
MCU 5 × SUVIN	2.52	3.54	0.08*	21.09	1.13	8.82**
L 1058 × GSB 40	2.74	2.47	0.16**	22.00	1.08	2.87*
L 1058 × DB 16	2.52	-0.96	0.36**	24.13	1.64	3.43*
L 1058 × DB 11	2.00	0.15	0.15**	23.67	1.05	-0.12
L 1058 × GSB 41	2.93	2.84	0.61**	24.72	1.49	0.07
L 1058 × TCB 37	2.33	3.96	2.94**	22.76	1.19	2.90*
L 1058 × SUVIN	2.48	2.03	0.23**	24.04	1.13	-0.18
L 762 × GSB 40	1.96	1.90*	-0.02	23.61	1.26	-0.11
L 762 × DB 16	1.93	-0.44	0.01	23.26	1.00	-0.60
L 762 × DB 11	2.26	-1.52	0.07*	24.56	1.27	14.83**
L 762 × GSB 41	2.74	1.40	0.27**	23.26	1.38	1.56
L 762 × TCB 37	1.85	0.87	0.01	22.26	0.96	13.13**
L 762 × SUVIN	2.59	1.70	-0.01	22.79	0.82	1.72
Population mean	2.43			23.40		

*Significant at 5% level

**Significant at 1% level

Table 4.42. Stability parameters for number of bolls plant⁻¹ and boll weight in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) as per Eberhart and Russell model during *kharif*, 2014-15

Hybrid	No. of bolls plant ⁻¹			Boll weight (g)		
	Mean	bi	s ² di	Mean	bi	s ² di
NDLH 1938 × GSB 40	71.04	1.40	8.04	3.72	1.26	-0.01
NDLH 1938 × DB 16	73.15	0.81	89.76**	3.67	0.86	-0.04
NDLH 1938 × DB 11	71.94	1.38	16.91*	3.56	1.56	0.33**
NDLH 1938 × GSB 41	76.93	1.32	4.45	3.48	2.16	0.02*
NDLH 1938 × TCB 37	74.02	0.58	160.65**	3.13	1.32	0.04**
NDLH 1938 × SUVIN	65.35	-0.30	130.05**	3.09	0.81	0.00
H 1442 × GSB 40	73.74	1.07	615.11**	3.36	1.67	0.01
H 1442 × DB 16	78.91	0.03	-1.35	3.74	0.24	-0.01
H 1442 × DB 11	75.26	0.90	4.06	3.12	2.01	0.15**
H 1442 × GSB 41	75.18	0.28	4.59	3.97	0.44	0.00
H 1442 × TCB 37	62.50	-0.22	244.27**	3.29	0.69	0.09**
H 1442 × SUVIN	67.46	0.19**	-4.14	3.05	1.52	0.00
ADB 542 × GSB 40	72.24	-0.52	125.49**	3.30	0.76	0.13**
ADB 542 × DB 16	76.52	-0.06*	-3.55	3.70	0.07	0.00
ADB 542 × DB 11	70.054	2.02	160.69**	3.78	0.36	0.00
ADB 542 × GSB 41	60.370	0.16	12.20*	3.61	-0.16	0.37**
ADB 542 × TCB 37	69.91	-0.61	80.39**	3.16	1.85	0.00
ADB 542 × SUVIN	51.70	0.96	-3.57	3.03	1.87*	-0.01
ADB 532 × GSB 40	66.96	2.22	108.86**	3.84	-0.77	0.03*
ADB 532 × DB 16	58.78	1.01	-2.12	3.81	-0.20	0.13**
ADB 532 × DB 11	65.94	0.53	111.83**	3.47	1.86	0.02*
ADB 532 × GSB 41	63.073	0.69	-3.50	3.43	1.73	0.12**
ADB 532 × TCB 37	63.09	-0.60	53.97**	3.22	2.52	0.02*
ADB 532 × SUVIN	61.07	0.90	20.85*	3.29	1.39	0.00
WGCV 48 × GSB 40	62.70	1.74	422.52**	3.49	1.81	0.10**
WGCV 48 × DB 16	67.02	-0.04*	-4.09	3.37	0.20	0.20**
WGCV 48 × DB 11	74.13	1.58	4.70	3.21	1.33	0.07**
WGCV 48 × GSB 41	67.89	0.66	84.21**	3.16	1.19	0.10**
WGCV 48 × TCB 37	62.05	0.94	161.64**	3.11	0.78	0.02
WGCV 48 × SUVIN	53.10	1.65	114.58**	3.12	-0.54	0.00
MR 786 × GSB 40	61.63	1.15	238.48**	3.67	1.89	0.48**
MR 786 × DB 16	67.24	0.55	16.22*	3.67	-0.50	0.02*
MR 786 × DB 11	68.22	1.22	6.03	3.44	1.63	0.02
MR 786 × GSB 41	72.68	0.05*	-4.10	3.63	0.21**	-0.01
MR 786 × TCB 37	69.02	2.10	-2.41	3.38	1.34	0.00
MR 786 × SUVIN	64.65	0.91	29.78**	3.39	1.79	0.07**

Table 4.42 (cont.)

Table 4.42 (cont.)

Hybrid	No. of bolls plant ⁻¹			Boll weight (g)		
	Mean	bi	s ² di	Mean	bi	s ² di
TSH 0250 × GSB 40	69.29	0.20*	-3.59	4.21	-0.27	0.01
TSH 0250 × DB 16	63.02	0.96	346.86**	3.06	-0.36	0.07**
TSH 0250 × DB 11	66.20	1.34	250.34**	2.94	0.88	0.00
TSH 0250 × GSB 41	66.83	0.87	27.86**	2.91	1.31	0.08**
TSH 0250 × TCB 37	44.29	1.20	141.19**	3.04	2.69	1.32**
TSH 0250 × SUVIN	57.59	1.46	45.35**	2.77	1.84	0.27**
BS 37 × GSB 40	67.85	3.52	35.95**	3.69	1.00	0.46**
BS 37 × DB 16	66.22	0.22	2.98	3.37	2.22	0.02
BS 37 × DB 11	58.74	2.07	186.76**	3.64	2.80	0.21**
BS 37 × GSB 41	77.89	0.75	53.72**	3.36	-0.08	0.02*
BS 37 × TCB 37	59.20	2.33	160.07**	3.23	1.05	0.32**
BS 37 × SUVIN	79.98	-1.36	152.47**	2.96	2.09	0.06**
SCS 793 × GSB 40	58.96	1.90	21.31*	3.05	0.98	0.15**
SCS 793 × DB 16	72.81	-0.19*	-3.91	3.32	0.86	0.06**
SCS 793 × DB 11	73.54	1.43	132.81**	3.21	1.35	0.09**
SCS 793 × GSB 41	75.74	-0.30	27.54**	3.13	1.37	0.36**
SCS 793 × TCB 37	62.11	1.75	457.76**	2.62	0.32	-0.01
SCS 793 × SUVIN	72.72	0.14	158.20**	2.67	0.40	0.01
MCU 5 × GSB 40	46.31	1.00	14.50*	3.11	1.92	0.88**
MCU 5 × DB 16	54.61	0.45	299.28**	3.31	-0.36	0.01
MCU 5 × DB 11	45.61	1.56	5.70	2.83	0.79	0.05**
MCU 5 × GSB 41	53.35	0.80	67.85**	2.92	0.33	0.02*
MCU 5 × TCB 37	53.35	-0.25	17.59*	3.01	1.30	0.22**
MCU 5 × SUVIN	52.96	0.06	68.00**	2.66	0.87	0.02
L 1058 × GSB 40	59.32	1.54	84.31**	3.24	-0.35	0.00
L 1058 × DB 16	63.76	2.88	17.18*	3.20	-0.48	0.05
L 1058 × DB 11	63.24	2.18	45.67**	3.52	-0.92*	0.00
L 1058 × GSB 41	63.29	3.16	158.67**	3.40	-1.47	0.08**
L 1058 × TCB 37	59.61	2.90	553.70**	3.21	2.24	0.12**
L 1058 × SUVIN	61.74	1.24	31.66**	3.11	1.24	0.04**
L 762 × GSB 40	65.04	1.13	7.05	3.29	1.88	0.03*
L 762 × DB 16	75.20	1.58	30.64**	3.27	1.22	0.00
L 762 × DB 11	71.83	1.84	3.18	3.24	2.21	0.04**
L 762 × GSB 41	66.96	1.13	349.11**	2.71	0.59	0.18**
L 762 × TCB 37	73.05	0.94	6.31	3.68	3.26	0.06**
L 762 × SUVIN	68.18	2.95	23.95**	3.21	0.35	0.15**
Population mean	65.63			3.30		

*Significant at 5% level

**Significant at 1% level

Table 4.43. Stability parameters for lint index and seed index in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) as per Eberhart and Russell model during *kharif*, 2014-15

Hybrid	Lint index (g)			Seed index (g)		
	Mean	bi	s ² di	Mean	bi	s ² di
NDLH 1938 × GSB 40	5.10	2.72	0.17**	11.99	0.99	-0.07
NDLH 1938 × DB 16	5.13	1.38	-0.01	12.41	0.96	0.82**
NDLH 1938 × DB 11	5.25	0.87	0.66**	11.42	0.93	1.99**
NDLH 1938 × GSB 41	5.39	-0.79	0.00	11.83	0.20*	-0.06
NDLH 1938 × TCB 37	5.28	-0.54	0.26**	12.38	0.58	10.60**
NDLH 1938 × SUVIN	4.39	1.38	0.03	12.89	0.84	1.47**
H 1442 × GSB 40	5.27	2.79	0.16**	13.04	1.99	-0.02
H 1442 × DB 16	5.35	0.33	-0.01	11.85	0.08*	-0.04
H 1442 × DB 11	4.95	1.74	0.16**	11.91	1.11	2.23**
H 1442 × GSB 41	5.72	0.29	0.00	11.62	0.14	-0.03
H 1442 × TCB 37	5.20	0.47	-0.01	12.22	0.55	0.17
H 1442 × SUVIN	4.89	2.36	0.36**	12.27	1.38	0.37*
ADB 542 × GSB 40	5.16	1.49	0.07**	12.90	1.23	1.16**
ADB 542 × DB 16	5.73	-0.27*	-0.01	11.59	-0.07*	-0.03
ADB 542 × DB 11	4.83	2.20	0.05*	12.75	1.92*	-0.06
ADB 542 × GSB 41	5.61	0.22**	-0.01	12.81	0.84	0.68**
ADB 542 × TCB 37	4.77	0.67	0.15**	12.44	0.95	2.14**
ADB 542 × SUVIN	4.85	-0.15	0.00	11.97	1.00	0.43**
ADB 532 × GSB 40	5.67	-0.97	0.00	14.34	0.87	-0.02
ADB 532 × DB 16	6.02	1.29	0.19**	14.22	0.82	0.11
ADB 532 × DB 11	4.75	1.76	0.01	12.88	1.30	0.40*
ADB 532 × GSB 41	5.44	1.60	0.16**	12.73	0.88	1.04**
ADB 532 × TCB 37	4.75	0.45	0.03	13.50	1.57	0.30*
ADB 532 × SUVIN	5.05	0.59	0.15**	13.52	1.46	-0.05
WGCV 48 × GSB 40	5.02	1.21	0.01	13.14	1.50	2.40**
WGCV 48 × DB 16	5.25	1.15	0.15**	12.78	1.11	2.86**
WGCV 48 × DB 11	5.21	0.60	0.00	12.06	1.49*	-0.07
WGCV 48 × GSB 41	4.90	0.92	0.02	11.94	0.96	1.99**
WGCV 48 × TCB 37	5.06	0.17	0.01	12.78	0.93	0.09
WGCV 48 × SUVIN	5.50	-0.17	0.02	13.42	1.07	5.48**
MR 786 × GSB 40	5.44	2.71*	-0.01	13.30	1.26	0.91**
MR 786 × DB 16	5.89	0.37	0.01	13.08	0.81	1.82**
MR 786 × DB 11	4.62	1.36	0.43**	12.79	0.90	0.15
MR 786 × GSB 41	5.72	-0.03	0.04*	11.54	-0.04	0.03
MR 786 × TCB 37	5.38	1.24	0.00	14.19	1.31	0.30*
MR 786 × SUVIN	5.46	-1.56	0.08**	12.29	0.58	0.15

Table 4.43 (cont.)

Table 4.43 (cont.)

Hybrid	Lint index (g)			Seed index (g)		
	Mean	bi	s ² di	Mean	bi	s ² di
TSH 0250 × GSB 40	5.93	0.13	0.05*	11.79	-0.02*	-0.04
TSH 0250 × DB 16	5.39	2.80	0.12**	12.67	1.60	0.95**
TSH 0250 × DB 11	4.99	0.13	0.03	13.28	1.33	0.26*
TSH 0250 × GSB 41	4.92	0.71	-0.01	12.09	0.76	1.28**
TSH 0250 × TCB 37	4.39	1.06	0.00	12.45	1.14	0.64**
TSH 0250 × SUVIN	4.07	2.59	0.20**	12.79	1.26	7.32**
BS 37 × GSB 40	5.18	0.67	-0.01	12.63	1.53	2.75**
BS 37 × DB 16	4.95	1.07	0.02	12.91	0.70	0.07
BS 37 × DB 11	4.37	1.74	0.01	12.61	1.14	0.19
BS 37 × GSB 41	5.12	1.70	0.12**	13.00	1.34	0.77**
BS 37 × TCB 37	4.19	0.39	0.03*	13.58	1.04	0.75**
BS 37 × SUVIN	4.26	2.89	0.07**	11.09	1.30	0.45**
SCS 793 × GSB 40	4.36	0.85	0.00	12.57	2.05	0.04
SCS 793 × DB 16	5.50	0.01	0.08**	13.06	0.85	0.77**
SCS 793 × DB 11	5.12	-0.36*	-0.01	13.32	0.89	3.00**
SCS 793 × GSB 41	4.52	-0.52	0.26**	13.12	1.32	3.74**
SCS 793 × TCB 37	4.93	0.01	0.33**	12.75	1.04	0.21*
SCS 793 × SUVIN	4.13	0.27	0.06**	12.32	0.95	1.42**
MCU 5 × GSB 40	4.35	3.76	0.11**	13.23	1.21	0.53**
MCU 5 × DB 16	5.36	0.90	1.99**	14.17	0.84	8.55**
MCU 5 × DB 11	4.76	-0.09	0.00	12.29	0.92	1.03**
MCU 5 × GSB 41	4.95	0.63	0.01	12.74	0.34	1.30**
MCU 5 × TCB 37	4.61	1.81	0.00	12.74	1.49	0.08
MCU 5 × SUVIN	4.84	2.21	0.32**	13.67	1.63*	-0.07
L 1058 × GSB 40	5.72	2.23	0.07**	13.94	1.12	0.22*
L 1058 × DB 16	6.07	2.43	0.40**	12.29	1.30	0.19
L 1058 × DB 11	5.55	0.81	0.10**	12.99	0.35	2.41**
L 1058 × GSB 41	5.39	2.57	2.29**	12.33	1.18	13.96**
L 1058 × TCB 37	5.67	2.65	0.10**	13.06	1.20	0.26*
L 1058 × SUVIN	5.36	1.40	0.33**	12.91	1.61	0.15
L 762 × GSB 40	5.07	1.55	0.34**	12.15	0.93	0.38*
L 762 × DB 16	5.43	0.32	0.02	11.46	0.61	0.38*
L 762 × DB 11	5.45	1.37	-0.01	12.41	0.64	-0.04
L 762 × GSB 41	5.32	0.73*	-0.01	11.47	0.56	0.09
L 762 × TCB 37	5.34	0.36	0.46**	11.36	0.75	0.62**
L 762 × SUVIN	5.57	0.39	0.01	12.26	0.69	-0.01
Population mean	5.12			12.64		

*Significant at 5% level

**Significant at 1% level

Table 4.44. Stability parameters for ginning out-turn and 2.5% span length in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) as per Eberhart and Russell model during *kharif*, 2014-15

Hybrid	Ginning out-turn (%)			2.5% span length (mm)		
	Mean	bi	s ² di	Mean	bi	s ² di
NDLH 1938 × GSB 40	29.81	-0.33	0.73	33.98	1.58*	-0.38
NDLH 1938 × DB 16	29.47	0.95	3.51**	33.49	1.15	0.34
NDLH 1938 × DB 11	31.73	1.51	0.16	32.97	0.96	-0.36
NDLH 1938 × GSB 41	31.34	0.97	-0.23	33.45	0.93	6.14**
NDLH 1938 × TCB 37	30.27	1.14	19.57**	34.73	1.18	2.33**
NDLH 1938 × SUVIN	25.50	0.33	1.19*	35.32	1.03	0.24
H 1442 × GSB 40	29.29	1.86	6.30**	34.29	1.37	-0.34
H 1442 × DB 16	31.08	-0.05	-0.06	36.69	0.07	0.17
H 1442 × DB 11	29.56	0.86	1.13*	33.23	1.16	-0.03
H 1442 × GSB 41	33.00	0.15	0.21	33.96	0.07*	-0.38
H 1442 × TCB 37	29.92	0.58	0.78	34.95	1.17	4.64**
H 1442 × SUVIN	28.63	0.25	9.68**	34.95	1.57	0.11
ADB 542 × GSB 40	28.86	1.05	0.44	34.07	0.92	-0.14
ADB 542 × DB 16	33.09	0.06	-0.29	34.98	0.04*	-0.36
ADB 542 × DB 11	27.99	1.58	-0.15	34.82	0.60	-0.37
ADB 542 × GSB 41	30.63	1.19	2.84**	34.88	0.75	0.44
ADB 542 × TCB 37	27.98	1.61	14.69**	35.06	1.23	0.79
ADB 542 × SUVIN	29.13	2.12	1.24*	36.67	1.21	-0.21
ADB 532 × GSB 40	28.49	1.83	1.46*	34.76	0.59	1.89*
ADB 532 × DB 16	29.80	0.25	3.83**	35.61	0.63	-0.04
ADB 532 × DB 11	27.15	1.05	3.10**	33.94	1.25	0.17
ADB 532 × GSB 41	30.00	0.52*	-0.33	35.49	0.64	0.08
ADB 532 × TCB 37	26.45	2.09	-0.26	35.92	0.31	-0.36
ADB 532 × SUVIN	27.53	1.72	1.75*	36.63	1.00	0.04
WGCV 48 × GSB 40	28.12	2.02	8.26**	35.75	1.33	0.16
WGCV 48 × DB 16	29.41	1.23	1.24*	34.69	1.15	-0.38
WGCV 48 × DB 11	30.66	2.35	-0.09	34.34	1.17	-0.29
WGCV 48 × GSB 41	29.40	1.47	9.36**	33.84	0.98	-0.31
WGCV 48 × TCB 37	28.57	1.32	1.80*	36.12	1.61	-0.37
WGCV 48 × SUVIN	29.45	1.56	13.00**	34.77	0.96	-0.07
MR 786 × GSB 40	29.09	0.13	1.17*	32.64	1.32	0.95
MR 786 × DB 16	31.20	0.92	8.65**	33.08	0.61	0.01
MR 786 × DB 11	26.61	0.90	13.38**	32.72	0.83	-0.21
MR 786 × GSB 41	33.13	-0.10*	-0.29	33.83	0.11*	-0.38
MR 786 × TCB 37	27.69	1.14	-0.14	34.21	1.25*	-0.39
MR 786 × SUVIN	30.85	1.92	8.48**	33.77	1.15	-0.24

Table 4.44 (cont.)

Table 4.44 (cont.)

Hybrid	Ginning out-turn (%)			2.5% span length (mm)		
	Mean	bi	s ² di	Mean	bi	s ² di
TSH 0250 × GSB 40	33.49	-0.05	0.05	36.78	0.09	-0.31
TSH 0250 × DB 16	30.09	0.55	6.29**	35.45	1.64*	-0.39
TSH 0250 × DB 11	27.67	2.06	-0.30	34.53	1.42*	-0.38
TSH 0250 × GSB 41	29.07	1.03	2.68**	33.29	0.80	-0.01
TSH 0250 × TCB 37	26.32	1.29	2.97**	36.57	1.57	1.76*
TSH 0250 × SUVIN	24.23	0.00	5.31**	35.37	1.99	-0.34
BS 37 × GSB 40	29.59	1.88	9.65**	36.62	0.23	-0.01
BS 37 × DB 16	27.77	0.26	1.01*	35.44	0.79	-0.16
BS 37 × DB 11	25.81	0.37	0.73	35.61	1.64	0.07
BS 37 × GSB 41	28.47	1.04	-0.26	35.14	0.39	0.22
BS 37 × TCB 37	23.80	1.43	3.32**	36.89	-0.29	1.22*
BS 37 × SUVIN	27.76	-0.19	3.24**	35.13	1.87	0.70
SCS 793 × GSB 40	26.53	2.66	0.18	35.69	0.98	0.07
SCS 793 × DB 16	29.80	1.43	0.23	33.69	0.84	-0.19
SCS 793 × DB 11	28.03	1.94	3.40**	33.84	0.95	-0.21
SCS 793 × GSB 41	26.09	2.55*	-0.31	33.32	0.80	-0.18
SCS 793 × TCB 37	28.09	1.36	12.19**	35.89	1.63	-0.16
SCS 793 × SUVIN	25.33	1.37	-0.15	33.80	0.68	-0.36
MCU 5 × GSB 40	24.56	-0.66	11.89**	37.29	1.05	2.04*
MCU 5 × DB 16	27.43	0.93	1.05*	36.57	1.29	-0.36
MCU 5 × DB 11	28.15	1.45	5.90**	34.49	1.52	-0.16
MCU 5 × GSB 41	28.05	0.17	1.35*	35.61	0.68	-0.15
MCU 5 × TCB 37	26.83	1.15	-0.03	36.92	0.65	1.37*
MCU 5 × SUVIN	26.35	0.60	3.48**	37.97	1.11	4.98**
L 1058 × GSB 40	29.15	0.31	-0.29	34.74	1.25	-0.35
L 1058 × DB 16	33.24	0.75	0.54	34.61	0.95	0.68
L 1058 × DB 11	29.97	0.10	1.56*	35.85	0.75	-0.28
L 1058 × GSB 41	30.50	0.58*	-0.33	35.86	1.27	-0.38
L 1058 × TCB 37	30.32	0.10	2.38**	35.94	0.88	-0.15
L 1058 × SUVIN	29.77	2.08	2.09**	37.02	2.37	-0.32
L 762 × GSB 40	29.51	0.79	1.94**	33.15	1.03	-0.20
L 762 × DB 16	32.25	1.21	2.65**	33.88	1.93	2.07*
L 762 × DB 11	30.56	0.23*	-0.33	33.74	0.77	-0.24
L 762 × GSB 41	31.76	0.68	0.26	33.80	0.48	-0.37
L 762 × TCB 37	32.13	1.49	0.64	33.83	0.94	0.17
L 762 × SUVIN	31.34	0.91	1.08*	34.66	1.00	0.19
Population mean	29.03			34.91		

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

Table 4.45. Stability parameters for uniformity ratio and micronaire value in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) as per Eberhart and Russell model during *kharif*, 2014-15

Hybrid	Uniformity ratio			Micronaire value (10 ⁻⁶ g/inch)		
	Mean	bi	s ² di	Mean	bi	s ² di
NDLH 1938 × GSB 40	46.71	7.79*	-0.47	3.03	1.59	0.00
NDLH 1938 × DB 16	46.75	4.39**	-0.47	3.26	1.78	0.01*
NDLH 1938 × DB 11	46.31	2.00	-0.47	3.12	1.80	0.00
NDLH 1938 × GSB 41	46.45	-1.69	-0.39	2.73	0.76	0.00
NDLH 1938 × TCB 37	45.82	1.31	0.63	2.65	0.33	0.00
NDLH 1938 × SUVIN	45.43	-7.76*	-0.45	2.95	1.76	0.06**
H 1442 × GSB 40	46.34	5.57	-0.45	3.06	1.93	0.00
H 1442 × DB 16	46.22	-0.33	-0.23	2.80	0.87	0.02**
H 1442 × DB 11	46.06	6.29	-0.38	2.84	1.47	0.00
H 1442 × GSB 41	46.43	-5.82	1.40*	3.32	1.66	0.13**
H 1442 × TCB 37	45.87	-0.54	0.43	2.99	1.56	0.00
H 1442 × SUVIN	45.32	-0.43	0.13	3.00	2.01	0.01*
ADB 542 × GSB 40	45.87	7.36	-0.05	3.03	1.22	0.01*
ADB 542 × DB 16	45.96	-3.44	-0.08	3.40	1.33	0.03**
ADB 542 × DB 11	46.30	-0.15	0.44	2.72	1.00	0.00
ADB 542 × GSB 41	46.05	3.39	0.93	2.85	0.53*	0.00
ADB 542 × TCB 37	45.73	-3.86	-0.17	2.85	1.14	0.01*
ADB 542 × SUVIN	45.03	11.55	-0.07	3.12	1.68	0.03**
ADB 532 × GSB 40	46.09	-7.45	-0.20	2.57	0.08	0.00
ADB 532 × DB 16	45.04	5.01	1.41*	2.83	0.83	0.00
ADB 532 × DB 11	46.32	-0.60	-0.09	2.69	0.19	0.05**
ADB 532 × GSB 41	45.76	7.35	-0.36	2.71	0.09	0.00
ADB 532 × TCB 37	44.86	4.29	0.65	2.91	1.00	0.00
ADB 532 × SUVIN	44.69	3.49**	-0.47	2.62	0.72	0.00
WGCV 48 × GSB 40	45.33	4.92*	-0.47	2.96	0.98	0.05**
WGCV 48 × DB 16	45.24	2.53	-0.46	2.91	1.12	0.02**
WGCV 48 × DB 11	47.42	8.07	2.11*	3.01	1.91*	0.00
WGCV 48 × GSB 41	45.88	2.26	-0.39	3.06	1.47	0.01*
WGCV 48 × TCB 37	44.55	-3.37	-0.44	2.91	1.52	0.00
WGCV 48 × SUVIN	45.71	-2.79	1.19	2.98	1.39	0.03**
MR 786 × GSB 40	47.27	0.01	-0.05	2.79	0.86	0.04**
MR 786 × DB 16	46.37	-2.22	0.27	2.94	1.23	0.00
MR 786 × DB 11	46.44	-5.01	1.61*	2.69	0.24	0.03**
MR 786 × GSB 41	47.47	6.08	-0.24	3.02	1.57*	0.00
MR 786 × TCB 37	47.50	-4.03	-0.11	2.92	1.58	0.00
MR 786 × SUVIN	44.87	-2.67	-0.47	2.58	0.57	0.00

Table 4.45 (cont.)

Table 4.45 (cont.)

Hybrid	Uniformity ratio			Micronaire value (10^{-6} g/inch)		
	Mean	bi	s ² di	Mean	bi	s ² di
TSH 0250 × GSB 40	44.80	-1.46	-0.18	3.00	1.16	0.00
TSH 0250 × DB 16	45.31	1.12	0.16	2.80	1.09	0.01*
TSH 0250 × DB 11	45.82	1.78	1.10	2.66	0.70	0.00
TSH 0250 × GSB 41	45.01	5.69	-0.06	2.53	0.17	0.05**
TSH 0250 × TCB 37	44.45	-1.62	-0.46	2.73	0.69	0.06**
TSH 0250 × SUVIN	44.20	3.62	-0.41	2.61	-0.09	0.00
BS 37 × GSB 40	47.22	-6.53*	-0.46	2.84	0.81*	0.00
BS 37 × DB 16	44.83	9.65	-0.31	2.96	1.11	0.02*
BS 37 × DB 11	46.38	-3.49	1.83*	2.69	0.69	0.00
BS 37 × GSB 41	45.83	0.36	0.84	2.87	1.29	0.01*
BS 37 × TCB 37	44.85	3.45	0.81	2.68	0.58	0.00
BS 37 × SUVIN	45.07	-0.02	2.89**	2.88	1.11	0.00
SCS 793 × GSB 40	45.93	0.42	-0.38	2.87	0.86	0.02*
SCS 793 × DB 16	46.37	-2.08	-0.35	2.77	1.09	0.00
SCS 793 × DB 11	47.11	-3.21	1.93*	2.66	0.38	0.07**
SCS 793 × GSB 41	47.25	2.84	-0.42	2.81	0.73	0.00
SCS 793 × TCB 37	46.14	-9.54	-0.41	2.75	1.18	0.00
SCS 793 × SUVIN	45.19	1.73	-0.45	2.64	0.40	0.00
MCU 5 × GSB 40	46.11	6.05	0.80	2.67	0.35	0.00
MCU 5 × DB 16	43.87	2.88*	-0.47	2.65	1.00	0.03**
MCU 5 × DB 11	45.68	0.14	-0.34	2.62	0.62	0.00
MCU 5 × GSB 41	45.18	-3.02	-0.36	2.75	0.58	0.02*
MCU 5 × TCB 37	43.96	2.35	-0.37	2.79	0.98	0.00
MCU 5 × SUVIN	44.87	1.88	1.54*	2.66	0.73	0.00
L 1058 × GSB 40	45.56	-2.17	-0.46	2.82	1.48	0.03**
L 1058 × DB 16	44.91	0.53	-0.03	2.77	0.69	0.00
L 1058 × DB 11	45.90	0.31	-0.44	2.79	0.82	0.00
L 1058 × GSB 41	44.69	0.23	0.05	2.87	1.09	0.00
L 1058 × TCB 37	44.56	1.96	0.05	2.72	0.92	0.00
L 1058 × SUVIN	45.39	2.56	0.95	2.73	1.14	0.01*
L 762 × GSB 40	45.75	3.72	-0.34	2.93	1.36	0.01
L 762 × DB 16	46.50	1.16	2.32*	3.10	0.97	0.03**
L 762 × DB 11	45.26	3.29	-0.17	3.00	1.32	0.01*
L 762 × GSB 41	45.61	5.13	-0.04	3.03	1.11	0.00
L 762 × TCB 37	45.48	-3.73*	-0.47	2.99	0.65	0.00
L 762 × SUVIN	45.44	4.49	-0.47	2.77	0.54	0.08**
Population mean	45.72			2.85		

*Significant at 5% level

**Significant at 1% level

Table 4.46. Stability parameters for bundle strength and fibre elongation in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) as per Eberhart and Russell model during *kharif*, 2014-15

Hybrid	Bundle strength (g/tex)			Fibre elongation (%)		
	Mean	bi	s ² di	Mean	bi	s ² di
NDLH 1938 × GSB 40	27.25	1.24	0.12	5.06	1.36	-0.01
NDLH 1938 × DB 16	27.39	1.52	-0.18	5.25	0.89*	-0.01
NDLH 1938 × DB 11	26.16	1.74	0.20	4.98	1.80	0.01
NDLH 1938 × GSB 41	27.04	0.96	1.04*	4.96	0.97	-0.01
NDLH 1938 × TCB 37	27.18	1.50	1.03*	4.79	1.28	-0.01
NDLH 1938 × SUVIN	28.11	1.40	3.30**	5.06	1.36	0.01
H 1442 × GSB 40	26.48	1.24	1.10*	4.92	1.18	-0.01
H 1442 × DB 16	29.66	0.30	0.20	4.97	2.08	0.00
H 1442 × DB 11	26.13	0.83	0.45	4.97	1.81*	-0.01
H 1442 × GSB 41	26.92	-0.05	0.00	4.94	1.03	-0.01
H 1442 × TCB 37	26.79	1.25	0.51	4.73	0.97	-0.01
H 1442 × SUVIN	27.01	1.87	0.19	4.97	1.46	0.01
ADB 542 × GSB 40	25.59	0.81	-0.19	4.96	1.43	0.01
ADB 542 × DB 16	27.25	-0.07	-0.15	5.15	0.20*	-0.01
ADB 542 × DB 11	26.86	1.22	0.20	4.88	1.10	-0.01
ADB 542 × GSB 41	27.79	0.11	-0.19	5.05	0.96	-0.01
ADB 542 × TCB 37	26.01	1.02	1.39**	4.85	0.51	0.00
ADB 542 × SUVIN	27.22	0.97	-0.16	5.06	0.51*	-0.01
ADB 532 × GSB 40	28.19	0.14	-0.08	4.88	0.68	0.00
ADB 532 × DB 16	28.32	0.58	-0.18	5.12	1.61	-0.01
ADB 532 × DB 11	26.15	1.52	-0.23	4.96	0.62	-0.01
ADB 532 × GSB 41	28.49	1.01	-0.24	5.04	1.28	0.04*
ADB 532 × TCB 37	28.45	0.68	-0.01	4.89	1.15	-0.01
ADB 532 × SUVIN	27.45	1.02	1.80**	4.88	1.32	-0.01
WGCV 48 × GSB 40	27.16	0.88	-0.18	4.89	1.27	-0.01
WGCV 48 × DB 16	27.37	1.07	0.22	4.95	0.67	0.01
WGCV 48 × DB 11	26.37	1.44	0.47	4.96	1.73	0.00
WGCV 48 × GSB 41	26.13	0.86*	-0.24	5.08	0.72	0.09**
WGCV 48 × TCB 37	27.52	0.85	-0.22	4.78	-0.18	0.00
WGCV 48 × SUVIN	27.23	1.45	-0.22	4.89	1.72	0.00
MR 786 × GSB 40	25.20	1.45	-0.17	4.82	1.22	0.00
MR 786 × DB 16	26.31	0.81	-0.16	5.09	1.41	0.00
MR 786 × DB 11	24.99	1.50	-0.20	4.69	0.64	-0.01
MR 786 × GSB 41	26.49	-0.07	0.07	5.15	1.38	0.02
MR 786 × TCB 37	27.16	0.54	0.61	5.03	1.09	-0.01
MR 786 × SUVIN	25.07	1.64	0.18	4.73	0.54	-0.01

Table 4.46 (cont.)

Table 4.46 (cont.)

Hybrid	Bundle strength (g/tex)			Fibre elongation (%)		
	Mean	bi	s ² di	Mean	bi	s ² di
TSH 0250 × GSB 40	27.67	-0.01*	-0.23	4.83	0.28	0.05**
TSH 0250 × DB 16	27.51	1.09	-0.23	5.04	0.33	0.00
TSH 0250 × DB 11	26.85	2.04	0.20	4.86	1.17	0.02*
TSH 0250 × GSB 41	26.43	0.82	0.20	4.85	0.67	0.06**
TSH 0250 × TCB 37	27.09	1.43	0.29	4.65	0.67	-0.01
TSH 0250 × SUVIN	26.89	1.70	-0.21	4.55	0.18	0.00
BS 37 × GSB 40	29.26	-0.12*	-0.23	5.19	-0.51	0.01
BS 37 × DB 16	26.41	0.60	0.03	4.86	0.87	0.00
BS 37 × DB 11	27.37	1.44	-0.04	4.97	0.84	0.03*
BS 37 × GSB 41	27.72	0.50	-0.03	5.01	0.84	-0.01
BS 37 × TCB 37	27.77	0.82	0.04	5.02	1.12	0.00
BS 37 × SUVIN	25.62	1.44	-0.21	4.87	1.18	0.11**
SCS 793 × GSB 40	27.34	0.95**	-0.24	5.03	0.64	0.00
SCS 793 × DB 16	26.88	0.42	0.27	5.01	0.84	0.00
SCS 793 × DB 11	28.42	-0.12	2.23**	4.99	0.44*	-0.01
SCS 793 × GSB 41	26.74	0.88	0.37	5.00	-0.22	0.02
SCS 793 × TCB 37	27.58	1.22	-0.23	4.89	0.81	0.00
SCS 793 × SUVIN	27.23	0.22**	-0.24	4.78	1.39	-0.01
MCU 5 × GSB 40	30.17	0.86	16.89**	4.96	0.37	0.03*
MCU 5 × DB 16	26.70	1.65	0.34	4.76	1.37*	-0.01
MCU 5 × DB 11	26.38	2.26	0.31	4.78	1.33	-0.01
MCU 5 × GSB 41	26.32	1.23	-0.15	4.75	1.50	0.00
MCU 5 × TCB 37	26.83	0.79	0.32	4.86	1.50	0.03*
MCU 5 × SUVIN	28.25	0.77	3.43**	4.83	1.10	-0.01
L 1058 × GSB 40	25.93	1.32	0.10	4.92	2.02	0.02
L 1058 × DB 16	26.16	1.18	4.35**	4.90	1.21	0.12**
L 1058 × DB 11	27.77	0.78	2.34**	5.05	0.50	-0.01
L 1058 × GSB 41	27.71	1.12	0.00	4.80	0.55	-0.01
L 1058 × TCB 37	27.12	0.34	-0.19	4.86	0.80	-0.01
L 1058 × SUVIN	28.55	1.72	1.73**	4.94	1.47	0.00
L 762 × GSB 40	25.41	1.13	-0.22	4.87	0.98	0.00
L 762 × DB 16	25.94	1.88	1.22*	5.12	1.24	0.03*
L 762 × DB 11	25.95	1.24	0.26	5.12	1.90	0.00
L 762 × GSB 41	25.54	0.95	-0.12	4.96	1.43	0.00
L 762 × TCB 37	26.04	1.00	0.17	4.93	0.47	0.03*
L 762 × SUVIN	27.05	1.29	-0.23	4.92	0.98	0.01
Population mean	27.02			4.93		

*Significant at 5% level

**Significant at 1% level

Table 4.47. Stability parameters for seed cotton yield plant⁻¹ and lint yield plant⁻¹ in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) as per Eberhart and Russell model during *kharif*, 2014-15.

Hybrid	Seed cotton yield plant ⁻¹ (g)			Lint yield plant ⁻¹ (g)		
	Mean	bi	s ² di	Mean	bi	s ² di
NDLH 1938 × GSB 40	223.16	1.92	30.41	66.03	0.77	86.01**
NDLH 1938 × DB 16	226.51	0.40	575.82**	68.16	1.60	50.05**
NDLH 1938 × DB 11	214.01	-0.08	243.92*	70.23	1.37	135.16**
NDLH 1938 × GSB 41	225.23	1.23	154.33	70.1	0.94	10.06
NDLH 1938 × TCB 37	195.12	0.14	88.60	58.85	-0.05	145.19**
NDLH 1938 × SUVIN	171.88	-1.26	79.77	43.64	-0.33	29.10*
H 1442 × GSB 40	206.68	-0.83	2844.57**	60.21	1.16	348.83**
H 1442 × DB 16	251.38	0.12	17.53	78.36	0.05	10.49
H 1442 × DB 11	197.62	-0.26	452.60**	58.62	0.05	3.42
H 1442 × GSB 41	253.36	0.19	-42.51	83.71	0.44*	-7.12
H 1442 × TCB 37	173.27	-0.59	392.76*	52.17	-0.04	108.63**
H 1442 × SUVIN	174.60	0.04	488.46**	49.54	-0.66	-4.89
ADB 542 × GSB 40	202.38	-0.52*	-70.15	58.55	0.19	10.78
ADB 542 × DB 16	240.49	0.13	-38.28	79.60	0.07	-1.61
ADB 542 × DB 11	224.46	2.25	4368.18**	63.75	2.91	246.17**
ADB 542 × GSB 41	185.06	1.10	-34.22	56.20	0.99	3.44
ADB 542 × TCB 37	187.72	-1.49	242.94*	51.79	-0.15*	-7.19
ADB 542 × SUVIN	131.68	0.73	85.32	38.48	0.93	-5.70
ADB 532 × GSB 40	219.57	2.55	7848.48**	63.88	3.43	489.43**
ADB 532 × DB 16	189.71	0.99	475.02**	56.45	0.78	28.54*
ADB 532 × DB 11	195.56	1.15	2874.90**	53.5	0.67	201.15**
ADB 532 × GSB 41	183.11	1.10	307.39*	54.83	0.62	44.14**
ADB 532 × TCB 37	172.41	-1.34	773.99**	44.87	-0.70	10.01
ADB 532 × SUVIN	169.46	0.63	-49.92	47.04	0.88	35.40*
WGCV 48 × GSB 40	180.63	-0.05	3190.04**	51.45	1.83	282.60**
WGCV 48 × DB 16	192.04	0.84	76.35	56.14	0.87	3.89
WGCV 48 × DB 11	202.29	2.23	118.66	62.57	2.31*	-6.77
WGCV 48 × GSB 41	181.28	0.66	-7.91	53.77	1.45	-5.47
WGCV 48 × TCB 37	163.11	0.02	1140.56**	47.22	0.73	190.62**
WGCV 48 × SUVIN	142.05	1.70	3266.66**	42.40	2.01	234.55**
MR 786 × GSB 40	188.76	1.47	692.64**	54.48	1.14	5.50
MR 786 × DB 16	210.44	0.99	698.90**	65.76	0.99	123.13**
MR 786 × DB 11	198.96	1.61	294.40*	53.40	1.50	109.64**
MR 786 × GSB 41	224.24	0.04	-62.82	74.76	0.02*	-6.64
MR 786 × TCB 37	195.89	2.21	-16.86	54.67	1.88*	-7.20
MR 786 × SUVIN	186.70	1.53	1151.47**	56.79	0.84	6.05

Table 4.47 (cont.)

Table 4.47 (cont.)

Hybrid	Seed cotton yield plant ⁻¹ (g)			Lint yield plant ⁻¹ (g)		
	Mean	bi	s ² di	Mean	bi	s ² di
TSH 0250 × GSB 40	248.02	0.59	3.74	83.08	0.66	-6.14
TSH 0250 × DB 16	166.08	2.54	805.17**	49.72	1.29	133.85**
TSH 0250 × DB 11	164.63	1.87	857.66**	45.44	1.40	26.15*
TSH 0250 × GSB 41	165.43	1.44	735.63**	48.31	1.03	103.20**
TSH 0250 × TCB 37	107.31	0.24	696.73**	28.11	0.16	25.57*
TSH 0250 × SUVIN	131.82	-0.11	106.74	32.04	0.34	-5.63
BS 37 × GSB 40	213.83	2.96	1457.77**	63.63	2.88	127.35**
BS 37 × DB 16	188.68	-0.08	694.05**	52.26	-0.48	9.48
BS 37 × DB 11	176.00	2.33	1592.60**	45.17	0.86	179.35**
BS 37 × GSB 41	222.46	0.22	1233.99**	63.81	1.14	140.67**
BS 37 × TCB 37	166.09	4.03	396.40*	40.46	2.59	132.67**
BS 37 × SUVIN	200.49	-3.08	407.74*	55.74	-2.64	40.27*
SCS 793 × GSB 40	153.95	2.79	-46.75	40.86	2.31*	-7.08
SCS 793 × DB 16	205.14	0.09	436.10**	60.67	0.08*	-7.17
SCS 793 × DB 11	197.91	1.34	607.35**	55.24	1.35	26.01*
SCS 793 × GSB 41	202.54	-2.49**	-72.27	52.41	-0.67	232.99**
SCS 793 × TCB 37	137.78	2.50	574.47**	37.79	1.30	46.43**
SCS 793 × SUVIN	164.67	-0.20	278.92*	41.91	0.57	62.04**
MCU 5 × GSB 40	118.42	-0.16	-31.17	28.97	0.00	21.60*
MCU 5 × DB 16	152.99	1.30	744.88**	41.88	0.76	80.48**
MCU 5 × DB 11	109.35	1.65	198.91	30.66	1.37	2.53
MCU 5 × GSB 41	133.15	1.43	139.20	37.65	0.89	70.23**
MCU 5 × TCB 37	137.19	-1.10	417.49*	36.57	-0.63*	-6.97
MCU 5 × SUVIN	119.84	0.02	566.48**	31.29	-0.33	1.38
L 1058 × GSB 40	163.48	2.35	-4.97	47.66	1.74	20.35
L 1058 × DB 16	176.54	4.25	1481.87**	58.42	3.85*	-3.37
L 1058 × DB 11	191.22	2.90	5060.08**	57.78	3.16	56.14**
L 1058 × GSB 41	182.71	4.75	2694.85**	56.05	4.18*	-6.62
L 1058 × TCB 37	164.67	4.62	3542.63**	49.05	2.15	949.54**
L 1058 × SUVIN	161.04	0.43	201.46	48.44	1.37	47.38**
L 762 × GSB 40	181.08	1.42	565.32*	53.39	0.98	105.36**
L 762 × DB 16	208.48	2.05	154.11	66.54	1.72	96.29**
L 762 × DB 11	194.98	1.82	19.10	59.48	1.15	67.55**
L 762 × GSB 41	157.30	2.57	1901.81**	49.92	1.39	420.11**
L 762 × TCB 37	226.02	0.01	2139.07**	70.77	-0.29	83.15**
L 762 × SUVIN	181.99	3.09	959.92**	57.45	2.88	-2.78
Population mean	184.10			53.90		

*Significant at 5% level

**Significant at 1% level

Table 4.38. Environment index values (I_j) for different characters in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) during *kharif*, 2014-15

Character	Environment		
	Bapatla	J M Puram	Lam Farm
Days to 50% flowering	-0.20	-2.11	2.31
Plant height (cm)	-15.18	1.35	13.83
No. of monopodia plant ⁻¹	0.02	0.25	-0.27
No. of sympodia plant ⁻¹	-4.66	4.11	0.55
No. of bolls plant ⁻¹	-8.35	-1.26	9.60
Boll weight (g)	0.05	0.19	-0.23
Seed index (g)	-0.11	1.96	-1.85
Lint index (g)	-0.07	0.35	-0.28
Ginning out-turn (%)	-0.20	-1.68	1.88
2.5% span length (mm)	0.05	1.58	-1.63
Uniformity ratio	0.11	0.08	-0.19
Micronaire value (10 ⁻⁶ g/inch)	-0.04	0.35	-0.31
Bundle strength (g/tex)	0.05	1.43	-1.48
Fibre elongation (%)	-0.02	0.16	-0.15
Seed cotton yield plant ⁻¹ (g)	-20.47	7.07	13.41
Lint yield plant ⁻¹ (g)	-6.54	-1.14	7.68

Table 4.39. Analysis of variance for stability of different characters in inter-specific hybrids of cotton (*G. hirsutum* L. × *G. barbadense* L.) as per Eberhart and Russell model during *kharif*, 2014-15

Source of variation	d.f	Days to 50% flowering	Plant height (cm)	No. of monopodia plant ⁻¹	No. of sympodia plant ⁻¹	No. of bolls plant ⁻¹	Boll weight (g)	Lint index (g)	Seed index (g)
Rep within Env.	6	0.51	19.48	0.02	0.40	6.03	0.05	0.01	0.04
Genotypes	71	17.48**	271.89**	0.54	10.86**	193.74**	0.31**	0.66**	1.57
Env+ (Genotypes × Env.)	144	11.00*	354.96**	0.47	25.00**	207.65**	0.15	0.30**	5.07**
Environments	2	353.94**	15243.12**	5.01**	1402.78**	5882.86**	3.25**	7.42**	261.43**
Genotypes × Env.	142	6.17	145.27	0.40	5.59	127.72	0.10	0.20	1.46
Environments (Lin.)	1	707.87**	30486.25**	10.02**	2805.55**	11765.73**	6.50**	14.84**	522.87**
Genotypes × Env.(Lin.)	71	4.57	167.13	0.39	6.60	152.93*	0.09	0.23	1.51
Pooled Deviation	72	7.66**	121.70**	0.41**	4.51**	101.08**	0.12**	0.17**	1.38**
Pooled Error	426	1.16	39.76	0.02	0.63	4.11	0.01	0.01	0.07
Total	215	13.14	327.53	0.49	20.33	203.05	0.20	0.42	3.91

Source of variation	d.f	Ginning out-turn (%)	2.5% span length (mm)	Uniformity ratio	Micronaire value (10 ⁻⁶ g/inch)	Bundle strength (g/tex)	Fibre elongation (%)	Seed cotton yield plant ⁻¹ (g)	Lint yield plant ⁻¹ (g)
Rep within Env.	6	0.22	0.26	0.16	0.02	0.25	0.03	36.82	3.83
Genotypes	71	14.42**	4.60**	2.13**	0.10**	3.12**	0.05**	3255.72**	461.01**
Env+ (Genotypes × Env.)	144	6.69**	3.55**	0.81	0.14**	3.17**	0.04**	1544.68*	166.70**
Environments	2	230.31**	185.06**	1.90	7.91**	153.38**	1.71**	23357.90**	3711.95**
Genotypes × Env.	142	3.54	1.00	0.79	0.04**	1.06	0.01	1237.45	116.76
Environments (Lin.)	1	460.61**	370.12**	3.81*	15.82**	306.76**	3.43**	46715.80**	7423.91**
Genotypes × Env.(Lin.)	71	3.60	1.28**	0.95*	0.05**	1.28*	0.01	1496.18*	139.40*
Pooled Deviation	72	3.42**	0.70**	0.63	0.02**	0.83**	0.02**	965.13**	92.82**
Pooled Error	426	0.34	0.39	0.48	0.00	0.24	0.01	74.42	7.29
Total	215	9.24	3.90	1.24	0.13	3.16	0.04	2109.72	263.89

* Significant at 5% level

** Significant at 1% level - When tested against pooled error