

**RNA SEQUENCE BASED QTL MAPPING AND GENETIC
INVESTIGATION FOR SEED COTTON YIELD AND
FIBRE STRENGTH IN *Gossypium hirsutum* L.**

MAHESH R. HAMPANNAVAR

**DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE, DHARWAD
UNIVERSITY OF AGRICULTURAL SCIENCES,
DHARWAD – 580 005**

JANUARY, 2020

**RNA SEQUENCE BASED QTL MAPPING AND GENETIC
INVESTIGATION FOR SEED COTTON YIELD AND
FIBRE STRENGTH IN *Gossypium hirsutum* L.**

Thesis submitted to the
University of Agricultural Sciences, Dharwad
in partial fulfillment of the requirements for the
Degree of

DOCTOR OF PHILOSOPHY

in

GENETICS AND PLANT BREEDING

By

MAHESH R. HAMPANNAVAR

**DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE, DHARWAD
UNIVERSITY OF AGRICULTURAL SCIENCES,
DHARWAD – 580 005**

JANUARY, 2020

**DEPARTMENT OF GENETICS AND PLANT BREEDING
COLLEGE OF AGRICULTURE, DHARWAD
UNIVERSITY OF AGRICULTURAL SCIENCES, DHARWAD**

CERTIFICATE

This is to certify that the thesis entitled “**RNA SEQUENCE BASED QTL MAPPING AND GENETIC INVESTIGATION FOR SEED COTTON YIELD AND FIBRE STRENGTH IN *Gossypium hirsutum* L.**” submitted by **Mr. MAHESH R. HAMPANNAVAR**, for the degree of **DOCTOR OF PHILOSOPHY** in **GENETICS AND PLANT BREEDING** to the University of Agricultural Sciences, Dharwad is a record of research work done by him during the period of his study in this University under my guidance and supervision and the thesis has not previously formed the basis for the award of any degree, diploma, associateship, fellowship or other similar titles.

**DHARWAD
JANUARY, 2020**

**(B. R. PATIL)
CHAIRMAN**

Approved by :

Chairman : _____
(B. R. PATIL)

Members : 1. _____
(B. S. JANAGOUDAR)

2. _____
(I. S. KATAGERI)

3. _____
(ARAVINDA KUMAR B. N.)

ACKNOWLEDGEMENT

Gratitude takes three forms, “A feeling from the heart, an expression in words and a giving in return.....”

On my personal note, floral salutations with serene tranquility and pure love may only contain towards my parents. It is an immense pleasure to express my sincere gratitude and heartfelt respects to the blessing of my family members father Sri. **RAJENDRA**, mother Smt. **SHASHIKALA**. younger brother **MANOJ**, whose undemanding, selfless scarifies, unwearing support, love and blessings in these days of testing and toiling, stand in a immaculate, may I be worthy to be upto their desires and expectations. It is my privilege to express sense of reverence, gratitude and thanks to **Dr. B. R. PATIL**, Professor, Department of Genetics and Plant Breeding, University of Agricultural Sciences, Dharwad and the esteemed chairman of my advisory committee for his constructive criticism throughout the period of investigation which enabled me to reach this mile stone in my life.

I express my sincere gratitude and thanks to the to the members of my advisory committee, **Dr. B. S. JANAGOUDAR**, Former Vice Chancellor UAS Dharwad, **Dr. I. S KATAGERI**, Dean (Forestry) College of Forestry, Sirsi, UAS, Dharwad and **Dr. ARAVINDA KUMAR B. N.**, Placement Cell Head and Professor of Agronomy College of Agriculture, UAS, Dharwad for constant encouragement during research work and critical suggestions during the preparation of thesis.

I avail this opportunity to express my sincere thanks to **Dr. B. D. Biradar**, Professor and Head, Department of Genetics and Plant Breeding, , **Dr. S. K. Deshpande**, Professor, **Dr. O. Sridevi**, Professor, **Dr. Vijayakumar** Special Officer Seed, UAS Dharawad, **Dr. M. C. Wali**, Professor and **Dr. S. A. Desai**, Professor, **Priya**, SRF, Department of Genetics and Plant Breeding, College of Agriculture, Dharwad for their help and co-operation during post graduation life at UAS, Dharwad.

I express my deep sense of gratitude to non-teaching staff Sri. Lobo, Miss. Veena, Sri. Hiremat, Sri. Manju Badiger, **Mr. Nagappa** and **Mr. Rudrappa** of the Department of Genetics and Plant Breeding, UAS, Dharwad.

Courageous guidelines help a lot to obtain desirable results in research work so I am happy to be associated with my lab mates and I extend special thanks to **Manoj**,

Vrinda, Lokeshkumar, Vinay, Sangamesh, Shreyas, Gopi, Ganesh, Shailaja and Maruti for their kind and selfless help during research.

I am very thankful to all my seniors Venkatesh, Vinod, Mani, Harivaraprasad Krishna, Saritha, and Suresh for their kind help and support during my stay here. Heartful special thanks to my batchmates Anjan, Kiran, Sowjanya, Lokesh, Lakshmiddevamma, Mahalaxmi and Anisa Nimbal for their constant support and encouragement during the tenure of whole Ph. D. programme.

I gratefully acknowledge Karnataka Government, for providing me financial support.

Any omission in this brief acknowledgement does not mean lack of gratitude.

DHARWAD

JANUARY, 2020

(MAHESH R. HAMPANNAVAR)

CONTENTS

Chapter No.	Chapter Particulars	Page No.
	CERTIFICATE	iii
	ACKNOWLEDGEMENT	iv
	LIST OF ABBREVIATIONS	viii
	LIST OF TABLES	ix
	LIST OF FIGURES	xi
	LIST OF PLATES	xii
	LIST OF APPENDICES	xiii
1.	INTRODUCTION	1-5
2.	REVIEW OF LITERATURE	6-41
	2.1 Construction of linkage map and identification of QTLs related to yield and fibre quality traits in cotton	7
	2.2 Genetic variability for yield, yield contributing and fibre quality traits in cotton	21
	2.3 Correlation and path analysis in cotton	32
	2.4 Intergeneration correlation and regression for yield and yield component traits and fibre quality traits yield	37
	2.5 Identification of transgressive segregants in the RIL population	40
3.	MATERIAL AND METHODS	42-73
	3.1 Experimental site location and weather condition	42
	3.2 Experimental material	42
	3.3 Experimental design and layout plan	48
	3.4 Observations recorded	48
	3.5 Biometrical analysis	51
	3.6 Molecular analysis	59
	3.7 Development of linkage map and QTL mapping in RIL population	70

Contd.....

Chapter No.	Chapter Particulars	Page No.
4.	EXPERIMENTAL RESULTS	74-152
	4.1 Analysis of variance	74
	4.2 Identification of QTLs for yield and fibre quality traits	76
	4.3 Genetic variability parameters for yield and yield attributes and fibre quality traits	108
	4.4 Character association and path analysis in the RIL population	113
	4.5 Intergeneration correlation and regression between the F ₄ Vs F ₅ and F ₅ Vs F ₆ generation	125
	4.6 Identification of transgressive segregants in RIL population	133
	4.7 Identification of superior recombinant inbred lines based on <i>per se</i> performance	140
	4.8 Identification of superior recombinant inbred lines (RIL) over the check varieties	144
5.	DISCUSSION	153-183
	5.1 Analysis of variance	153
	5.2 Identification of QTLs for yield and fibre quality traits	154
	5.3 Genetic variability parameters for yield and yield attributes and fibre quality traits	163
	5.4 Character association and path analysis in the RIL population	167
	5.5 Intergeneration correlation and regression between the F ₄ Vs F ₅ and F ₅ Vs F ₆ generation	177
	5.6 Identification of transgressive segregants in RIL population	180
	5.7 Identification superior lines over the commercial variety	182
	5.8 Identification of superior recombinant inbred lines based on <i>per se</i> performance	183
6.	SUMMARY AND CONCLUSIONS	185-189
	REFERENCES	190-216
	APPENDICES	217-249

LIST OF ABBREVIATIONS

$\mu\text{g inch}^{-1}$	- Microgam per inch
ANOVA	- Analysis of Variance
cm	- centi meter
DNA	- Deoxyribonucleic Acid
F ₂	- Second filial generation
F ₃	- Third filial generation
F ₄	- Fourth filial generation
F ₅	- Fifth filial generation
F ₆	- Sixth filial generation
g	- gram
g/tex	- gram per tex
HVI	- High Volume Instrument
Kg ha ⁻¹	- Kilogram per hectare
LM	- Linkage Map
LOD	- Logarithm Of The Odds
m	- meter
PCR	- Polymerase Chain Reaction
QTL	- Quantitative Trait Loci
RIL	- Recombinant Inbred Line
RNA	- Ribonucleic Acid
SDL	- Segregation Distortion Loci
SRAP Polymorphism	- Sequence Related Amplified
TRAP	- Target Region Amplified Polymorphism
TS	- Transgressive Segregation
UHML	- Upper Half Mean Length

LIST OF TABLES

Table No.	Title	Page No.
1.	List of recent studies on QTL mapping in <i>Gossypium</i> sp for various traits	14
2.	Characteristics of distorted loci on interspecific and intraspecific populations in <i>G. hirsutum</i>	20
3.	List of recent Genetic variability studies for yield, yield attributes and fibre quality traits in <i>Gossypium</i> sp.	23
4.	Table 4: Meteorological data parameters during the crop growth period at University of Agricultural Sciences, Dharwad	43
5.	Characteristics of parental lines viz., RHAP 12 and RHAP 15 of <i>G. hirsutum</i>	44
6.	Schematic representation of ANOVA table of simple lattice design	51
7.	Composition of CTAB DNA extraction buffer	60
8.	Concentration of each component in PCR mixture	62
9.	List of Sequence Related Amplified Polymorphism (SRAP) primers employed in <i>G. hirsutum</i>	64
10.	Thermo profile of PCR for SRAP markers	63
11.	List of Target Region Amplified Polymorphism (TRAP) primers employed in <i>G. hirsutum</i>	71
12.	Thermo profile of PCR for TRAP markers	66
13.	<i>Hirsutum barbadense</i> introgressed lines; HBS144 and HBS187 contrasting for fibre strength, fibre diameter and cellulose content at different fibre developmental stages	70
14.	Analysis of variance for yield and its component and fibre quality traits in the RIL population of <i>G. hirsutum</i>	75
15.	Trait performance of RIL (Recombinant Inbred Line) and its parent's viz., RHAP 12 and RHAP 15 of <i>G. hirsutum</i>	77
16.	List of polymorphic Sequence Related Amplified Polymorphic (SRAP) markers identified between the RHAP 12 and RHAP15 of <i>G. hirsutum</i>	88
17.	List of polymorphic Target Region Polymorphism (TRAP) markers identified between the RHAP 12 and RHAP 15 of <i>G. hirsutum</i>	91
18.	Summary of the SRAP and TRAP linkage map of the RHAP 12 × RHAP 15 derived RIL population of <i>G. hirsutum</i>	94

Contd.....

Table No.	Title	Page No.
19.	List of Segregation Distortion loci in the SRAP and TRAP linkage map of the RHAP 12 × RHAP 15 derived RIL population of <i>G. hirsutum</i>	99
20.	List of significantly segregation distortion loci in the genetic map of the RHAP 12 × RHAP 15 derived RIL population of <i>G. hirsutum</i>	99
21.	Biometrical parameters of individual QTL affecting the cotton yield, its attributes and fibre quality traits in RIL population derived from intraspecific hybridization between RHAP 12 and RHAP 15 of <i>G. hirsutum</i>	102
22.	Mean, range and components of variance of yield and its component traits and fibre quality traits in recombinant inbred lines of <i>G. hirsutum</i>	109
23.	Phenotypic correlation coefficient between seed cotton yield and its component traits and fibre quality traits in 222 recombinant inbred lines of <i>G. hirsutum</i>	114
24.	Genotypic correlation coefficient between seed cotton yield and its component traits and fibre quality traits in 222 recombinant inbred lines (RILs) of <i>G. hirsutum</i>	115
25.	Phenotypic path coefficient among seed cotton yield and its attributing and fibre quality traits in 222 recombinant inbred lines of <i>G. hirsutum</i>	119
26.	Genotypic path coefficient among seed cotton yield and its attributing and fibre quality traits in 222 recombinant inbred lines of <i>G. hirsutum</i>	120
27.	Intergeneration correlation and regression between the F ₄ vs F ₅ and F ₅ vs F ₆ generations of segregating population derived from hybridization of RHAP 12 and RHAP 15 of <i>G. hirsutum</i>	126
28.	Identification of Transgressive Segregants (TS) in the RIL population derived from hybridization between RHAP 12 and RHAP 12 of <i>G. hirsutum</i>	134
29.	List of top 20 superior lines based on per se performance for each trait in RIL population of <i>G. hirsutum</i>	141
30.	List of significantly superior lines over check variety for seed cotton yield per plant in RIL population of <i>G. hirsutum</i>	146
31.	List of significantly superior lines over check variety for ginning outturn in RIL population of <i>G. hirsutum</i>	148
32.	List of significantly superior lines over check variety for fibre strength in RIL population of <i>G. hirsutum</i>	150
33.	List of superior lines over check variety for upper half mean length (UHML) in RIL population of <i>G. hirsutum</i>	152

LIST OF FIGURES

Figure No.	Title	Page No.
1.	Time line of research programme	45
2.	Outline of Sequence Related Amplified Polymorphism (SRAP) marker	62
3.	Outline of Target Region Amplification Polymorphism (TRAP) marker	67
4.	Example for amplicons pattern and scoring pattern of dominant and recessive markers in the <i>QTL IciMapping</i> software	73
5.	Frequency distribution of agronomic and fibre quality traits in RIL population	78
6.	Construction of linkage map by employing the SRAP and TRAP markers in cotton RIL population.	95
7.	Number of Markers (%) per linkage group	98
8.	Genome coverage by each linkage group	98
9.	Percentage of segregation distortion in linkage map	100
10.	Genetic linkage map and the location of QTLs for yield and its attributing and fibre quality traits in the intraspecific RIL linkage map	103
11.	Graphical representation of phenotypic and genotypic coefficient of variance of yield and fibre quality traits in RIL population of upland cotton	110
12.	Path analysis of seed cotton yield per plant in 222 recombinant inbred lines derived from RHAP 12 and RHAP 15 genotypes	121
13.	Parent offspring linear regression graph for the yield and its attributing traits and fibre quality traits across the segregating generation	127

LIST OF PLATES

Plate No.	Title	Page No.
1.	Parental lines viz., RHAP 12 and RHAP 15 of <i>G. hirsutum</i> utilized to develop intraspecific derived RIL population	46
2.	Field general view during <i>kharif</i> 2018	47
3.	Electron microscopic view of fibrillar arrangement in <i>Hirsutum barbadense</i> introgressed lines HBS144 and HBS187 contrasting for fibre strength used for RNA sequencing by illumina biseq method	69
4.	<i>Hirsutum barbadense</i> introgressed lines HBS144 and HBS187 contrasting for fibre strength used for RNA sequencing by illumina biseq method	68
5.	Monomorphic and Polymorphic behavior of Sequence Related Amplified Polymorphism (SRAP) markers between RHAP 12 and RHAP 15 of <i>G. hirsutum</i>	84
6.	Monomorphic and Polymorphic behavior of Target Region Amplified Polymorphism (TRAP) markers between RHAP 12 and RHAP 15 of <i>G. hirsutum</i>	85
7.	Genotyping the 222 RILs using SRAP marker viz., me8-em8 at 150 bp	87

LIST OF APPENDICES

Appendix No.	Title	Page No.
I	Chi-square value of poly morphic SRAP and TRAP markers employing in genotype of RIL population	217
II.	Phenotypic observation on yield and its attributes and fibre quality traits in RIL population delivered from intraspecific hybridization between RHAP 12 $\times$ RHAP 15 of <i>G. hirsutum</i>	219
IIIa.	Phenotypic observation on yield and its attributing traits in F ₄ , F ₅ and F ₆ segregating population delivered from intraspecific hybridization between RHAP 12 $\times$ RHAP 15 of <i>G. hirsutum</i>	230
IIIb.	Phenotypic observation on fibre quality traits in F ₄ , F ₅ and F ₆ segregating population delivered from intraspecific hybridization between RHAP 12 $\times$ RHAP 15 of <i>G. hirsutum</i>	240

1. INTRODUCTION

The genus *Gossypium* is the most important source of natural textile fibre (Wakelyn and Chaudhry, 2010). The cotton plant is a perennial shrub or tree that belongs to order Malvales, family Malvaceae, genus *Gossypium* L. The genus comprises 50 species (Fryxell, 1992 and Wendel and Cronn, 2003), out of that 45 are diploid ($2n=2x=26$) and five are allotetraploid ($2n=4x=52$). The geographical distribution of species spans the tropical and subtropical regions of the world. The two A genome diploid species and two AD genome tetraploid species are grown for their lint (Wakelyn and Chaudhry, 2010). The tetraploid cotton would have arisen on the American continent from the unique hybridization event, which was then followed by diversification. Globally 90 per cent cotton area is under *G. hirsutum*, eight per cent is under *G. barbadense* and just two per cent is under *G. arboreum* and *G. herbaceum*. India has the peculiarity of growing all the four cultivated cotton species viz., *G. arboreum*, *G. herbaceum* (both diploids, $2n = 2x = 26$), *G. hirsutum* and *G. barbadense* (both tetraploids, $2n = 4x = 52$). India is the leading producer of cotton and contributes 26 per cent of total production of world. In India cotton is cultivated in an area of 12.2 million hectares with a production of 36.1 million bales and productivity of 501 kg ha^{-1} . In Karnataka it has covered an area of 0.575 million hectares with a production of 1.8 million bales and productivity of 532 kg ha^{-1} (Anon., 2019).

Cotton is known as “White Gold” due to revenue gain in agriculture as well as textile industrial economy. In India the 65 per cent of raw material is supplied from cotton to textile industry. However, low seed cotton yield and poor fibre quality were major constraint in cotton production (Wakelyn and Chaudhry, 2010). Therefore, breeder should concentrate on developing genotypes with high fibre yield along with superior fibre quality. The fibre yield and fibre quality can be attributed by a set of measurable characters so we need to focus on these independent traits. The set of traits which influence the yield are plant height, sympodia branches per plant, number of monopodia branches per plant, number of bolls per plant, lint index, seed index, boll weight and ginning outturn and many more. Some of fibre quality traits viz., fibre strength, fibre length and fibre fineness are the primary quality properties that influence textile processing. Earlier cotton industries were giving preference in the order of fibre

length, fibre fitness, fibre maturity and lastly to the fibre strength. Due to modernization of textile industry through increased automation of spinning and weaving, there is demand for change in the order of preference where, fibre strength is at top place (Wakelyn and Chaudhry, 2010). Higher preference should be given to fibre strength under cotton fibre quality parameters for making our cotton quality comparable and competitive with man made fibre. Hence, there is a need to develop cotton varieties and/or hybrids with high fibre strength along with high yield.

However, the available breeding material has a narrow genetic base and less variability for seed cotton yield and fibre quality traits. Hence, it is essential to expand the genetic base through hybridization among the contrasting lines. Hybridization has been practised long before the onset of Mendalian genetics. In hybridization two genetically diverse genotypes are crossed to produce an array of variation in segregating population. Whereas recombination is another natural phenomenon, where two or more loci recombine to form new combination/s of alleles; particularly recombination of an additive allele from either of the parents which gives rise to a transgressives. Hence, the transgressive segregants are the result of hybridization and recombination between the parental genomes (Nolte and David, 2005). The transgressive segregants are helpful for extending the limit of character expression in the parents.

Traditional breeding procedures are difficult to improve the complex traits because of long duration and low selective efficiency. The long duration could be overcome by early generation selection. The early generation selection in the population is determined by the intergeneration correlation of the particular trait. The selection efficiency could be increased by studying the intergeneration regression of the particular trait. The intergeneration regression helps to analyse the potential of the parent to transfer the trait value to its progeny. By estimating the intergeneration correlation and regression for the agronomic and fibre quality characters in cotton, we could improve the selection efficiency.

Since hybridization breeding was initiated in plants, significant achievements have been attained in cotton improvement. The innovations in textile technology and improvements in living standards continuously occur, thus increasing the requirement in cotton fibre yield and quality. Improving yield and fibre quality simultaneously is a

long-term challenge for cotton breeders. Instead of improving the yield and fibre quality from conventional breeding, new technologies such as biotechnology increase the likelihood of success (Ortiz, 1998; Ruttan, 1999; Huang *et al.*, 2002). One field of biotechnology, the DNA markers, derived from research into molecular genetics and genomics, offers great potential for plant breeding. Based on the study of quantitative trait locus (QTL), a locus (DNA section) correlates with a variation of a quantitative trait in the phenotype of an organism population (Miles and Wayne, 2008). This is often an early step in identifying and sequencing the actual genes that cause the trait variation. The DNA markers linked to allelic variation in the genes underlying these traits. By using those DNA markers in plant breeding, efficiency and precision could be greatly increased. The use of DNA markers in plant breeding is called marker-assisted selection (MAS) and is a component of the new discipline of 'molecular breeding' (Huang *et al.*, 2002). To identify a particular marker linked to the genomic region governing the trait of interest requires much background work viz., linkage map and QTL mapping.

The QTLs are the genomic regions that link the information between phenotypic (trait measurement) and genotypic data (molecular markers) and explain the genetic basis of variation in complex traits. There is a need for QTL analysis to explore the individual QTLs and discover more of their action, interaction and precise location in the genome of a crop species. However, for QTL mapping, there is a requirement to develop suitable mapping population from phenotypically contrasting parents and genetic markers to construct the linkage group. There are four types of mapping populations; F₂, backcross and Recombinant Inbred Lines (RILs), Near Isogenic Lines (NILs) which have been popularly used for plant genetic mapping. The recombinant inbred lines (RILs) are stable and are developed by using single seed descent method from second filial generation. It involves continuous selfing until homozygosity is obtained in all the individuals. Each cycle of selfing results in enhanced recombination frequency and these populations are highly suitable for saturated mapping. To date, majority of cotton genetic maps have been developed based on interspecific populations, which had little usage in upland cotton breeding programs. The intraspecific genetic maps of upland cotton help to detect QTLs for fibre quality and yield traits. However, due to low levels of intraspecific DNA marker polymorphisms in

upland cotton, most intraspecific maps have relatively low density and cannot satisfy for MAS and map-based cloning purposes. Therefore, it is necessary to develop new type of markers which can enable mapping of intraspecific upland cotton populations to obtain high polymorphism.

The Sequence Related Amplified Polymorphism (SRAP) markers are simple, dominant and codominant, efficient markers (Li and Quiros, 2001). This marker system can be adapted for a variety of purposes in different crops, including genomic and gene tagging, cDNA fingerprinting, map-based cloning and map construction (Comlekcioglu *et al.*, 2010). It has several advantages over other marker systems such as ease, reasonable throughput rate, discloses numerous co-dominant markers, allows easy isolation of bands for sequencing and most notably, it targets open reading frames (ORFs) (Li and Quiros, 2001). Target Region Amplified Polymorphism (TRAP) marker is also a PCR based marker to detect the polymorphism at Express Sequence Tag (ESTs) sites. The TRAP markers are employed for various purposes *viz.*, assessment of genetic diversity (Alwala *et al.*, 2006 and Hu *et al.*, 2005), isolation of an express gene, gene tagging and construction of genetic map (Li *et al.*, 2006 and Yang *et al.*, 2005). The combination of SRAP and TRAP markers facilitated to identify sufficient polymorphic loci in between the parents. These markers are low cost and high throughput in nature. These two markers assist in construction of high-density linkage map furthermore assists in identifying the QTLs around the candidate gene (Miklas *et al.*, 2006; Lim *et al.*, 2008).

Hence, considering various limitations in cotton breeding, in the present experiment, an effort has been done to identify the transgressive segregants with respect to fibre quality and seed cotton yield traits in comparison to superior parents and superior line over the commercial check varieties. The intergeneration correlation and regression were assessed between the segregating generations for early generation selection. For a better understanding of QTL governing quantitative traits, a genetic linkage map of tetraploid cotton was sought through Sequence Related Amplified Polymorphism (SRAP) and Target Region Amplified Polymorphism (TRAP) markers in the cotton RIL population.

Objectives of the investigation

1. To construct the genetic linkage map in cotton using RNA *seq.* based polymorphic markers.
2. To detect QTLs *vis a vis* association with molecular markers for seed cotton yield, its components and fibre quality traits.
3. To study the intergeneration correlation in F₄ Vs F₅ and F₅ Vs F₆ generation for yield and yield attributes.
4. To identify the transgressive segregants for seed cotton yield, its components and fibre quality traits.

2. REVIEW OF LITERATURE

The cotton plant is a perennial shrub or tree that belongs to order Malvales, family Malvaceae, genus *Gossypium* L. The genus *Gossypium* (*G. hirsutum*, *G. barbadense*, *G. herbaceum* and *G. arboreum*) produces the spinnable fibres. The *Gossypium* genus is subdivided into four sub-genus, six sections and 15 subsections (Fryxell, 1979). In total *Gossypium* genus comprises 50 species (Fryxell, 1992; Wendel and Cronn, 2003), 45 of which are diploid ($2n=2x=26$) and five are allotetraploid ($2n=4x=52$). In addition, genus includes 9 distinct morphological and cytological genomic groups in which first eight groups are diploid in nature and designated by letters A to G and K, the ninth group is tetraploid and carries the A and D genomes (Percival *et al.*, 1999).

The molecular investigation suggested that the tetraploid cotton arose on the American continent (new world) during the Pleistocene period, through a unique interspecific hybridization event- which explains the monophyletic origin of tetraploid cotton, involving an A genome and a D genome species (Wendel and Cronn, 2003). The A genome of the AD tetraploid species was derived from a type close to *G. herbaceum*, while the D genome would originate from a D genome species nowadays extinct, but close to that of *G. raimondii*. The geographical distribution of *Gossypium* sp. spans the tropical and subtropical regions of the world.

Today, plant breeding can be considered as an evolutionary science and backbone of a scientific discipline that developed by integrating approaches from the various scientific fields (including molecular technology). It allows breeders to increase their efficiency and more thoroughly exploit the genetic resources.

Calhoun and Bowman (1999) stated that breeding objectives should be based on market requirements and genetic resources. Cotton breeders focused on at least three distinct markets *viz.*, cotton manufacturers, textile processors and end-users. The cotton breeder would increase the yield and fibre quality to reach these three separate markets. A cultivar carrying all the desired characteristics could ensure that upland cotton remains dominant over the synthetic fibres in the competitions.

The fibre quality parameters like fibre length, uniformity, fineness, maturity, fibre elongation and especially fibre strength is a major consideration in development of upland cultivars. The emphasis on fibre strength is prompted mostly by change in textile technology that allows the more rapid processing. Along with fibre quality, seed cotton yield is very important trait for the cotton producers. It would not be exaggeration to say that whole genome of a plant contributes to its final yield (Worley *et al.*, 1974). The quantitative inheritance of seed cotton yield and fibre quality traits makes them complex traits whose expression depends upon the action of multigene. Hence, the present study focuses on improving the seed cotton yield and fibre quality simultaneously by using novel techniques.

2.1 Construction of linkage map and identification of QTLs related to yield and fibre quality traits in cotton

In the present study, we employed the Sequence Related Amplified Polymorphic (SRAP) and Target Region Amplified Polymorphism (TRAP) markers to construct the linkage map in the RIL population. In this section the genetic markers, mapping population, linkage mapping and QTL mapping with respect to yield and fibre quality traits in cotton is reviewed.

The linkage phenomenon was exploited by Sturtevent in 1913 to construct the first-ever linkage map in *Drosophila*. “A linkage map is a schematic representation of the relative location of various genetic markers present in the chromosomes of an organism as determined from the frequency of recombination between pair of markers”. The Linkage is one of the phenomena which deviate from the Mendel second law *i.e* law of independent assortment. The recombination frequency between the adjacent markers is calculated from the appropriate mapping population. Considering above said facts, to construct the linkage map two equipments are fundamental *viz.*, genetic marker and mapping population.

2.1.1 Genetic Markers employed in the construction of a linkage map

In the genomic analysis, molecular markers, especially PCR-based markers are widely used. The main applications of these markers have been in taxonomy, map construction, evolution and gene cloning. These markers differ in reliability, complexity

and throughput. Some of the markers include Amplified Fragment Length Polymorphism (AFLP), Random Amplified Polymorphic DNA (RAPD), Simple Sequence Repeat polymorphism (SSR) and a few others (Lee, M., 1995; Rafalski *et al.*, 1996). Each marker has its own advantages and disadvantages. For example low reproducing capacity and random amplification of RAPD marker, complex procedure in detecting of AFLP markers and expensive nature of SSR markers (Vos *et al.*, 1995). By considering these limitations, we employed the Sequence Related Amplified Polymorphism (SRAP) and Target Region Amplified Polymorphism (TRAP) markers. These markers generates good amplification and exhibit high polymorphism in various crops viz., citrus, potato, rice, lettuce, garlic, apple, rapeseed (*B. napus*), and celery (Li and Quiros, 2001).

a. Sequence Related Amplified Polymorphism (SRAP) markers

SRAP is a PCR-based marker system which consists of two primers, a forward primer of 17 bases and a reverse primer of 18 bases. The forward primer consists of 10 bases at 5' end which has filler sequence with no specific combination, followed by CCGG sequence *i.e.* core sequence along with three selective nucleotides at 3' end. The variation in these selective nucleotides generates the set of primers. The reverse primer shares the same property as forward primer except four nucleotide sequence (CCGG) in forward, whereas in reverse primer AATT replaces core sequence (Fig. 2). During construction of primers there should be consideration 40-50 per cent GC content along with avoidance of secondary structure and the filler sequence from both forward and reverse primer must be different from each other (Li and Quiros, 2001).

Lin *et al.* (2003) developed the first linkage map in cotton using the SRAP marker in F₂ population derived from an interspecific cross (Handan208 × Pima90). The 285 loci exhibited the polymorphism between the parents, which were harbored on 39 linkage groups at LOD of 3. The total length of the map was 3030.7 cM which covered 65.4 % of the whole cotton genome and the average distance between adjacent markers was 12.79 cM. All the markers were distributed evenly among the linkage groups without clustering of loci.

This SRAP marker was used in combination with other markers to increase the map length. Zhang *et al.* (2009) constructed the linkage map in RIL population derived

from an interspecific cross of T586 × Yumian 1 using the four types of markers including 509 SSR, 29 SRAP, eight morphological markers, and 58 introns targeted intron-exon splice junction (IT-ISJ) marker. These polymorphic loci genotyped in 270 (F_{2:7}) RIL populations. The map spanned length of 3,140.9 cM with 60 linkage groups furthermore an average interval of 5.2 cM between adjacent markers, approximately accounting for 70.6 % of the cotton genome. The high density linkage map was constructed by Yu *et al.* (2007) using 129 SRAP, 697 SSRs, 171 TRAPs, 98 AFLP and two morphological markers in 186 F₂ populations derived from interspecific cross (CRI 36 × Hai 7124). The total map length spanned 4536.7cM with an average genetic distance of 4.1 cM per marker. This map provides an essential resource for high resolution mapping of quantitative trait loci and molecular breeding in cotton.

In nutshell, the SRAP markers are simple, dominant and codominant. The marker system that can be adapted for a variety of purposes in different crops, including gene tagging, cDNA fingerprinting, map based cloning and map construction (Comlekcioglu *et al.*, 2010). It has several advantages over other marker systems such as ease, reasonable throughput rate, discloses numerous co-dominant markers, allows easy isolation of bands for sequencing and most notably, it targets Open Reading Frames (ORFs).

b. Target Region Amplified Polymorphism (TRAP) Markers

Target Region Amplified Polymorphism (TRAP) marker is also one of important PCR based marker to detect the polymorphism at Express Sequence Tag (ESTs) sites. The TRAP marker has complementarity with SRAP marker, in which one of the primers is designed using the sequence information from Express Sequence Tags (ESTs) sites and the other primer is an arbitrary sequence with either a GC or AT rich core anneals to an exon or intron regions (Fig. 3). During the genetic analysis this combination pair of primer will be attached to specific gene (Hu and Vick, 2003). The TRAP primer with the average length of 18 base pairs furthermore first five cycles annealing temperature is 35°C followed by 35 cycles with an annealing temperature of 50°C.

The TRAP markers are being used for various purposes like an assessment of genetic diversity (Alwala *et al.*, 2006 and Hu *et al.*, 2005), isolation of expressed gene, gene tagging and construction of genetic map (Li *et al.*, 2006 and Yang *et al.*, 2005).

Yu *et al.* (2007) reported the first linkage map using the TRAP marker in F₂ population (186) derived from interspecific crosses CRI 36 × Hai 7124. Along with TRAP markers, employed SRAP, SSR, AFLP and morphological marker for construction of linkage map. This map was spanned length of 4536.7 cM with an average genetic distance of 4.1 cM per marker.

A linkage map was constructed by Yang *et al.* (2005) in wheat crop by employing 612 simple sequence repeats (SSRs) and 12 Target Region Amplified Polymorphism (TRAP) markers. He concluded that TRAP markers assists in identifying new QTL governing the resistance to Fusarium head blight (FHB). In wheat RIL population (79) Yang *et al.* (2005) constructed a linkage map which consisted of 172 polymorphic markers. He concluded that "TRAP marker failed to identify the new QTLs for the trait, but marker significantly increased map density and the region amplified using TRAP primer was far from the expected region. The above said results could be due to complex genome structure of wheat and/or EST regions used for preparation of TRAP primer might be far from QTLs. As a result, use of TRAP markers for fine mapping may need cautiousness. Liu *et al.* (2005) concluded that TRAP markers were spread throughout the wheat genome and assisted in filling the gaps in the linkage map. The TRAP marker exhibited similar properties as SSR in assigning the linkage groups to chromosomes. TRAP markers are mostly dominant therefore more useful in Recombinant Inbred Lines (RILs) and Double haploids (DH) population.

The TRAP markers are highly efficient in generating great numbers of polymorphic loci (Liu *et al.*, 2005; Hu *et al.*, 2005; Alwala *et al.*, 2006) and could be used to significantly boost map density by connecting the linkage groups and filling the gaps (Yang *et al.*, 2005).

2.1.2 Mapping population utilized for genotyping

A population that is suitable for linkage map using genetic markers is known as a mapping population. Mapping populations are developed by crossing the contrastingly

different parents and handling of progenies of parents in a definite fashion (Paterson, 1996). The mapping populations are used for identifying the region on chromosome and genetic distance between two loci. The genetic markers aid in construction of map using recombination frequency and identifying the QTLs. The markers, which are shown the linkage with the QTL can be used in Marker Assisted Selection (MAS) for trait of interest (Paterson, A. H., 1996). Based on taxonomic relationship between parents, mapping population is two types viz., intraspecific and interspecific population. There are several different types of mapping population in the crops based on the development; each one has its own advantage and disadvantages (Paterson, 1996).

The biparental mapping populations are derived from two contrasting parents viz., F_2 , $F_{2:3}$, near isogenic lines, double haploids, recombinant inbred lines, immortal F_2 population and chromosomal segment substitution lines (Schneider *et al.*, 2001). The development of mapping population depends on per cent of inbreeding depression in the species, time available for developing and trait to be mapped (Schneider *et al.*, 2001). The double haploid and RILs are immortal mapping populations. The lines are true-breeding lines or homozygous lines. This permitted the evaluation of these lines in multiple environments. The double haploids population requires the regeneration capacity of plants which is lack in most of the crops so only option left to produce the immortal population is Recombinant Inbred Lines (RILs). Hence, in the present investigation recombinant inbred lines were utilized for genotyping.

Recombinant inbred lines (RILs) are a set of homozygous lines produced by continuous inbreeding/selfing of individual F_2 plants (Burr *et al.*, 1988). In self pollinate crops or crops which show negligible inbreeding depression the RIL population developed through Single Seed Descent (SSD) method. In case of crops which exhibiting the high inbreeding depression, RILs can be produced by sib mating. The use RIL population in linkage map construction was first done in mouse (Schneider *et al.*, 2001).

If there is a possibility to developing the RILs through selfing then there is no need to use the sib mating as the rate of decrease in heterozygote with selfing is one half of that in the previous generation, while in sibmating it is one-fourth. Each line in RIL population contains different combination of linkage blocks from original parents,

which provides the basis for linkage analysis. The information obtained from RIL is twice the F_2 population. Due to continuous selfing leads to homozygosity (Darvasi and Soller, 1995) in RIL which can be maintained indefinitely. The expected ratio of homozygosity in RILs population is 1:1. This makes the RILs an essentially a perpetual or permanent mapping population (Burr *et al.*, 1988). Often RIL populations are called as immortal but any biological entity is indeed mortal, therefore the term perpetual is preferable. The amount of information obtained from dominant and codominant markers are same. The RIL population helps to know the additive and additive $\times$ additive gene action.

The cotton crop is essentially self pollinated crop which exhibits very negligible inbreeding depression and hence opens the gate to develop RIL population in cotton. There are many studies conducted in cotton using the RIL population to identify the QTLs with respect to fibre quality, yield and its component traits (Wang *et al.*, 2006; Shen *et al.*, 2007; Wang *et al.*, 2007; Lacape *et al.*, 2009; Zhang *et al.*, 2009; Tan *et al.*, 2014; Hantao *et al.*, 2015; Liu *et al.*, 2015; Shang *et al.*, 2015; Wang, *et al.*, 2015; Zhang *et al.*, 2015; Jia *et al.*, 2016; Li *et al.*, 2016; Zhang *et al.*, 2017). They concluded that RIL population helps in construction of fine QTL mapping alongwith identifying both minor QTLs and stable QTL across the environments.

Segregation distortion is a potential evolutionary force (Taylor and Ingvarsson, 2003). The segregation distortion was first reported in maize by Mangelsdorf and Jones (1926). The segregation distortion is more in RIL population compared to F_2 population in cotton (Tan *et al.*, 2018). Segregation distortion is a more serious concern in RIL population because of genetic drift (Zhang *et al.*, 2009). This genetic drift is due to artificial and natural selection for several generations, during which partial female or male sterility, time lethality, gametic selection, zygotic selection and/or pollen spine development occur naturally (Xian-Liang *et al.*, 2006). The SNP maps constructed for RIL populations of upland cotton showed the segregation distortion ranging from 13.29 per cent to 63.77 per cent (Zhou *et al.*, 2014; Wang *et al.*, 2015; Li *et al.*, 2016; Zhang *et al.*, 2017). However, the influence of segregation distortion in identification of QTLs could be negligible (Xian-Liang *et al.*, 2006). The observed segregation distortions in some of studies are listed in Table 2. There are many cotton molecular maps which have

been constructed and published. An overview of all recent genetic linkage map published in cotton is presented in Table 1.

2.1.3 QTL mapping for yield and yield attributes and fibre quality traits in cotton

The regions which govern the quantitative traits are called quantitative trait loci (Collard *et al.*, 2005). Locating the regions of quantitative trait loci (QTL) through linkage maps is called QTL mapping (Paterson *et al.*, 1996). QTL analysis was done by following principle; partitioning the mapping population by using the molecular information into different genetic groups along with calculating the significant difference between the genotypic groups with respect to trait value. QTL mapping programs can be roughly classified into different groups according to the number of markers or genetic models and analytical approaches applied. According to, the statistical analyses of associations between phenotype and genotype in a population to detect QTLs include single-marker mapping (Luo and Kearsey, 1989), simple interval mapping (SIM) (Lander and Botstein, 1989) and composite interval mapping (CIM) (Zeng, 1994), multiple interval mapping (MIM) (Jiang and Zeng, 1995 and Ronin *et al.*, 1995). In our study we used the inclusive composite interval mapping which is modification of composite interval mapping. The detailed discussion of composite and inclusive composite interval mapping is done in below section.

Composite interval mapping

Jansen (1993), Zeng (1993) and Zeng (1994) independently proposed combining SIM with multiple regression analysis in mapping, which is termed as "composite interval mapping" (CIM). The CIM evaluates the possibility of identification of target QTL at multiple analysis points across each inter marker interval. However, at each point, it also includes the effect of one or more background markers that are often referred as cofactors. The purpose of using cofactors is to minimize the effects of QTLs in the remainder of the genome when attempting to identify a QTL in a particular region. The inclusion of cofactors in the analysis helps in one of two ways, depending on whether the background markers and the target interval are linked. If they are not linked, inclusion of the background markers makes the analysis more sensitive to the presence of a QTL in the target interval. If they are linked, inclusion of the background

Table 1: List of recent studies on QTL mapping in *Gossypium* sp for various traits

Sl. No.	Parents	Mapping Population		Marker	Map Length (cM)	No. Linkage groups	Traits and Number of QTL for the trait	Reference
		Type	size					
1	<i>G. hirsutum</i> L. cv. Acala-44 × <i>G. barbadense</i> L. cv. Pima S-7.	F ₂	94	AFLPs (33), SSRs (47) and RFLPs (12)	3,287	42	Total 28 QTLs for 11 fiber-related traits	Mei <i>et al.</i> (2004)
2	<i>Gh</i> TM-1 × <i>Gb</i> 3-79	F ₂	171	RFLPs (216) and RAPDs (139)	4766	50	FS (4), FL (3), MIC (6),	Russell <i>et al.</i> (2004)
3	<i>Gh</i> Handan208 × <i>Gb</i> Pima90	F ₂	69	SSRs (205), RAPDs (107), SRAPs (437)	5141.8	41	FS (2), FL (4), MIC (7),	Lin <i>et al.</i> (2005)
4	<i>Gh</i> Yumian-1 x <i>Gb</i> T586	F _{2:3}	117	SSR (55), AFLP (12) and morphological loci (3)	525	20	LP (4), FL (3), FL (2), FU (3), FE (2), MIC (2)	Zhang, <i>et al.</i> (2005)
5	<i>Gh</i> Zhongmiansuo12 (ZMS12) × <i>Gh</i> 8891	RIL	180	SSR (127), AFLP (18), SRAP (30)	865 .20	26	FL (4), FS (4), MIC (7), MAT (5), FR (8), FB (7), FE (8),SFI (8)	Wang <i>et al.</i> (2006)
6	<i>Gh</i> 7235 × <i>Gh</i> TM-1	RIL	258	SSR (156)	1,024.4	31	FS (7), FL (8), MIC (5), FU (3), FE (4), BS (5), LP (6), SI (5), NB (5), SCY (1), LY (4),	Shen <i>et al.</i> (2007)
7	<i>Gh</i> Zhongmiansuo-12 × <i>Gh</i> 8891	RIL	180	SSR (127) , AFLP (18), RAPD (2), SRAP (1)	865.20	32	SCY (7), LY (4), BW (5), LP (7), LI (6), SI (5)	Wang <i>et al.</i> (2007)

Contd...

Sl. No.	Parents	Mapping Population		Marker	Map Length (cM)	No. Linkage groups	Traits and Number of QTL for the trait	Reference
		Type	size					
8	<i>Gh</i> (Handan 208) × <i>Gb</i> (Pima 90)	RIL	121	SSR (834) SRAP (121) RAPD (62)	5472.3	26	LI (4), SI (8), LY (4), SCY (4), SB (1), FS (3), FL (4), MIC (7),	He <i>et al.</i> (2007)
9	(Simian-3 × Sumian-12) × (Zhong-4133 × 8891)	4WC	280	SSR (285)	2113.3	56	NB (1), BW (1), SI (2), LP (2), LI (2), LY (1), FL (5), FS (4), FM (2), FE (3), FU (1)	Hongde <i>et al.</i> (2008)
10	<i>Gh</i> Guazuncho 2 × <i>Gb</i> VH8-4602	RIL	140	597 SSR (597) AFLPs (525)	2,044	18	Total 25 QTLs of fiber-related traits	Lacape <i>et al.</i> (2009)
11	<i>Gh</i> Yumian 1 × <i>Gh</i> T586	RIL	270	SSR (509), IT-ISJ (58), SRAP (29) morphological loci (8)	3,140.9	60	Fl (4), FLU (3), FS (2), MIC (2), FE (2)	Zhang <i>et al.</i> (2009)
12	<i>Gh</i> TM-1 × <i>Gb</i> NM24016	RIL	98	SSR (538) SNP (491)	2061	117	BZ (1), LY (1), FS (1), FL (1), FU (2)	Michael <i>et al.</i> (2014)
13	<i>Gh</i> TM-1 × <i>Gb</i> NM24016	RIL	98	SSR (429) and SNP (412)	2061.06	117	28 QTL for 10 traits, FS (2),	Michael <i>et al.</i> (2014)
14	Suyuan 7235 × ‘Sealand 883’	F ₂₃	175	SSR (52)	8.7	1	FS (1) on chromosome 24	Kumar <i>et al.</i> (2012)
15	<i>Gh</i> CCRI-35 × <i>Gh</i> Yumian-1	RIL	180	SSR (1,274)	3076.4	26	FLU (10), FS (9), FE (10), MIC (15)	Tan <i>et al.</i> (2014)
16	<i>Gh</i> Yumian-1 × <i>Gh</i> 7235	RIL	180	SSR (1478)	2842.06	26	FL (12), FU (13), MIC (13), FE (11), FS (11)	Tang <i>et al.</i> (2015)
17	<i>Gh</i> Baimian1 × <i>Gh</i> TM-1	F ₂₃	200	SSR (144)	1273	37	SCY (4), LY (8), LP (10), BN (5), BS (10), LI (6), SI (7)	Xia <i>et al.</i> (2014)

Contd.....

Sl No.	Parents	Mapping Population		Marker	Map Length (cM)	No. Linkage groups	Traits and Number of QTL for the trait	Reference
		Type	size					
18	<i>Gh</i> DH962 × <i>Gh</i> Jiminia5	RIL	178	SSR (532), InDels (32), SNP (46)	2016.44	53	FL (10), FS (18), MIC (13), FE (16), FU (7), SCW (19), LW (20), LP (13), BN (14), SI (2), LI (2)	Hantao <i>et al.</i> (2015)
19	<i>Gh</i> Yumian-1 × <i>Gh</i> T586	RIL	270	SSR (1675)	3338.2	26	LP (8)	Liu <i>et al.</i> (2015)
20	<i>Gh</i> Prema × <i>Gh</i> 86-1	RIL	179	RAD (5771) SSR (304)	3499.69	103	FS (13)	Wang, <i>et al.</i> (2015)
21	<i>Gh</i> GX1135 × <i>Gh</i> GX100-2	RIL	177	SSR (610)	3714.4	26	FL (8), FS (3), FE (5), MIC (4)	Shang <i>et al.</i> (2015)
22	<i>Gh</i> 0–153 × <i>Gh</i> sGK9708	RIL	196	SSR (210)	178.8	1 (Chro 25)	FS (7), FL (5), FM (5)	Zhang <i>et al.</i> (2015)
23	<i>G. arboreum</i> (acc. SMA-4, PI529740) × <i>G. herbaceum</i> (acc. A-97, PI529670)	F ₂	94	AFLP (539), SSR (50), TRAP (17)	1109	37	FL (4), FU (3), SFI (5), FS (2), UI (1), SI (2)	Ashok and Gerald, (2015)
24	<i>Gh</i> 0–153 × <i>Gh</i> sGK9708.	RIL	196	SSR (851)	4110	26	FL (31), FS (35), FE (32), FU (32), MIC (35)	Jamshed <i>et al.</i> (2016)
25	<i>Gh</i> HS46 × <i>Gh</i> MARCABUCAG8US-1-88	RIL	188	SNP (2618)	1784.28	26	FL (12), FU (8), MIC (10), FE (9), FS (8), BW (8), LP (15)	Li <i>et al.</i> (2016)
26	<i>Gh</i> GX1135 × <i>Gh</i> GX100-2	RIL	178	SSR (653)	3889.9	26	FL (8), FS (3), FE (4), FM (4)	Lianguang <i>et al.</i> (2016)
27	<i>Gh</i> CCRI-36 × <i>Gb</i> G2005	RIL	137	SNP (6,434)	4,071.98	26	PH (11)	Jia <i>et al.</i> (2016)

Contd...

Sl. No.	Parents	Mapping Population		Marker	Map Length (cM)	No. Linkage groups	Traits and Number of QTL for the trait	Reference
		Type	size					
28	<i>Gh</i> PD 94042 × <i>Gm</i> (AD)4-08	F ₂	92	EST-SSR (1134)	5595	26	FE (14)	Wang <i>et al.</i> (2016)
29	<i>Gb</i> TM-1 × <i>Gh</i> TX-256	IL	115	SSR (80)	1104.15		FE (6), FL (10), FS (10), MIC (6), FU (2)	Shu-Wen <i>et al.</i> (2016)
30	<i>Gh</i> 0-153 × <i>Gh</i> sGK9708	RIL	196	SNP (2376) SSR (77)	2865.73	26	FS (40)	Zhang <i>et al.</i> (2017)
31	Yumian 1 × Acala Maxxa	F _{2:8}	180	SNP (12116)	3,741.81	26	FL (21), FU (16), FS (27), MIC (18), FE (22)	Tan <i>et al.</i> (2018)
32	<i>Gh</i> Yumian 1 × <i>Gb</i> CA3084	RIL	180	SNP (33288)		26	FL (20), FS (21), MIC (22), FL (13), FU (19)	Ali <i>et al.</i> (2018a)
33	<i>Gb</i> Suvin × <i>Gb</i> BCS 23-18-7	F ₂	185	SNP (525)	1219.4	41	Yield component traits (13) and Fiber quality traits (16) Major QTLs : UHML (2), FS (1), EL (1)	Kumar <i>et al.</i> (2018)
34	MBI7561 × CCRI45	CSSLs BC ₅ F ₂ BC ₅ F _{2:3} BC ₅ F _{2:3}	310 253 250	SSR (81)	138.11	18	129 QTLs for agronomic and fibre quality traits FS (27)	Li <i>et al.</i> (2019)
35	<i>Gh</i> NC05AZ06 × <i>Gh</i> NC11-2091	RIL		SNP (3129)	4422.44	26	Fiber quality QTLs (59), Yield Trait (38), Agronomic traits (2)	Kuanga (2019)
36	<i>Gossypium hirsutum</i> × <i>G. tomentosum</i>	IL	107	SNP (3157)	-	26	Mic (4), FL (10), FU (1), FS (6), FE (9), BW (7), LW (3), LP (13), HSW (11), PH (3), BN (4), FBN (1), SI (2)	Ayaz <i>et al.</i> (2018)

Contd.....

Sl. No.	Parents	Mapping Population		Marker	Map Length (cM)	No. Linkage groups	Traits and Number of QTL for the trait	Reference
		Type	size					
37	<i>Brassica oleracea</i> L.	DH		SRAP (130) AFLP (120)	2165	-	SRAP markers are potential markers and wider genome coverage because of targets the ORF	Li and Quiros, (2001)
38	<i>Brassica napus</i> L.	RIL	188	SRAP (96) SSR (59) AFLP (6) TRAP (6)	1248.5	19	SRAP markers is efficient marker in detecting the QTLs.	Jin <i>et al.</i> (2007)
39	<i>Brassica napus</i> L	F ₂	184	SRAP (142) AFLP (117) SSR (160)	2054.51	20	SRAP marker act as functional markers	Li <i>et al.</i> (2007)
40	<i>Vitis vinifera</i>	F ₁	149	SSR (86) SRAP (92)	1272.8	21	SRAP markers lengthened the map further more increase the map density	Guo <i>et al.</i> (2014b)
41	<i>Zoysia japonica</i>	F ₁	120	SRAP (293) RAPD (33)	1211	24	SRAP markers produces the high number of polymorphic loci	Guo <i>et al.</i> (2014a)
42	<i>Pisum sativum</i> L. (DDR11 and Zav25)	F ₂	45	SRAP (208 polymorphic bands)	528.8	7	SRAP markers were efficient markers in map construction	Guindon <i>et al.</i> (2016)
43	Durum wheat	RIL	120	TRAP (148)	2043	14	TRAP markers helps in fill the gap in linkage map in addition to that marker may join or separate the linkage group	Menzo <i>et al.</i> (2013)
44	Sunflower	F _{2:4}	123	TRAP (180) SSR (32) Morphological marker (2)	1797.6	19	TRAP marker takes the benefit of annotated EST information, QTL near to this region facilitate the cloning of candidate gene.	Yue <i>et al.</i> (2008)

Contd.....

Sl. No.	Parents	Mapping Population		Marker	Map Length (cM)	No. Linkage groups	Traits and Number of QTL for the trait	Reference
		Type	size					
45	<i>Zea mays</i> L.	F ₂	146	AFLP (151) TRAP (14)	593	10	TRAP marker might no ideal for construction of genetic markers	Shridar <i>et al.</i> (2008)
46	Wheat * Maize	DH	120	SSR (410) TRAP (218) RFLP (1) Phenotypic markers (3)	3811.5	21	Telomeric based TRAP markers allowed in define the linkage group ends	Chu <i>et al.</i> (2008)

Table 2: Characteristics of distorted loci on interspecific and intraspecific populations in *G. hirsutum*

Population	Parents	Population type	Polymorphic loci / distorted loci	Percentage of distorted loci	Reference	Favored parent
Interspecific population	<i>G. hirsutum</i> × <i>G. barbadense</i>					
	Guazuncho 2 × VH8-4602	BC ₁	888/76	8.50	Lacape <i>et al.</i> (2003)	-
	Acala-44 × Pima S-7	F ₂	392/30	7.65	Mei <i>et al.</i> (2004)	Pima S-7
	Handan208 × Pima90	F ₂	749/135	18.02	Lin <i>et al.</i> (2005)	Handan208
	CRI 36 × Hai 7124	F ₂	1252/249	19.90	Yu <i>et al.</i> (2007)	CRI 36
	Handan208 × Pima90	F ₂	834/173	20.74	He <i>et al.</i> (2007)	CRI 36
	Emian22 × Pima3-79	BC ₁	917/107	11.67	Zhang <i>et al.</i> (2008)	-
	Emian22 × Pima3-79	BC ₁	2521/423	16.80	Yu <i>et al.</i> (2011)	-
	TM-1 × Hai7124	BC ₁	3414/300	8.79	Zhao <i>et al.</i> (2012)	-
	SG 747 × Giza 75	BIL	392/100	25.50	Yu <i>et al.</i> (2013)	-
Intraspecific population	<i>G. hirsutum</i> × <i>G. hirsutum</i>					
	7235 × TM-1	F ₂	127/56	44.10	Shen <i>et al.</i> (2005)	7235
	7235 × TM-1	RIL	181/95	52.49	Shen <i>et al.</i> (2007)	7235
	Zhongmiansuo 35 × Yumian 1	F ₂	178/57	32.02	Chen <i>et al.</i> (2008)	-
	T586 × Yumian 1	RIL	618/150	24.27	Zhang <i>et al.</i> (2009)	-
	sGK9708 × 0-153	F ₂	229/110	48.00	Sun <i>et al.</i> (2012)	sGK9708
	sGK9708 × 0-153	RIL	217/93	43.30	Sun <i>et al.</i> (2012)	sGK9708
	Prema × 86-1	RIL	304/247	81.25	Ning <i>et al.</i> (2014)	86-1
	Yumian 1 × 7235	RIL	1582/662	41.80	Tang <i>et al.</i> (2015)	7235

marker may help to separate the target QTL from other linked QTL on the far side of the background marker (Zeng, 1993 and Zeng, 1994).

Inclusive composite interval mapping is the modification of CIM algorithms. Two genetic assumptions used in ICIM are (1) the genotypic value of an individual is the summation of effects from all genes affecting the trait of interest; (2) linked QTL are separated by at least one blank marker interval. Under the two assumptions, they proved that additive effect of the QTL located in a marker interval can be completely absorbed by the regression coefficients of the two flanking markers, while the QTL dominance effect causes marker dominance effects as well as additive by additive interactions between the two flanking markers. By including two multiplication variables between flanking markers, the additive and dominance effects of one QTL can be completely absorbed. As a consequence, an inclusive linear model of phenotype regressing on all genetic marker can be used to fit the positions and additive effects of all QTL in the genome (Li *et al.*, 2007; Wang, 2009, Zhang *et al.*, 2008).

The brief review on QTLs mapping in cotton using different marker systems is presented in Table 1.

2.2 Genetic variability for yield, yield contributing and fibre quality traits in cotton

In crop improvement programme selection is one of the essential phases and the genetic variability is prerequisite for selection. The amount of genetic variability decides the success of most crop improvement programs in a crop for desirable traits. The quantitative characters, such as agronomic traits: plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant; yield attributing traits: Seed cotton yield per plant (g), seed Index (g), boll weight (g), lint Index (g), ginning outturn (%); fibre quality traits: fibre strength (g/text), fibre length (mm), micronaire value ($\mu\text{g}/\text{inch}$), maturity ratio, fibre elongation length (%), fibre uniformity ratio (%). The variability in these traits is assessed through genetic parameters viz., genotypic variance, phenotypic variance, heritability and genetic advance. The absolute values of phenotypic and genotypic variance cannot be used for comparing because units of measurement of the characters may be different. Hence the

coefficient of variation helps to bring the genetic and phenotypic variance to common platform as result we can compare the variability among the different traits (Khan *et al.*, 2005).

The phenotypic variability is the sum of genotype and environment components among them only genotypic component is heritable in nature. The breeder would have considered mainly the genotypic variability during selection for traits and adoption of selection strategy. The mean and range parameters of different traits helps to know the extent of improvement can be possible in the population.

One of the important components that has been considered during the selection is heritability which comprises of broad sense heritability and narrow sense heritability. The heritability with respect to broad sense is the ratio of genetic variance to phenotypic variance. In case of narrow sense heritability is the ratio of the additive variance to phenotypic variance (Lush, 1949).

The genetic gain expected for a particular character through selection is the product of its heritability, phenotypic standard deviation and selection differential as proposed by Burton and Devane (1953). The theoretical outcome of selection can be estimated by considering the heritability along with genetic advance. (Johnson *et al.*, 1955b).

According to Panse (1940), if heritability is mainly due to non-additive effects (dominance and epistasis), the genetic gain will be low whereas, if the heritability is due to additive effects it could be associated with high genetic advance. Swarup and Chagule (1962) observed that high heritability need not be associated with high genetic advance.

A brief review of genetic variability has been presented in Table 3 and some most related studies discussed below.

Choudki *et al.* (2012) reported that high GCV for seed cotton yield, seed index, ginning outturn, lint index in interspecific RIL populations. The characters like seed cotton yield, 2.5 per cent span length and fibre strength recorded high heritability besides high genetic advance in seed cotton yield, seed index, lint index and micronaire value.

Table 3: List of recent Genetic variability studies for yield, yield attributes and fibre quality traits in *Gossypium* sp.

SL No.	Characters	PCV	GCV	h^2	GA	GAM	References
01	Seed cotton yield	High	High	High	High	--	Dhivya <i>et al.</i> (2014) and Fakhar <i>et al.</i> (2015).
		High	High	High	High	High	Ahsan <i>et al.</i> (2015) and Nagaraju (2016)
		Mod	Mod	High	--	High	Gitte <i>et al.</i> (2007)
		Mod	Mod	High	High	High	Tuteja <i>et al.</i> (2006) and Muhammad <i>et al.</i> (2015)
		High	High	High	Low	High	Choudki <i>et al.</i> (2012)
		Mod	Mod	Low		High	Eswari <i>et al.</i> (2016)
			Low	High			Richard <i>et al.</i> (2006)
		High	High	High	Mod	High	Ramesh <i>et al.</i> (2018)
		Mod	Mod	High			Raza <i>et al.</i> (2016)
		Mod	Mod	High		High	Jarwar <i>et al.</i> (2018)
02	Plant height	Low	Low	Mod	Mod	Mod	Muhammad <i>et al.</i> (2015) and Nagaraju (2016)
		Mod	Mod	High	High	--	Fakhar <i>et al.</i> (2015)
		Mod	Mod	Mod	--	Mod	Dhivya <i>et al.</i> (2014)
		Mod	Mod	High	--	High	Vineela <i>et al.</i> (2013)
		Low	Low	Low	Low	Low	Tuteja <i>et al.</i> (2006)
		Low	Low	Low	High	Mod	Gitte <i>et al.</i> (2007)
		High	High	High	High		Hafiz <i>et al.</i> (2013)
		Low	Low	High	Mod	Low	Ramesh <i>et al.</i> (2018)
			High	High			Richard <i>et al.</i> (2006)
		Mod	Mod	High		High	Deyi <i>et al.</i> (2016)

Contd.....

SL No.	Characters	PCV	GCV	h^2	GA	GAM	References
03	Number of monopodia per plant	High	High	High	Low		Fakhar <i>et al.</i> (2015)
		High	Mod	Mod	High	Mod	Tuteja <i>et al.</i> (2008)
		High	High	High	Low	High	Nagaraju (2016)
		High	Mod	High	--	High	Vineela <i>et al.</i> (2013)
		High	High	High	--	High	Choudki <i>et al.</i> (2012)
		Mod	Mod	High	--	High	Gitte <i>et al.</i> (2007)
		Mod	High	Mod		High	Eswari <i>et al.</i> (2016)
		High	High	High	Mod		Hafiz <i>et al.</i> (2013)
		High	Mod	High	Mod	High	Ramesh <i>et al.</i> (2018)
		High	High	Mod			Raza <i>et al.</i> (2016)
04	Number of sympodia per plant	High	Mod	High	High		Fakhar <i>et al.</i> (2015) and Gitte <i>et al.</i> (2007)
		Mod	Mod	High	Low	High	Nagaraju (2016)
		Mod	Mod	High	--	High	Choudki <i>et al.</i> (2012)
		Mod	Low	Low	--	Low	Choudki <i>et al.</i> (2012) and Tuteja <i>et al.</i> (2006)
		Mod	Mod	High		Mod	Eswari <i>et al.</i> (2016)
		High	High	High		High	Hafiz <i>et al.</i> (2013)
		Mod	Low	High	Mod	Low	Ramesh <i>et al.</i> (2018)
		Mod	Low	High		Mod	Deyi <i>et al.</i> (2016)
		Mod	Mod	High		High	Jarwar <i>et al.</i> , (2018)

Contd.....

SL No.	Characters	PCV	GCV	h^2	GA	GAM	References
05	Number of bolls per plant	High	High	High	Mod	High	Muhammad <i>et al.</i> (2015)
		Mod	Mod	High	Low	High	Nagaraju (2016)
		High	Mod	High	High	--	Fakhar <i>et al.</i> (2015)
		Mod	Mod	Mod	--	High	Dhivya <i>et al.</i> (2014)
		Mod	Mod	Mod	--	Mod	Vineela <i>et al.</i> (2013)
		Mod	Low	Mod	Low	Low	Choudki <i>et al.</i> (2012) and Tuteja <i>et al.</i> (2006)
		Mod	Mod	High	--	High	Gitte <i>et al.</i> (2007)
		High	High	High		High	Eswari <i>et al.</i> (2016)
		High	High	High	High		Hafiz <i>et al.</i> (2013)
		Mod	Low	Low	Mod	Low	Ramesh <i>et al.</i> (2018)
		Mod	Mod	Mod			Raza <i>et al.</i> (2016)
		Mod	Mod	High		High	Deyi <i>et al.</i> (2016)
		Mod	Low	Mod		Low	Jarwar <i>et al.</i> (2018)
06	Ginning outturn	Mod	Mod	High	Mod	High	Muhammad <i>et al.</i> (2015)
		Mod	Low	High	Low	Mod	Nagaraju (2016)
		Low	Low	High	Low	--	Fakhar <i>et al.</i> (2015)
		Mod	Low	Mod	--	Low	Dhivya <i>et al.</i> (2014)
		Low	Low	High	Low	Low	Choudki <i>et al.</i> (2012)
		Mod	Mod	High	--	High	Gitte <i>et al.</i> (2007)
		Mod	Low	High	--	Low	Tuteja <i>et al.</i> (2006)
		Mod	Mod	High	Mod	High	Muhammad <i>et al.</i> (2015)
		Mod	Low	High	Low	Mod	Nagaraju (2016)

Contd.....

SL No.	Characters	PCV	GCV	h ²	GA	GAM	References
06	Ginning outturn	Mod	Low	Mod	--	Low	Dhivya <i>et al.</i> (2014)
		Low	Low	High	Low	Low	Choudki <i>et al.</i> (2012)
		Mod	Mod	High	--	High	Gitte <i>et al.</i> (2007)
		Mod	Low	High	--	Low	Tuteja <i>et al.</i> (2006)
		Low	Low	High		Mod	Eswari <i>et al.</i> (2016)
		Low	Low	High	Low	Low	Ramesh <i>et al.</i> (2018)
			Low	High			Richard <i>et al.</i> (2006)
		Mod	Low	Low		Low	Jarwar <i>et al.</i> (2018)
07	Lint index	High	High	High	Low	High	Muhammad <i>et al.</i> (2015)
		High	High	High	High	High	Ahsan <i>et al.</i> (2015)
		Mod	Mod	High	Low	Mod	Nagaraju (2016)
		Mod	Mod	High	Low	--	Fakhar <i>et al.</i> (2015)
		Mod	Mod	Mod	--	Mod	Dhivya <i>et al.</i> (2014)
		Low	Low	Mod	--	Low	Choudki <i>et al.</i> (2012)
		Mod	Mod	High	Mod	Mod	Ramesh <i>et al.</i> (2018)
		Low	Low	High		Mod	Deyi <i>et al.</i> (2016)
		Mod	Mod	Mod		High	Jarwar <i>et al.</i> (2018)
08	Seed index	High	High	High	Low	High	Muhammad <i>et al.</i> (2015)
		Mod	Mod	High	Low	--	Fakhar <i>et al.</i> (2015)
		Low	Low	High	Low	Mod	Nagaraju (2016)
		Mod	Mod	Mod	--	High	Dhivya <i>et al.</i> (2014)
		Low	Low	Low	Low	Low	Choudki <i>et al.</i> (2012)

Contd.....

SL No.	Characters	PCV	GCV	h^2	GA	GAM	References
08	Seed index	Mod	Mod	High	Mod	Mod	Ramesh <i>et al.</i> (2018)
		Low	Low	High		Mod	Deyi <i>et al.</i> (2016)
		Mod	Mod	Mod		High	Jarwar <i>et al.</i> (2018)
09	Boll weight	Mod	Mod	High	High	High	Muhammad <i>et al.</i> (2015) and Choudki <i>et al.</i> (2012)
		Mod	Mod	High	Low	Mod	Nagaraju (2016)
		Mod	Mod	High	High	--	Fakhar <i>et al.</i> (2015) and Gitte <i>et al.</i> (2007)
		Mod	Low	Low	--	Mod	Dhivya <i>et al.</i> (2014)
		Mod	Mod	High	--	High	Vineela <i>et al.</i> (2013)
		Low	Mod	Low	Low	Low	Tuteja <i>et al.</i> (2006)
		Mod	Mod	High		high	Eswari <i>et al.</i> (2016)
		Mod	Mod	Mod	Mod	Mod	Ramesh <i>et al.</i> (2018)
		Low	Low	Mod			Raza <i>et al.</i> (2016)
		Mod	Low	Mod		Low	Jarwar <i>et al.</i> (2018)
10	Fibre length	Low	Low	High	Low	--	Fakhar <i>et al.</i> (2015)
		Low	Low	High	Low	Low	Nagaraju (2016)
		Low	Low	High	--	High	Dhivya <i>et al.</i> (2014)
		Low	Low	High	--	Mod	Malagouda <i>et al.</i> (2014) and Gitte <i>et al.</i> (2007)
		Low	Low	Mod	Low	Low	Choudki <i>et al.</i> (2012) and Tuteja <i>et al.</i> (2006)
		Low	Mod	High		Mod	Eswari <i>et al.</i> (2016)
		Mod	Low	High		Low	Hafiz <i>et al.</i> (2013)
		Low	Low	High	Low	Mod	Ramesh <i>et al.</i> (2018)
			Low	High			Richard <i>et al.</i> (2006)
		Low	Low	High		Low	Deyi <i>et al.</i> (2016)
		Low	Low	High		Mod	Jarwar <i>et al.</i> , (2018)

Contd.....

SL No.	Characters	PCV	GCV	h ²	GA	GAM	References
11	Fibre strength	Low	Low	High	High	--	Fakhar <i>et al.</i> (2015)
		Low	Low	High	Low	Mod	Nagaraju (2016)
		Low	Low	Mod	--	Mod	Malagouda <i>et al.</i> (2014)
		Low	Low	High	Low	Low	Choudki <i>et al.</i> (2012)
		Low	Mod	High		Mod	Eswari <i>et al.</i> (2016)
		Low	Low	High	Low	Mod	Ramesh <i>et al.</i> (2018)
		Low	Low	High		Low	Deyi <i>et al.</i> (2016)
12	Micronaire (Fibre fineness)	Low	Low	High	Low	--	Fakhar <i>et al.</i> (2015)
		Mod	Mod	High	Low	Mod	Nagaraju (2016)
		Low	Low	Low	--	Low	Malagouda <i>et al.</i> (2014)
		Low	Low	High	Low	Low	Choudki <i>et al.</i> (2012)
		High	High	Low	Low		Hafiz <i>et al.</i> (2013)
		Low	Low	High	Low	Mod	Ramesh <i>et al.</i> (2018)
			Low	High			Richard <i>et al.</i> (2006)
		Low	Low	High	Low		Deyi <i>et al.</i> (2016)
13	Elongation	Low	Low	High	--	Mod	Malagouda <i>et al.</i> (2014)
		Low	Low	High	Low	Low	Nagaraju (2016)
		Low	Low	Low	Low	Low	Choudki <i>et al.</i> (2012)
		Low	Low	High	Low	Low	Ramesh <i>et al.</i> (2018)
		Low	Low	High		Low	Deyi <i>et al.</i> (2016)

Contd.....

--

SL No.	Characters	PCV	GCV	h^2	GA	GAM	References
14	Uniformity ratio	Low	Low	High	Low	--	Fakhar <i>et al.</i> (2015)
		Low	Low	Mod	--	Low	Malagouda <i>et al.</i> (2014)
		Low	Low	High	Low	Low	Choudki <i>et al.</i> (2012) and Nagaraju (2016)
		Low	Mod	High		Mod	Eswari <i>et al.</i> (2016)
		Low	Low	High	Low	Low	Ramesh <i>et al.</i> (2018)
15	Maturity ratio	Low	Low	High	Low	Low	Choudki <i>et al.</i> (2012) and Nagaraju (2016)
		Low	Low	High	Low	Mod	Ramesh <i>et al.</i> (2018)

Where,

PCV - Phenotypic coefficient of variation

GCV - Genotypic coefficient of variation

h^2 - heritability

GA – Genetic advance

GAM - Genetic advance as per cent mean

Mod - moderate

Alkuddsi *et al.* (2013b) evaluated the segregating F₅ generation of sea Island cotton where he observed high GCV, PCV, heritability and genetic advance exhibited for seed cotton yield.

Dhivya *et al.* (2014) reported high PCV and GCV for seed index, plant height, lint index and boll weight in 54 *G. hirsutum* lines. The number of sympodia per plant, single plant yields, seed index and micronaire value exhibited high heritability along with high genetic advance.

Erande *et al.* (2014) reported that number of sympodia, number of bolls and seed cotton yield displayed high GCV and PCV in 20 phenotypically diverse *arboreum* cotton accessions. The number of monopodia, number of sympodia, plant height, number of bolls, boll weight, seed cotton yield, 2.5 per cent span length and micronaire accounted for high heritability coupled with high genetic advance.

A study on genetic variability in 53 cotton cultivars by Farooq *et al.* (2014) revealed that plant height, number of sympodia, ginning outturn, fibre length, fibre strength and micronaire recorded low GCV, PCV and high heritability while, high GCV and PCV were recorded for seed cotton yield.

Malagouda *et al.* (2014) reported that phenotypic and genotypic coefficients of variation were low in all traits in diploid recombinant inbred lines (RILs). The uniformity ratio recorded the lowest PCV and GCV whereas, highest PCV for micronaire and highest GCV for fibre elongation were observed. The highest was heritability observed in 2.5 per cent span length and fibre elongation coupled with moderate genetic advance as per cent mean whereas, fibre strength recorded moderate heritability with low genetic advance as per cent mean.

Muhammad *et al.* (2015) reported that the number of bolls per plant, lint index and seed cotton yield per plant revealed highest genotypic (GCV) and phenotypic coefficient of variation (PCV) in eight accessions. He observed that GCV had a similar trend as PCV. The lint index, the number of bolls per plant and seed cotton yield per plant displayed the high heritability and high genetic advance.

Reddy and Sarma (2014) conducted a study on genetic variation in 13 varieties of *arboreum* cotton for all important traits. The high GCV, PCV, heritability and genetic advance was observed for seed cotton yield and number of bolls.

A study on genetic variation in 202 accessions conducted by Wadeyar and Kajjidoni (2014) reported high GCV, PCV, heritability and genetic advance for the number of bolls and seed cotton yield, whereas low GCV, PCV and heritability was recorded for boll weight, ginning outturn, lint index while and seed index.

A genetic variability study was conducted by Dhivya *et al.* (2014) in 54 upland cotton genotypes. The highest PCV and GCV was recorded for seed index, plant height, lint index and boll weight. The PCV and GCV followed a similar trend for all traits. High heritability along with high genetic advance was observed for traits viz., the number of sympodia per plant, single plant yields, seed index and micronaire value. The combinations of high heritability with high genetic advance will provide a base for the reliability of that particular character in selection of variable entries.

Khan *et al.* (2015) reported that high PCV, GCV and heritability were observed in number of monopodia, number of sympodia, number of bolls and seed cotton yield. The boll weight, lint index and seed index displayed the moderate GCV, PCV and high heritability.

A study on genetic variability revealed that seed cotton yield had high GCV, PCV and high heritability coupled with high GAM in 200 RILs (Ramesh, 2015). While, moderate GCV, PCV with high heritability were observed for monopodia per plant, number of bolls per plant and lint yield.

Deyi *et al.* (2016) stated that lint yield per hectare followed by bolls per plant accounted for the highest GCV and PCV. The plant height, bolls per plant and lint yield per hectare recorded high heritability along with the high response to selection which indicated that the additive gene function model in the inheritance of these traits and direct selection can be profitably applied on them.

Eswari *et al.* (2016) analyzed the variance in eleven cotton genotypes for different traits, in this number of monopodia per plant exhibited the high GCV and

PCV. The difference between the estimates of PCV and GCV were low for all the characters except the number of monopodia per plant which indicated the lesser role of the environment in the expression of these characters. The number of bolls per plant, boll weight and seed cotton yield per plant recorded high heritability coupled with high genetic advance as per cent of mean.

Raza *et al.* (2016) reported that number of monopodia per plant exhibited the high PCV, GCV, h^2 and GAM among 59 F_4 populations of upland cotton. The lowest value of PCV and GCV were observed for number of bolls. Results further revealed that F_4 populations with moderate to high heritability could guide intensive selection for improvement in segregating populations.

Ramesh *et al.* (2018) reported that seed cotton yield exhibited higher genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) in 220 RIL population. Most of the traits recorded moderate PCV and GCV. The high genetic advance over a mean (GAM) was recorded for number of monopodia and seed cotton yield. The moderate GAM was accounted for boll weight, seed index, lint index, UHML, fibre strength, micronaire value and maturity ratio.

2.3 Correlation and path analysis in cotton

2.3.1 Correlation between yield, yield attributes and fibre quality traits in cotton

In plant breeding, the correlation coefficient estimates the mutual relation between various plant traits and determines the component characters on which selection could be made for genetic improvement in the desired trait. The prime objective of the breeder is improving the plant yield but the yield is the dependent character which depends on many independent characters. Hence, by selecting those characters which influence the yield, we can achieve the yield improvement in the trait. The correlation coefficient provides the degree of association and direction of the association between the traits.

The correlation studies provide a better understanding of yield components which helps the plant breeder during the selection (Johnson *et al.*, 1955a). The association between two characters can be directly observed and termed as phenotypic

correlation. It includes both genotypic and environmental effect. The genotypic correlation indicated that the association of two variables is heritable. The basic concept of correlation was elaborated and discussed by Fisher (1918) and Wright (1921b) for plant breeding program.

Some of the recent and relevant correlation studies in cotton are discussed below.

Richard *et al.* (2006) reported positive phenotypic correlation between 2.5 and 50 per cent span lengths with fibre strength in interspecific RIL population. In addition, a positive significance association was observed between lint yield and plant height.

Dhamayanthi *et al.* (2010) studied correlation in 25 *Gossypium barbadense* L. genotypes and reported that characters like sympodia per plant, fruiting point per plant, number of nodes per plant, number of bolls per plant and lint index were positively correlated with seed cotton yield per plant.

Salahuddin *et al.* (2010) observed that number of sympodia, bolls per plant, boll weight and ginning outturn had a significant positive phenotypic correlation with seed cotton yield in *Gossypium hirsutum* L. cultivars.

Tulasi *et al.* (2012) reported that a significant positive correlation was found between seed cotton yield and the number of bolls per plant, boll weight, ginning outturn, seed index and lint index had a positive correlation. These positively correlated traits can be considered as selection indices for improving seed cotton yield.

The correlation study was done by Alkuddsi *et al.* (2013a) in 92 inter-specific cotton hybrids. The seed cotton yield had a significant positive phenotypic correlation of with boll weight, lint index and ginning outturn.

Hafiz *et al.* (2013) evaluated the upland cotton germplasm and found positive significant correlation among the monopodial and staple length, fibre fineness, sympodial branches and number of bolls at both genotypic and phenotypic level.

Erande *et al.* (2014) reported that seed cotton yield had a significant positive correlation with plant height, number of monopodia, number of sympodia, boll weight,

number of bolls and ginning outturn in 20 phenotypically diverse *arboreum* cotton accessions at genotypic and phenotypic level.

Farooq *et al.* (2014) reported that number of bolls, boll weight, plant height and ginning outturn had a significant and positive correlation with seed cotton yield in 53 cotton cultivars. They also revealed that fibre length was negatively correlated with fibre fineness.

Saeed *et al.* (2014) studied correlation fibre quality and some yield contributing traits in 101 cotton genotypes and found significant associations among boll weight and fibre related trait and staple length.

Baloch *et al.* (2015) mentioned that significant and positive correlation between seed cotton yield and number of sympodia per plant, number of bolls per plant and boll weight in eight cotton genotypes. They noticed seed cotton yield had a negative significant correlation with micronaire value.

Ramesh (2015) reported that 2.5 per cent span length had significant positive phenotypic and genotypic correlation with fibre strength, fibre elongation level however 2.5 per cent span length had a significant negative association with uniformity ratio, micronaire value and maturity ratio. He also observed that uniformity ratio at both phenotypic and genotypic level had a significant positive correlation with micronaire value and maturity.

Gopi and Patil (2017) observed that seed cotton yield per plant was positively and significantly associated with number of locules per boll, plant height and number of bolls per plant in F₂ generation of the interspecific cross of *Gossypium arboreum* and *Gossypium herbaceum* (QTP 5 × ASH 90).

An association study was conducted by Kumar and Katageri (2017) between the yield and fibre quality traits in 1329 F₂ individuals of *G. barbadense* derived from Suvin × BCS 23-18-7. The seed cotton yield exhibited a significant and positive association with plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, lint yield per plant and boll weight. With respect to

fibre quality traits, fibre strength had a significant and positive association with UHML, seed index and seed cotton yield but negatively significant association with micronaire value, maturity ratio, fibre elongation and lint index.

Malagouda *et al.* (2014) reported that fibre length was positively significant with following quality traits viz., fibre strength and fibre elongation. Whereas, the significant negative correlation was observed between fibre strength and micronaire. He concluded that to improve the fibre quality selection should be based on 2.5 per cent span length, fibre strength and micronaire.

Raza *et al.* (2016) observed the following traits viz., plant height, number of monopodia per plant, number of bolls per sympodia, boll weight and seeds per boll in 59 F₄ generation segregants. Whereas except monopodia per plant all traits showed the significant association with seed cotton yield.

Deyi *et al.* (2016) mentioned that fibre length, strength and fineness had favorable associations in long staple lines of cotton. Where they concluded that there is a great potential in the population for further enhancing yield while maintaining high fibre quality.

Muhammad *et al.* (2018) reported that seed cotton yield had a positive significant correlation with plant height, sympodia branches, seeds per bolls and number of bolls. The fibre strength had positive significant correlation with fibre length in parental and F₁ population.

Javed *et al.* (2016) studied the association of ginning outturn, staple length and micronaire value in eight cotton genotypes. Only micronaire value exhibited the negative correlation with plant height, monopodia per plant, sympodia per plant, number of bolls and seed cotton yield.

2.3.2 Path analysis in cotton genotypes

The path coefficient analysis suggested by Dewey and Lu (1959) specified the effective measure of direct and indirect causes of association and also depicts the relative importance of each factor involved in contributing to the final product that is yield.

In order to find out the cause and effect relationship between grain yield and its related characters, path analysis was taken up in the present investigation. The path coefficient analysis also measures the relative importance of causal factors involved. This is simply a standardized partial regression analysis, where in total correlation value is subdivided into causal scheme.

Saifullah (2010) evaluated the fifteen genotypes (six parents, nine crosses) of American upland cotton (*Gossypium hirsutum* L.) and reported that the characters having most influence on seed cotton yield were bolls per plant and boll weight, which should be taken care of while selecting for higher yields in further breeding programme.

Vinodhana *et al.* (2013) mentioned that number of sympodia per plant, number of bolls per plant, boll weight, seed index and lint index directly influenced the seed cotton yield with high direct effects. It was concluded that these characters could be considered as significant selection criteria for seed cotton yield improvement in cotton.

Alkuddsi *et al.* (2013) indicated that a high positive direct effect of monopodia per plant (0.619) and mean boll weight (0.321) on kapas yield. Sympodia per plant exhibited high positive indirect effect on kapas yield via seed index (0.374) the result of this mean boll weight had high positive correlation with kapas yield and sympodia per plant recorded low positive correlation with kapas yield.

Rao and Gopinath (2013) evaluated the 28 interspecific hybrids and 8 parents of *hirsutum* cotton. Path coefficient analysis showed that number of bolls per plant exhibited maximum direct effect on seed cotton yield per plant followed by boll weight, number of sympodia per plant and lint index. The maximum positive indirect effect on seed cotton yield per plant was observed through number of bolls per plant. Thus due emphasis should be given to number of bolls per plant, boll weight and lint index for improvement in seed cotton yield

Reddy *et al.* (2017) evaluated upland cotton for yield and yield contributing characters in using 17 characters. Path analysis revealed high positive direct effect of bolls per plant, boll weight and lint yield per plant on seed cotton yield per plant. Selection based on these characters would improve seed cotton yield. So weightage should be given in selection process with more bolls per plant and more boll weight and

there should be economic balance among these traits to get higher seed cotton yield per plant.

Mahendra (2017) evaluated the forty genotypes of cotton (*Gossypium hirsutum* L.) for seed cotton yield, fibre quality and bio chemical traits. The path analysis revealed that number of bolls per plant and boll weight had high direct effect on seed cotton yield per plant.

Ali *et al.* (2018b) evaluated fifteen F₄ lines and a cotton standard variety (S12). The path coefficient analysis showed ginning outturns, number of bolls and boll weight have direct impact on the seed cotton yield. Consequently, revealed that ginning out turn, number of bolls and boll weight should be considered substantial while selecting the genotypes for the breeding purpose.

Nikhil *et al.* (2018) reported that boll weight and number of bolls per plant had highest direct effect on seed cotton yield per plant, whereas traits like plant height, UHML, fibre strength and lint index had direct negative effect on yield revealing that due weightage should be given in selection process with more number of bolls per plant and more boll weight can be considered as principal yield determining components.

2.4 Intergeneration correlation and regression for yield and yield component traits and fibre quality traits

The only limitation of crop improvement is long duration because selection in segregating generation or early generation is not recommended. However, above statement is not true in all situation or characters. We can select the genotype in early segregating generation also if that trait exhibited the similar performance in advance generations. The success of early generation selection usually depends on high correlation between performance of the genotypes selected in one generation and the performance of their progeny in the following generation. The parent-offspring coefficient of correlation and simple linear regression between different generations shows lesser influence of environmental effect and is very fruitful for selection in segregating population for the production of improved genotypes (Whan *et al.*, 1981; Rahman and Bahl, 1986).

In the present investigation, parent progeny correlation and regression was evaluating between F_4 vs F_5 and F_5 vs F_6 for economical important traits. Some of the relevant studies were discussed below.

Meredith and Bridge, (1973) analyzed the relationship between F_2 and selected F_3 generation in upland cotton for yield, it's component and quality traits. The cotton yield had non-significant association between F_2 and F_3 generations. However, significant association between the F_2 and F_3 for seed index, lint per cent, fibre length, elongation and strength were detected. It indicated that early generation may be ineffective for improvement of yield through direct selection.

Wynne (1976) reported that in peanut fruit length, SMK in F_2 generation were correlated with similar measures in F_5 generation. The yield was not significantly associated with the above generations.

Lungu *et al.* (1990) reported about intra and inter generation correlation in F_2 , F_3 and F_4 generation of wheat crop. He concluded that F_2 generation yield had positive significant relation with yield in F_3 and F_4 generation.

Simple linear regression analysis carried out in F_2 and F_3 and also between F_3 and F_4 by Ntare (1999) in peanut crop. He concluded that selection for yield in an early generation may be ineffective. This helps to determine the early generation selection accurately predicts the performance in later generation The results derived from parent-offspring correlation were almost similar to regression.

Ulloa *et al.* (2002) assessed the heritability and intergeneration correlation in okra leaf type of cotton for agronomic and fibre traits. Boll weight, lint percentage, seed weight and all the fibre quality traits had significant correlation between $F_{2:3}$ and $F_{2:6}$.

In cotton early generation testing was done by Jones and Smith (2005) for lint yield, fibre strength, fibre elongation, micronaire value, lint percentage, uniformity ratio. Above traits had a significant positive correlation between F_3 and F_6 generation except fibre elongation. He concluded that intergenerational correlation is effective tool for early generation selection to improve lint yield, fibre strength, micronaire value, lint percentage, uniformity ratio.

Barma *et al.* (2011) assessed membrane thermostability (MTS) during screening for heat tolerance in spring wheat. The MTS showed a significant intergeneration correlation (F_4 Vs F_5).

Barman and Barah (2012) stated that in case of mutant rice strains, intergeneration correlation between F_2 and F_3 revealed that plant height, number of panicles per plant, days to 50 per cent flowering and grain density had positive significant correlation and regression. This showed the efficiency of selection for these characters in early generations.

Muralidhara *et al.* (2015) reported that early generation (F_2) yield evaluation can be used as a reliable predictor of the performances at the F_3 generation in green gram as yield had a significant and positive correlation between F_2 and F_3 .

Suwarto *et al.* (2015) reported in case of segregating rice lines plant height, number of grain per panicle, panicles length, and flowering (days to 50 per cent flowering) had significant correlation and regression between F_2 and F_3 generation. This indicates that early generation selection for above traits could be effective. The yield per clump revealed non significant association hence selection for yield during early generation selection was futile.

Govintharaj *et al.* (2017) estimated parent-offspring correlation in early segregating rice lines for various traits. The significance association was observed for panicle length ($r=0.30$, $P<0.05$), single plant yield ($r=0.35$, $P<0.01$) and number of productive tillers ($r=0.47$, $P<0.01$) in F_2 and F_3 generation indicates that selection was productive in early generation for these traits.

The intergeneration correlation and regression calculated in four crosses of wheat crop by Singh *et al.* (2017). He pointed that plant height had a significant intergeneration correlation between F_2 and F_3 progenies of all crosses (Raj3765 x Syn 27, WH1105 x Syn27, Raj3765 x WH711 and WH1105 x WH711) and in the crosses like Raj3765 x Syn 27 and WH1105 x Syn27 yield per plant had significant intergeneration correlation among F_2 and F_3 segregating progenies. Hence, for improvement of plant height the selection at F_2 generation was recommended in all cross derivative populations.

In rice Koli and Patidar (2018) reported that number of panicles per plant, plant height, number of grains per panicle and days to 50 per cent flowering had significant positive correlation and regression between F_2 and F_3 generation. However, between the above generations, grain yield showed non significant correlation. This showed that selection for grain yield during early generation was not be desirable. Also they reported that in case of F_3 and F_4 for all the traits showed a significant positive correlation including the grain yield.

Manohara and Shashidhara (2018) analyzed the selection efficiency for grain yield and its attributed traits in early segregating generations of rice under aerobic condition. They concluded that intergeneration correlation and heritability values were higher in case of test weight, grains per panicle, number of panicles per hill and number of tillers per hill between F_2 and F_3 . Whereas, with respect to yield, plant height and days to fifty per cent flowering had non significant correlation and low values of heritability were observed. Therefore in early segregating generations selection for component traits can be more effective than direct selection on yield *per se*.

The inter generation correlation between lines for particular trait in any two generations increased as the generation were advanced. The intergeneration correlation is higher in consecutive generation compared to generation two or more apart. Associations between years of lines from the same or different generations were low and often non-significant (Whan *et al.*, 1981). Along with correlation the estimation of regression helps to know the degree of dependence of generation over previous generation. The estimation of regression between the generations called as parent-offspring regression or parent progeny regression. The parent-offspring regression helps to know the amount of genetic potential transferred from parents to its progenies. The parent-offspring regression could assist in estimating the degree of transferring the genetic potentials of the trait from one generation to other generation.

2.5 Identification of transgressive segregants in the RIL population

Miller and Rawlings (1967), Kamalanathan and Manivasakam (1987), Narayanan *et al.* (1987), Percy and Turcotte (1988), Girase *et al.* (2001), Pradeep and Sumalini (2003), Basamma *et al.* (2010) and Ramesh *et al.* (2018) conducted investigation on the identification of transgressive segregation in cotton

The study of transgressive segregants helps to know the potential of the parents. The success in producing the favorable transgressive segregants depends on genetic recombination between both linked and unlinked alleles (Briggs and Allard, 1953). The transgressive segregants are helpful for extending the limit of character expression beyond the parent.

3. MATERIAL AND METHODS

The present investigation was initiated during summer 2017 at Department of Genetics and Plant Breeding, Botanical garden, Agriculture College, Dharwad, University of Agricultural Sciences, Dharwad, The field evaluations were conducted during *kharif* 2017-18 and 2018-19. The time frame and flow of investigation is depicted in a flow chart (Fig. 1). The details of experimental materials and methods adopted under present investigation were described here under. The weather data during the investigation is presented in Table 4.

3.1 Experimental site location and weather condition

The field experiment was conducted on a medium deep black soil at University of Agricultural Sciences, Dharwad which is situated in the Northern Transitional Zone (Zone No. 8) of Karnataka state with latitude of 15.48° N, longitude of 74.98° E and at the altitude of 678 meter above the mean sea level. The total rainfall during the cropping period (*kharif* 2018-19) in Dharwad was 535.6 mm (Table 4).

3.2 Experimental material

The Recombinant Inbred Line (RIL) population was derived from intraspecific hybridization between cotton (*Gossypium hirsutum* L) genotypes viz., RHAP 12 and RHAP 15, which are contrastingly different *w.r.t* fibre strength and seed cotton yield (Table 5 and Plate 1). Both parental lines were stabilized segregating lines were developed at AICRP on cotton, Main Agriculture Research Station (MARS), Raichur. RHAP 12 was derived from hybridization between HGHV 99/300 and Pusa 1927 upland cotton lines whereas RHAP 15 was drawn from crossing between Surabhi and GMR 5 of *Gossypium hirsutum* L. genotypes. A Recombinant Inbred Line (RIL) population was developed using Single Boll Descent (SBD) method from F₂ generation and carry forwarded upto F₆ generation (Plate 2). The population consisted of 222 Recombinant Inbred Lines (RILs) and these lines exhibited no variation within line due to continuous selfing from F₂ generation onwards (Fig. 1). The experimental material comprises of 222 F₆ lines, two parents and check (MCU 5, Sahana and HBS 144). The F₄ and F₅ segregating material were evaluated during the *kharif* 2017 and *kharif* 2018 respectively.

Table 4: Meteorological data parameters during the crop period at University of agricultural sciences Dharwad

Months	Year	Temperature		RH (%)	Normal Rainfall (mm)	Rainfall (mm)	Year	Temperature		RH (%)	Normal Rainfall (mm)	Rainfall (mm)
		Max. °C	Min. °C					Max. °C	Min. °C			
June	2017	29.2	21.0	90.83	106.60	74.7	2018	28.8	21	87.7	106.60	115.4
July		26.3	21.0	92.35	155.92	146.0		25.8	20.6	90.1	155.92	128.8
August		26.4	20.6	92.71	102.34	112.2		25.9	20.2	89.7	102.34	72.2
September		27.1	20.1	90.00	109.32	73.4		29.6	18.9	83.7	109.32	69.6
October		29.7	18.8	75.61	126.50	44.8		31.6	18.3	73.3	126.50	76.8
November		30.8	14.4	57.10	32.13	5.8		30.5	16.3	66.4	32.13	34.4
December		30.0	14.0	59.32	5.10	0.0		28.8	14.6	70.7	5.10	38.4
January	2018	30.1	14	59.81	0.80	0.4	2019	29.5	13.0	60.5	0.80	0.0
February		33.6	17.9	62.45	11.34	0.2		32.8	15.9	54.8	11.34	0.0

Where,

RH = Relative humidity

Max = Maximum

Min = Minimum

Table 5: Characteristics of parental lines viz., RHAP 12 and RHAP 15 of *G. hirsutum*

Sl. No.	Traits	RHAP 12	RHAP 15
1	Plant height (cm)	124.70	131.10
2	Number of monopodia per plant	3.00	3.65
3	Number of sympodia per plant	10.60	12.90
4	Number of bolls per plant	25.40	18.50
5	Seed cotton yield per plant (g)	70.00	55.00
6	Seed index (g)	7.40	6.45
7	Boll weight (g)	3.35	2.64
8	Ginning outturn (%)	38.80	35.85
9	Lint index (g)	4.69	3.61
10	Fibre strength (g/tex)	29.30	22.20
11	Upper half mean length (mm)	27.50	25.10
12	Micronaire value ($\mu\text{g}/\text{inch}$)	3.83	3.54
13	Uniformity index (%)	88.80	84.50
14	Maturity ratio	0.47	0.55
15	Fibre elongation length (%)	6.40	6.90



Fig. 1: Time line of research programme

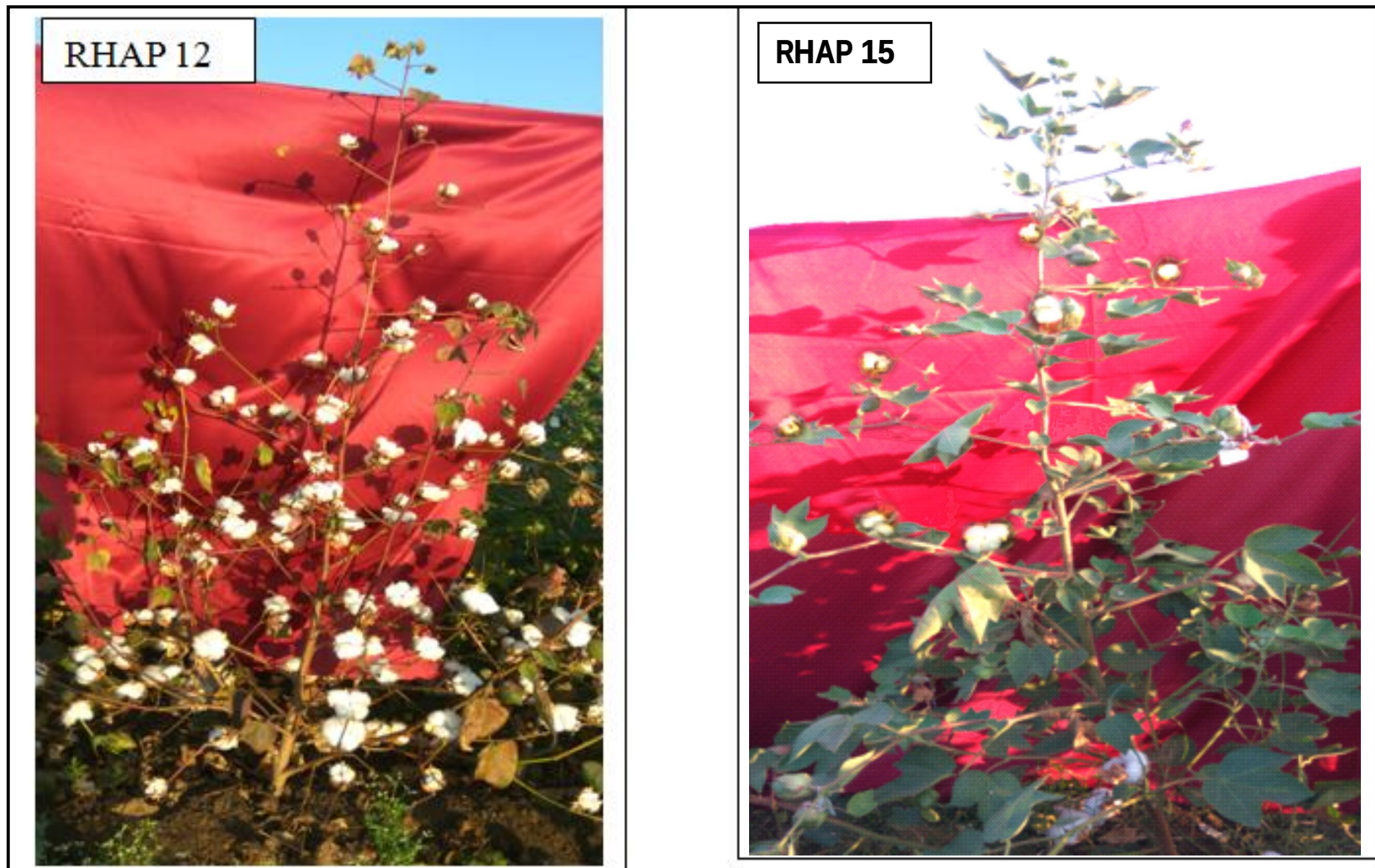


Plate 1: Parental lines viz., RHAP 12 and RHAP 15 of *G. hirsutum* utilized to develop intraspecific derived RIL population



Plate 2: A) Field general view during *kharif* 2018 (RIL Population) B) RIL 54 line C) RIL 54 line closer view

3.3 Experimental design and layout plan

The experimental material was laid out in simple lattice design with two replications. The blocks were spaced one meter apart and each block comprised of 222 RILs, check varieties viz., sahana, MCU 5, HBS 144. The two parental lines viz., RHAP 15 and RHAP 12 were evaluated in separate block. Each genotype in a block was grown in one row of 5 m length with a spacing of 90 cm between rows and 30 cm between plants.

3.4 Observations recorded

3.4.1 Yield and its attributing parameters

Five plants were selected at random and tagged in each line and observations of the following characters were recorded on tagged plants. The mean of five plants observation was used for statistical analysis.

3.4.1.1 Plant height (cm)

Plant height was measured in centimeter from the base of the plant to the apex of the plant at maturity.

3.4.1.2 Number of monopodia per plant

Number of branches on main stem which were lateral and axillary in position with vertical growth in acropetal succession was counted at maturity stage, avoiding small sprouts.

3.4.1.3 Number of sympodia per plant

Branches which are extra axillary in position and normally horizontal with zigzag pattern of fruiting points were taken as sympodia; the number of such sympodia on main stem was recorded at maturity stage.

3.4.1.4 Boll weight (g)

Seed cotton obtained from a random sample of 20 bolls collected from each line of RIL population was used to determine the boll weight in grams.

3.4.1.5 Number of bolls per plant

The number of bolls on the plant, which contributed to the seed cotton yield were counted and recorded at the time of harvest.

3.4.1.6 Seed cotton yield per plant (g)

The seed cotton yield harvested up till final picking from five plants in each line and average yield from those five plants used to calculate the seed cotton yield per plant.

3.4.1.7 Ginning outturn (%)

A random sample of 300 (g) seed cotton from each entry was ginned and the lint yield obtained was utilized for working out the ginning outturn by the formula.

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

3.4.1.8 Seed index (g)

Hundred good and bold seeds were weighed to determine the seed index in grams.

3.4.1.9 Lint index (g)

It is the weight of lint obtained from 100 seeds and expressed in grams. This was calculated by using the formula,

$$\text{Lint index (\%)} = \frac{\text{Weight of 100 seeds} \times \text{Ginning outturn}}{100 - \text{Ginning outturn}} \times 100$$

3.4.2 Fibre quality characters

The fibre quality parameter included fibre strength, Upper Half Mean Length (UHML), micronaire value, fibre elongation length and uniformity index. Following characters were analyzed under HVI (high volume instrument) at plus enterprise private limited Dharwad.

3.4.2.1 Fibre strength (g/tex)

It is the force required to break bundle of fibre of unit linear density. The fibre strength was expressed in gram per tex.

3.4.2.2 Upper half mean length (mm)

Upper half mean length (UHML) is defined as the longest 50 per cent of the fibres of the sample being tested. Fibre length was expressed in millimeter (mm).

3.4.2.3 Micronaire value ($\mu\text{g inch}^{-1}$)

It is the average weight per unit length of fibre. It is used in determining the fibre fineness, the linear density of fibre was expressed in microgram per inch ($\mu\text{g inch}^{-1}$).

3.4.2.4 Uniformity index (%)

Ratios of upper half mean length to mean staple length. It indicates the uniformity of fibre length. Fibre uniformity ratio was expressed in percentage (Anthony, 1999).

$$\text{Uniformity index (\%)} = \frac{\text{Upper Half Mean Length}}{\text{Mean staple length}} \times 100$$

3.4.2.5 Fibre elongation length

It is a measure of per cent increase in jaw separation under load at the time of fibre rupture, expressed in percentage (%).

$$\text{Fibre elongation (\%)} = \frac{\text{Apparent length} - \text{Initial length}}{\text{Initial length}} \times 100$$

3.4.2.6 Maturity ratio

It is an index of the extent of fibre development. The maturity depends mainly on the degree of secondary thickening of fibre (Anthony, 1999). The ratio of lumen and cell wall is less than one in case of mature fibre, 1-2 for half mature fibre and more than two for immature fibre.

3.5 Biometrical analysis

3.5.1 Genetic Variability

3.5.1.1 Analysis of Variance

The analysis of variance for different characters was carried out using simple lattice design as suggested by Cochran and Cox (1957).

Table 6: Schematic representation of ANOVA table of simple lattice design

Source of variation	Degrees of freedom (df)	Sum of squares (SS)	Mean square	Computed <i>F</i>	F ratio
Replication	$r - 1$	SSR	MSR	$\frac{MSR}{MSE}$	$\frac{\frac{MST (unadj)}{MSE}}{\frac{MSB (adj)}{MSE}}$
Genotypes (unadjusted)	$k^2 - 1$	$SSg (unadj.)$	$MSg (unadj.)$	$\frac{MST (unadj)}{MSE}$	
Blocks within replication (adjusted)	$r (k-1)$	$SSB (adj.)$	$MSB (adj.)$	$\frac{MSB (adj)}{MSE}$	
Intra-block error	$(k-1) (rk-k-1)$	SSE	MSE		
Total	$rk^2 - 1$	$SSTO$			

Where, r = Number of replications, k^2 Number of treatments (genotypes)

The adjusted variable mean differences were tested for significance as follows

Source of variation	df	Sum of squares	Mean square	F ratio
Genotypes (adjusted)	k^2-1	SSg	G	G/Ee
Error (intra block)	$(k-1) (rk-k-1)$	SSE	Ee	

The computed *F* value was compared with the table *F* value at (k^2-1) and $(k-1)$ $(rk-k-1)$ degrees of freedom for 5 % and 1 % level of significance.

To test significance of the differences between any two adjusted genotypic means, the standard error of mean was computed using the formula

$$S.E = [2Ee/r (1 + 2ku/k + 1)]^{0.5}$$

Where, S.E = Standard error of mean

Ee = Mean sum of squares for error (intra block)

r = Number of replications

k = Number of genotypes in each sub-block

u = Weightage factor computed

3.5.2 Population Mean and Variances

A. Arithmetic Mean: It is also simply known as mean or average, is computed by dividing the sum of all observations in a sample by their number.

$$\text{Mean} = \frac{\sum X}{n}$$

Where,

X = sum of all the observations

n = number of observations

B. Variance: It measures the variability and it is defined as average of square of deviations from the mean.

$$\sigma^2 = \frac{1}{n} \sum (X_i - X)^2$$

Where, σ^2 = variance, X_i = observation, X = mean

C. Standard Deviation (SD) : It is dispersion of individual values (X) around the population mean.

$$SD = \sqrt{\sigma^2}$$

D. Standard Error of Mean (SE) : It is dispersion of family mean around the estimated population mean.

$$\text{Standard Error} = \frac{SD}{\sqrt{n}}$$

Where,

SD = Standard deviation

n = number of observations

In fact, S.E. is the SD of mean *i.e.* represented by $\bar{X} \pm \text{S.E.}$.

E. Coefficient of Variability (CV): when variation has to be compared for different characters, each represented by different units. We can compare different traits by converting units of all characters on the same scale using coefficient of variability. Coefficient of Variability (CV) is expressed as percentage ratio.

$$\text{CV(\%)} = \frac{\text{SD}}{\bar{X}} \times 100$$

3.5.1.3 Estimation of Genetic Variability Parameters

Genetic variability among the genotypes for all recorded characters were estimated as mentioned below.

A. Genotypic co-efficient of variability (GCV)

$$\text{GCV\%} = (\sigma^2_g) / \bar{X} \times 100$$

B. Phenotypic co-efficient of variability (PCV)

$$\text{PCV\%} = (\sigma^2_p) / \bar{X} \times 100$$

C. Environmental coefficient of variability (ECV)

$$\text{ECV\%} = (\sigma^2_e) / \bar{X} \times 100$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

σ^2_e = Error variance

$\bar{X}$ - Grand mean of the character.

PCV and GCV were classified based on the scale given by Robinson *et al.* (1949) and presented below:

0-10 %	Low
>10 -20 %	Moderate
>20 %	- High

D. Heritability percentage (h^2)

It is the ratio of genetic variance to the phenotypic variance. The estimates of heritability in the broad sense were obtained by applying formula given by Singh and Chaudhary (1977).

$$h^2 = \left(\frac{\sigma^2_g}{\sigma^2_p} \right) \times 100$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

As suggested by Johnson *et al.* (1955a), heritability values are categorized as follows:

Low	- less than 30 %
Moderate	- >30-60 %
High	- more than 60 %

E. Genetic Advance (GA)

Genetic advance was computed by using the formula elucidated by Johnson *et al.* (1955a)

$$\text{Genetic advance} = \frac{\sigma^2_g}{\sigma^2_p} \times K$$

Where,

σ^2_g = Genotypic variance

σ^2_p = Phenotypic variance

K = selection difference a constant value of which is 2.06

F. Genetic advance over per cent of mean (GAM) :

Genetic advance over per cent mean was calculated as follows:

$$\text{GA \% over mean} = (\text{GA}/\text{Mean}) \times 100$$

3.5.3 Correlation and regression Coefficients and Path analysis

Both genotypic and phenotypic coefficients of correlation between all pairs of characters were determined by using variance and covariance components as suggested by Johnson *et al.* (1955b). Analysis was done using the “GENRES” computer programme.

$$r_{p(xy)} = \frac{\text{Cov}_p(X, Y)}{\sqrt{V_{px} V_{py}}}$$

$$r_{g(xy)} = \frac{\text{Cov}_g(X, Y)}{\sqrt{V_{gx} V_{gy}}}$$

Where,

r_p and r_g are phenotypic and genotypic correlations respectively.

$\text{Cov}_p(x, y)$ and $\text{Cov}_g(x, y)$ are phenotypic and genotypic covariance between the characters, x and y

V_{px} and V_{py} are the phenotypic variances for the characters x and y

V_{gx} and V_{gy} are the genotypic variances for the characters x and y

The calculated value of 'r' was compared with 't' table value with n-2 degree of freedom at 5 and 1 *per cent* level of significance.

Simple linear regression analysis

In statistics, simple linear regression is a linear regression model with a single explanatory variable. In simple linear regression, each observation consists of two values. One value is for the dependent variable and one value is for the independent variable.

$$Y = a + bX$$

Where,

Y = dependent variable

X = independent variable

b = slope of line

a = y intercept

Path Co-efficient analysis

Path-coefficient analysis was carried out using phenotypic correlation values of yield components on yield as suggested by Sewall wright (1921) and illustrated by Dewey and Lu (1959). Standard path coefficients which are the standardized partial regression coefficients were obtained using statistical software package. These values were obtained by solving the following set of "P" simultaneous equations by using the above package.

$$P_{01} + P_{02} r_{12} + \text{-----} + P_{0P} r_{1P} = r_{01}$$

$$P_{01} + P_{12} r_{02} + \text{-----} + P_{0P} r_{2P} = r_{02}$$



$$P_{01} + r_{1P} + P_{02} r_{2P} \text{-----} + P_{0P} = r_{0P}$$

The direct and indirect effects are rated as follows.

0.00 – 0.09 : Negligible

0.10 – 0.19 : Low

0.20 – 0.29 : Moderate

0.30 – 1.00 : High

More than 1.00 : Very high

3.5.4 t Test

A t-test is a type of inferential statistic used to determine if there is a significant difference between the means of two groups, which may be related in certain features.

T test assuming the equal variance

$$T - value = \frac{mean_1 - mean_2}{\sqrt{\frac{(n_1 - 1) \times var1^1 + (n_2 - 1) \times var2^2}{n_1 + n_2 - 1}}} \times \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}$$

Where,

mean1 and mean2=Average values of each of the sample sets

var1 and var2=Variance of each of the sample sets

n1 and n2=Number of records in each sample set

$n_1 + n_2 - 2$ = Degrees of Freedom

The outcome of the t-test produces the t-value. This calculated t-value is then compared against a value obtained from a critical value table (called the T-Distribution Table). This comparison helps to determine how likely the difference between the means occurred by chance or whether the data sets really have intrinsic differences. The t-test questions whether the difference between the groups represents a true difference in the study or if it is likely a meaningless statistical difference.

3.5.5 Kurtosis and skewness

The average and measure of dispersion like range can describe the distribution but they are not sufficient to describe the nature of the distribution. For this purpose we use other concepts known as Skewness and Kurtosis.

Skewness: The coefficient of Skewness is a measure the degree of symmetry in the variable distribution (Sheskin, 2011).

$$\text{Skewness} = \frac{1}{N} \sum_{i=1}^N \left[\frac{(X_i - \bar{X})}{\sigma} \right]^3$$

Where,

X_i = value of i^{th} individual

$\bar{X}$ = mean

σ = standard deviation

N = number of individuals

The skewness value can be positive or negative, or undefined. A zero value means that the tails on both sides of the mean balance out overall; this is the case for a symmetric distribution,

Kurtosis: The coefficient of Kurtosis is a measure for the degree of tailedness in the variable distribution (Westfall, 2014).

$$\text{Kurtosis} = \frac{1}{N} \sum_{i=1}^N \left[\frac{(X_i - \bar{X})}{\sigma} \right]^4$$

Where,

X_i = value of i^{th} individual

$\bar{X}$ = mean

σ = standard deviation

N = number of individuals

The kurtosis of any univariate normal distribution is 3. It is common to compare the kurtosis of a distribution to this value. Distributions with kurtosis less than 3 are said to be *platykurtic*, although this does not imply the distribution is "flat-topped" as sometimes reported. Rather, it means the distribution produces fewer and less extreme outliers than does the normal distribution. An example of a platykurtic distribution is the uniform distribution, which does not produce outliers.

3.5.6 Chi- square test

The goodness of test to Mendelian segregation of banding pattern in the segregating populations was tested by Chi- square test.

$$\chi^2 = \frac{\sum(O_i - e_i)^2}{e_i}$$

oi = Observed frequency

ei = Expected frequency

The significance of Chi-square value was tested against table value with n-1 degrees of freedom, where "n" is the total number of segregating classes (Pearson, 1900).

3.6 Molecular analysis

3.6.1 Isolation of DNA from population and parents

DNA isolation is a process of purification of DNA from sample by a combination of physical and chemical methods. DNA was extracted from both the parents and RILs using CTAB method with few modifications (Zhang and Stewart, 2000). The procedure for DNA extraction is as follows;

- The fresh leaf (1g) was taken in 2ml eppendorf tubes for DNA extraction.
- The leaves were crushed with micro pastel in liquid nitrogen to make fine powder.
- Then the pre heated DNA extraction buffer/ CTAB buffer (Table 7) was added to sample and later samples kept in water bath for 45 minute at 65°C with intermittent shaking.
- After previous step samples were taken out from water bath and allow for cooling.
- Added 1ml of chloroform: Isoamyl alcohol (24:1) and mixed well with the samples.

- The solution was centrifuged at 13,000 rpm for 10 minutes and only clear supernatant was transferred to fresh eppendorf tube and discard the debris.
- Again equal volume chloroform: Isoamyl alcohol solution was added to supernatant and centrifuged at 13,000 rpm for 10 min.
- By using micropipette, supernatant was collected and transferred to new 1.5 ml eppendorf tube. Then added 700 μ l of isopropanol and 50 μ l sodium acetate and kept at -20°C overnight for precipitation.
- Next day tubes were removed from the deep freezer and kept outside to attain room temperature. After that, centrifuged at 5,000 rpm for 5 min afterward supernatant was decanted without disturbing the pellet. The alcohol (70 %) was added to that pellet and centrifuged for 5,000 rpm for 5 min. After centrifuge alcohol was decanted without disturbing the pellet.
- Later Pellet was dried and suspended in 50 μ l of 1 X T₁₀E₁ buffer.
- To remove the RNA from sample RNase was added (1 mg/ml) and incubated at 37°C in water bath for half an hour.
- The finally DNA was stored at -20°C

Table 7: Composition of CTAB DNA extraction buffer

Components	Concentration	g/100ml	Quantity
EDTA (pH 8.0)	0.5M	18.612 g/100 ml	4 ml
Tris HCL (pH 8.0)	1M	15.76 g/100 ml	10 ml
CTAB	10 per cent	10 g/100 ml	20 ml
NaCl	4M	23.376 g/100 ml	35 ml
PVP	-	-	100 mg
β Mercaptoethanol	-	-	1 ml
Doubled distilled water	-	-	30 ml
Total	-	-	100 ml

3.6.1.1 Quantification of DNA- Agarose gel electrophoresis

In molecular biology, quantification performed to determine the average concentration of nucleic acid present in mixture as well as their purity. There are two methods to quantify the DNA such as i) Spectrophotometer ii) gel electrophoresis. We have quantified the DNA with gel electrophoresis because it's more sensitive than the other method. The 4 μ l of each sample was loaded on ethidium bromide stained agarose (1 %) gel and was electrophoresis at 100 volts. After electrophoresis, gel viewed under UV trans-illuminator. Quantification was done based on the intensity of the bands.

3.6.1.2 Normalization of DNA concentration for PCR

Normalization of DNA was done to bring all DNA concentrations to a relatively equal level (40ng/ μ l) by appropriate serial dilutions. Dilutions were done with T₁₀E₁ buffer.

3.6.2 Polymerase chain reaction

1. Template DNA: purified genomic DNA (40ng) of recombinant lines used as template DNA per reaction.
2. Primers: the primers utilized in investigation were listed in table 9 and 11.
3. dNTPs: individual dNTPs viz., dATP, dGTP, dCTP and dTTP were mixed in equal concentration and added to master mix.
4. *Taq* DNA polymerase: *Taq* DNA polymerase (3units per μ l) and 10x *Taq* buffer were obtained from M/S Bangalore Genei Pvt. Ltd., Bangalore.
5. Thermal cycler: Appendorf Thermal cycler

3.6.2.1 Amplification reaction mixture

The polymorphism find between the parents using SRAP and TRAP primers by PCR assay. The DNA master mix was done for polymorphism study in parents while primer master mix was done during the genotyping work in mapping population. The required master mix was prepared afresh to avoid handling errors. The total reaction

volume of PCR mixture was 20 μ l. the concentration of each component in PCR mixture has mentioned in Table 8.

Table 8: Concentration of each component in PCR mixture

Sl. No.	Components	Quantity
1	Template DNA (40 ng/ μ l)	2.0 μ l
2	10X assay buffer	2.0 μ l
3	dNTP mix (2.5 mM each)	1.6 μ l
4	Primer	
	a. Forward (5 pM/ μ l)	2.0 μ l
	b. Reverse (5 pM/ μ l)	2.0 μ l
5	Taq DNA polymerase (3U/ μ l)	0.2 μ l
6	Sterile double distilled water	7.6 μ l

3.6.3 Agarose gel electrophoresis

The PCR products were run on 2 per cent agarose gel to verify amplification. The gel electrophoresis was done in 1X TAE at 60 V for 120-160 min. The gel was stained with ethidium bromide solution (1 μ l/20 ml), allowed for electrophoresis in the gel electrophoresis unit and observed under UV trans illuminator.

3.6.4 Markers adopted in molecular analysis

i. Sequence Related Amplified Polymorphism (SRAP)

SRAP is also one of the PCR-based marker system which consist of two primers, a forward primer of 17 bases and a reverse primer of 18 bases. The forward primer consist of 10 bases at 5'end are filler sequence with no specific combination, followed by CCGG sequence and then three selective nucleotides at 3' end. The variation in these selective nucleotides generates the set of primers sharing the same core sequence. The reverse primer shares the same property as forward primer except four nucleotide sequence (CCGG) in forward, where as in reverse AATT replace those nucleotides (Fig. 2). Other cares like avoided the secondary structure and 40-50 % GC

content taken during the primer construction. Along with that, the filler sequence from both forward and reverse primer must be different each other.

In this experiment, SRAP primers were designed as mentioned in Li and Quiros, 2001 paper. All primers were commercially synthesized (Scigenom Hyderabad). In assay 9 forward primers and 17 reverse primers however a total of 153 different combinations were employed (Table 9). For PCR amplification, 20 µl of PCR reaction mixture used and concentration of different component mentioned in Table 8. The PCR amplification for SRAP analysis was performed according to Li and Quiros, 2001. The amplification conditions were as follows (Table 10).

Table 10: The Thermo profile of PCR for SRAP markers

Steps	Temperature °C	Time (min.)	Cycles
Initial Denaturation	95	5	
Denaturation	94	1	5
Annealing	35	1.30	
Extension	72	2	
Denaturation	94	0.55	33
Annealing	50	1.30	
Extension	72	2	
Final Extension	72	10	

ii. Targeted Region Amplified Polymorphism (TRAP)

TRAP markers are rapid and efficient PCR-based technique (Hu and Vick 2003), these markers utilizes the bioinformatics tools and expresses sequence tag (EST) database information to generate the polymorphic markers around the targeted candidate gene sequences. This target region amplification polymorphism (TRAP) technique uses 2 primers of 18 nucleotides to generate markers. One of the primers is fixed primer which was designed from the targeted EST sequence in the database; the second primer,

Table 9: List of Sequence Related Amplified Polymorphism (SRAP) primers employed in *G. hirsutum*

SL No.	SRAP forward primers (3'- 5')	
1	me1	TGAGTCCAAACCGGATA
2	me 2	TGAGTCCAAACCGGAGC
3	me3	TGAGTCCAAACCGGAAT
4	me 4	TGAGTCCAAACCGGACC
5	me 5	TGAGTCCAAACCGGAAG
6	me6	TGAGTCCAAACCGGTAG
7	me 7	TGAGTCCAAACCGGTTG
8	me8	TGAGTCCAAACCGGTGT
9	me 9	TGAGTCCAAACCGGTCA
SL.No.	SRAP reverse primers (3'- 5')	
1	em1	GACTGCGTACGAATTAAT
2	em2	GACTGCGTACGAATTTGC
3	em3	GACTGCGTACGAATTGAC
4	em4	GACTGCGTACGAATTTGA
5	em5	GACTGCGTACGAATTAAC
6	em6	GACTGCGTACGAATTGCA
7	em7	GACTGCGTACGAATTATG
8	em8	GACTGCGTACGAATTAGC
9	em9	GACTGCGTACGAATTACG
10	em10	GACTGCGTACGAATTTAG
11	em11	GACTGCGTACGAATTTCG
12	em12	GACTGCGTACGAATTGTC
13	em13	GACTGCGTACGAATTGGT
14	em14	GACTGCGTACGAATTCAG
15	em15	GACTGCGTACGAATTCTG
16	em16	GACTGCGTACGAATTCGG
17	em17	GACTGCGTACGAATTCCA

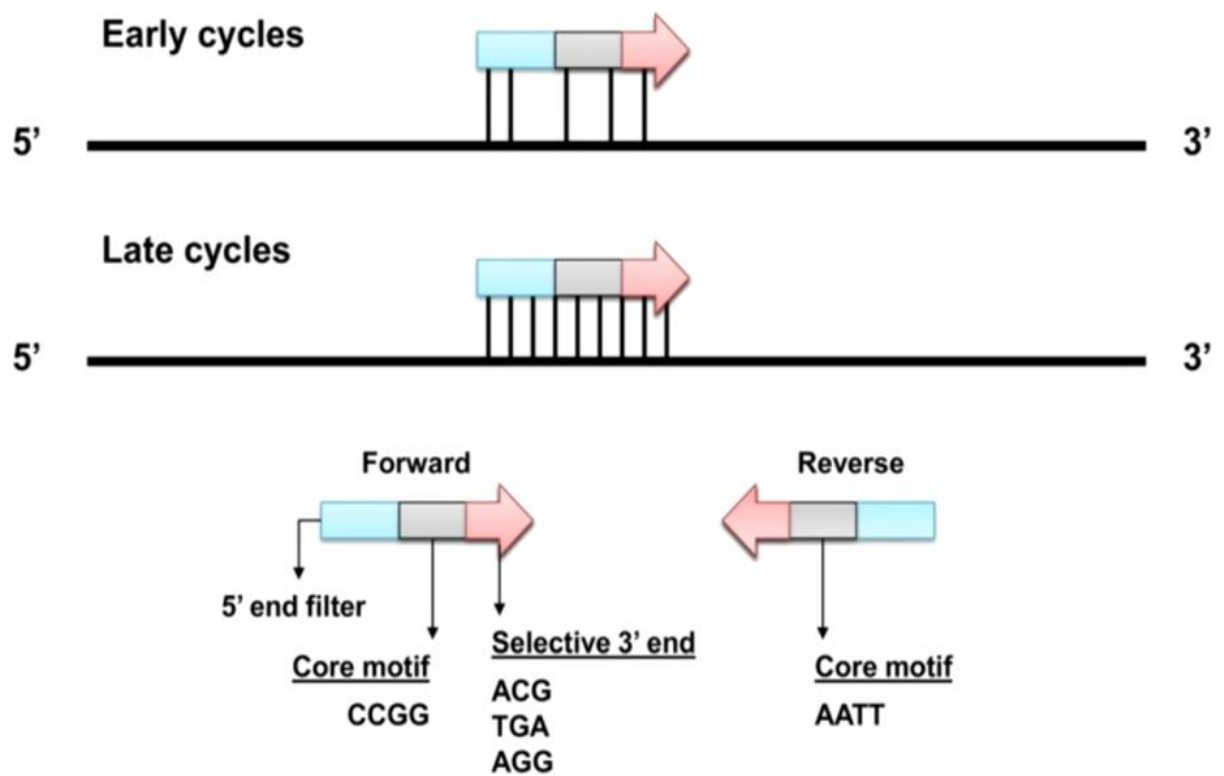


Fig. 2. Outline of Sequence Related Amplified Polymorphism (SRAP) marker

the arbitrary primer, is an arbitrary sequence with either an AT- or GC-rich core to anneal with an intron or exon, respectively (Fig. 3). The origin of fixed primer information is discussed in next section. The PCR amplification for TRAP analysis was performed according to Yu *et al.* (2007). The amplification conditions are as follows (Table 12).

Table 12. The Thermo profile of PCR for TRAP markers

Steps	Temperature °C	Time (min.)	Cycles
Initial Denaturation	95	2	
Denaturation	94	0.45	5
Annealing	35	0.45	
Extension	72	1	
Denaturation	94	0.45	33
Annealing	50	0.45	
Extension	72	1	
Final Extension	72	7	

3.6.4.1 Origin of fixed primer for TRAP

HBS 144 and HBS 187 (Plate 3) are the selected stabilized *hirsutum barbadense* introgressed lines contrastingly different for fibre strength, developed at ARS, Dharwad farm, University of Agricultural Sciences, Dharwad. The high fibre strength line HBS144 (28.0 g tex⁻¹) and low fibre strength line, HBS 187 (20.0 g tex⁻¹). fibre's micrograph indicated that HBS 144 had more thickened fibrillar structure possibly due to cellulose deposition (Vrinda, 2018 and Loheshkumar, 2018) which was less in HBS 187 (Plate 4). A fibre diameter of 17µm was observed in HBS144 while, a 10 µm fibre diameter was recorded in HBS 187. The fibrils which relate to deposition of cellulose had a diameter of 0.2 µm for HBS 144 and 0.1 µm for HBS 187 respectively (Patil, 2015). Cellulose deposition pattern of two contrasting cotton genotypes HBS144 and

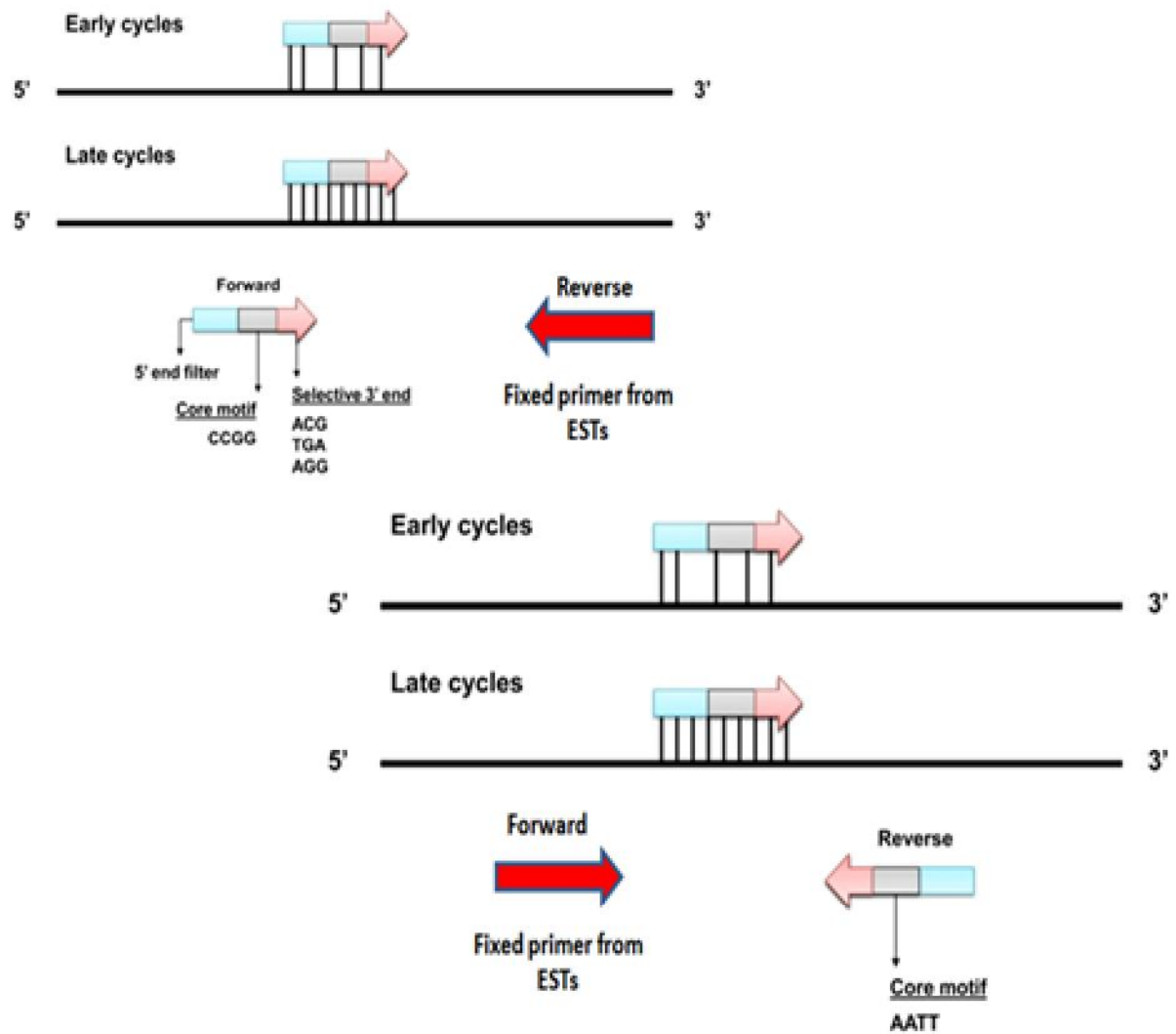
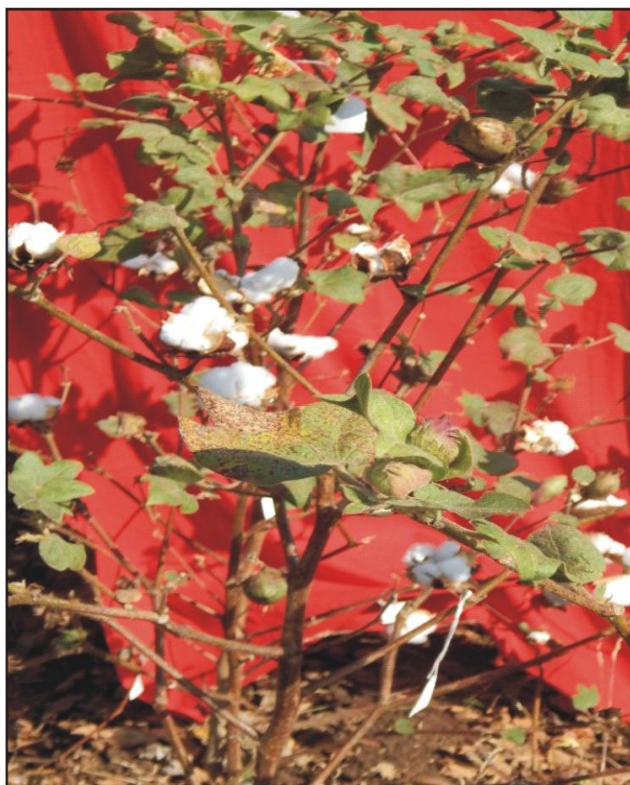


Fig. 3: Outline of Target Region Amplification Polymorphism (TRAP) marker

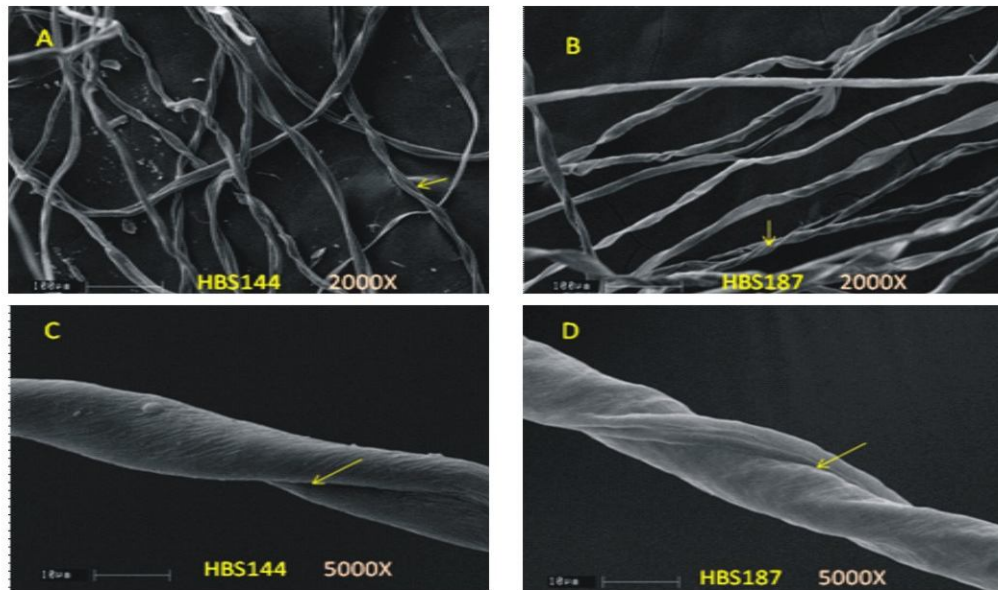


a) HBS144

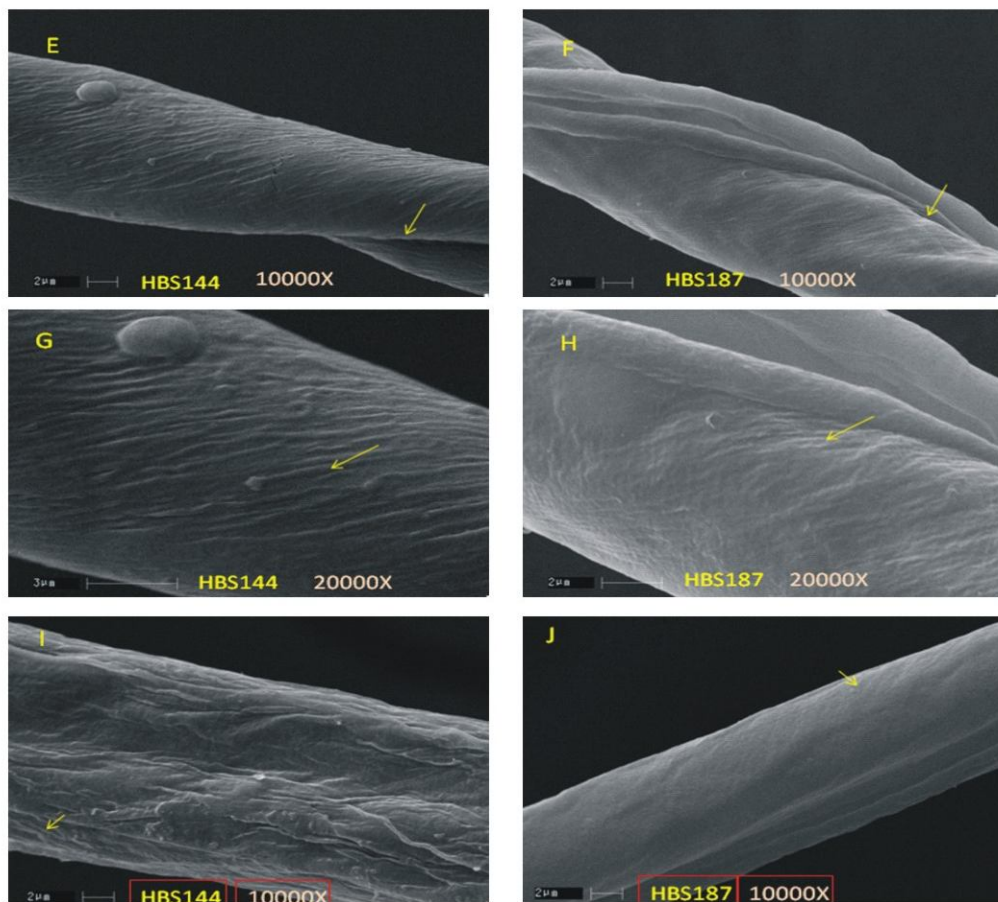


b) HBS187

Plate 3: *Hirsutum barbadense* introgressed lines HBS144 and HBS187 contrasting for fibre strength used for RNA sequencing by illumina biseq method



a) Images of cotton fibre under scanning electron microscope



b) Images of cotton fibre under scanning electron microscope

Plate 4: Electron microscopic view of fibrillar arrangement in *Hirsutum barbadense* introgressed lines HBS144 and HBS187 contrasting for fibre strength used for RNA sequencing by illumina biseq method

HBS 187 during fibre development period is presented in Table 13. Two cDNA libraries included mRNA from four different fibre development stages viz., 12 DPA (days to post anthesis), 18 DPA, 24 DPA and 30 DPA from each sample were generated from two cotton genotypes and sequenced by Illumina Hiseq method. In the present investigation fixed primers for TRAP was derived from the differentially expressed genes (DGE) of cotton of two contrasting parents HBS 144 and HBS 187. Differentially expressed P-significant and Q- significant genes from these two genotypes were used as one of the fixed primers in synthesis of TRAP markers. List of fixed primers for TRAP markers presented in Table 11.

Table 13: *Hirsutum barbadense* introgressed lines HBS144 and HBS187 contrasting for fibre strength, fibre diameter and cellulose content at different fibre developmental stages (Patil, 2017).

Sl. No.	Genotypes	Fibre strength (g tex ⁻¹)	Fibre Diameter (µm)	Fibril Diameter (µm)	Cellulose content (µg ml ⁻¹)			
					12DPA	18DPA	24DPA	30DPA
1	HBS 144	28.00	17	0.2	54.1	62.7	83.8	110.5
2	HBS 187	20.00	10	0.1	31.7	53.9	58.4	71.5

3.7 Development of linkage map and QTL mapping in RIL population

3.7.1 Mapping population utilized for genotyping

The genetic material consisted of 222 RIL population obtained from cross of RHAP 12 and RHAP 15 of *Gossypium hirsutum* L.

3.7.2 Genotyping of RIL population

3.7.2.1 DNA extraction

Young leaves from 21-days old seedlings were collected from 222 RILs of cross RHAP 12 × RHAP 15 and genomic DNA was extracted and its quality and quantity were estimated as per protocol described in 3.6.1.

Table 11: List of Target Related Amplified Polymorphism (TRAP) primers employed in *G. hirsutum*

SL	Primer ID	Gene	Forward sequence (5'- 3')
1	1F	42183	GGGTGGTGGATAATCTGTTGT
2	2F	55398	CCAAGTCCCGTTTCTGGTATT
3	3F	43908	TATGGAACAAGGGATGTGCATG
4	4F	32671	GGATCACACCTGTTGGTCATTA
5	5F	55808	GGACAAGGCTCAGGCTATAATG
6	6F	41929	GATAGGGATAGGGCGAGAGAA
7	7F	60537	GCTCTTCTTCCGGCTCTAATCGC
8	8F	24332	TGGGTTTCGCCCTTTGACTATC
9	9F	47473	GGCCATTCTGATGCAAAGATAC
10	10F	12657	CCATGCTCTAGTCTCACTTCTTT
11	11F	59335	GACTTTGGCTTCGGTCTTATACT
12	12F	27890	TGTCATTCTGGGAGCAGAAAC
			Reverse sequence (3'- 5')
13	1R	42183	GTGAAGCTGAGGAAATGTTTGG
14	2R	55398	TCTTGACTGGGCTCTTCTCT
15	3R	43908	GCTGGAGACAAACTGGAAC
16	4R	32671	GTGCTGTCAAGCTCTCTCTATG
17	5R	55808	ACGGCAAGTCCATGATTCTAC
18	6R	41929	GGAGCGTTTGCCATCAAATC
19	7R	60537	GCTAAGCACTTTGGCACATAC
20	8R	24332	CTTTGATGTCTGCCCTTCTCT
21	9R	47473	GGCCCACAACCTAAACCTATT
22	10R	12657	GCACTTCACTCCCACGTATT
23	11R	59335	CCCTGGTCCCTCATATCATTTTC
24	12R	27890	GAGCGACCCATCTGACATTATT

SL No.	Primer ID	SRAP forward primers (3'- 5')
1	me1	TGAGTCCAAACCGGATA
2	me 2	TGAGTCCAAACCGGAGC
3	me3	TGAGTCCAAACCGGAAT
4	me 4	TGAGTCCAAACCGGACC
5	me 5	TGAGTCCAAACCGGAAG
6	me6	TGAGTCCAAACCGGTAG
7	me 7	TGAGTCCAAACCGGTTG
8	me8	TGAGTCCAAACCGGTGT
9	me 9	TGAGTCCAAACCGGTCA

3.7.2.2 SRAP and TRAP marker assay

The 222 RILs of cross RHAP 12 × RHAP 15 were genotyped by employing a total of 38 polymorphic SRAP markers with 79 loci and 22 polymorphic TRAP markers with 67 loci. The protocol for PCR program as described in section 3.6.2 was followed. The genotype profiles produced by SRAP and TRAP markers on RIL population were scored manually. Example for polymorphic amplicons pattern and scoring pattern of SRAP and TRAP markers for the *QTL IciMapping* software is presented in Fig. 4.

3.7.2.3 Detection of segregation distortion (SD) of SRAP and TRAP markers

The genotypes of RIL at each SRAP and TRAP marker is expected to segregate in 1:1 ratio. The markers whose genotypic segregation deviated significantly ($p < 0.01$) from the expected 1:1 ratio as indicated by chi-square statistic at one degree of freedom were declared as distorted ones.

3.7.3 Genetic linkage map construction

The genetic linkage maps were constructed using software *QTL IciMapping* (Meng *et al.*, 2015). The genotype scores of the 222 RILs for the sets of polymorphic markers (146) were used for the construction of linkage map with a minimum LOD of 3 and maximum recombination fraction of 0.5. The Kosambi mapping function was used to convert the recombination frequencies into centiMorgan (cM) map distance (Kosambi *et al.*, 1943).

3.7.4 QTL analysis and mapping

QTL analysis was carried out using software *QTL IciMapping* v. 3.2 software (<https://www.integratedbreeding.net>). QTLs for various traits were identified by using the Inclusive Composite Interval Mapping (ICIM) method. Genome was scanned for QTLs at a walking speed of 1 cM and statistical significance of QTL for each trait was assessed by permuting each dataset 1,000 times, with a significance level of 0.05. For each trait, a minimum LOD value of 2.50 was used for the identification of QTL.

Gel	M	P1 (2)	P2 (0)	F1 (1)	Scoring of polymorphic amplicon	M	P1	P2	F1
A5	————	————	————	————	A5	————	————	————	————
A4	———— ———— ————		————	————	A4	———— ———— ————	2	10	10
A3	———— ———— ————	————	————	————	A3	———— ———— ————	————	————	————
A2	———— ————	————		————	A2	———— ————	12	0	12
A1	————	————	————	————	A1	————	————	————	————

Fig. 4: Example for amplicon pattern and scoring pattern of dominant and recessive markers in the QTL IciMapping software

4. EXPERIMENTAL RESULTS

The results obtained from the present investigation on RNA Sequence based QTL mapping and genetic investigation for seed cotton yield and fibre strength in *Gossypium hirsutum* L. are presented here under the following headings.

- 4.1 Analysis of variance
- 4.2 Identification of QTLs for yield and fibre quality traits
 - 4.2.1 Trait performance of RIL population and its parents
 - 4.2.2 Parental Polymorphism
 - 4.2.3 Linkage Analysis and map construction
 - 4.2.4 Segregation distortion
 - 4.2.5 QTL mapping for yield, yield related and fibre quality traits
- 4.3 Genetic variability parameters for yield and yield attributes and fibre quality traits
- 4.4 Character association and path analysis in the RIL population
- 4.5 Intergeneration correlation and regression between the F_4 Vs F_5 and F_5 Vs F_6 generation
- 4.6 Identification of transgressive segregants in RIL population
- 4.7 Identification of superior Recombinant Inbred Lines based on *per se* performance
- 4.8 Identification of superior Recombinant Inbred Lines (RIL) over the check varieties

4.1 Analysis of variance

Analysis of variance for yield and its component traits and fibre quality traits are presented in Table 14. Analysis of variation showed significant differences among the lines for all the traits viz., plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, seed cotton yield per plant (g), seed

Table 14: Analysis of variance for yield and its component and fibre quality traits in the RIL population of *G. hirsutum*

Source	df	Mean sum of squares								
		PH	NMP	NSP	NBP	SCYP	SI	BW	GOT	LI
Replications	1	778	8.19	375.81	61.03	263.03	5.75	0.27	6.91	3.93
Blocks	28	374.44	0.22	8.73	33.63	265.19	14.42	0.40	2.33	0.37
Treatments	224	283.77**	0.39**	3.65**	57.21**	712.39**	225.36**	0.95**	5.33**	0.60**
Error (Intra Block)	196	124.21	0.14	1.65	13.03	126.39	121.84	0.28	2.23	0.30
Total	449	220.75	0.29	3.88	36.46	427.70	387.38	0.62	3.79	0.46
Source	df	Mean sum of squares								
		UHML	FS	Mic	UI	MR	EL			
Replications	1	0.03	0.08	0.006	0.32	0.001	0.005			
Blocks	28	0.02	0.01	0.005	0.89	0.003	0.002			
Treatments	224	4.64**	8.43**	0.63**	37.05**	0.012**	0.387**			
Error (Intra Block)	196	0.02	0.01	0.006	0.89	0.003	0.001			
Total	449	2.33	4.21	0.18	18.92	0.008	0.194			

Where,

PH= Plant height (cm), NMP= Number of monopodia per plant, NSP = Number of sympodia per plants, NBP = Number of bolls per plant, SCYP= Seed cotton yield per plant (g), SI= Seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value (µg/inch), UI = Uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%), ** - Significance at 5 per cent.

index (g), boll weight (g), lint index (g), ginning outturn (%), fibre strength (g/text), fibre length (mm), micronaire value ($\mu\text{g}/\text{inch}$), fibre uniformity index (%), maturity ratio and fibre elongation length (%). Hence, above mentioned traits were considered for further analysis in Recombinant Inbred Lines (RILs).

4.2 Identification of QTLs for yield and fibre quality traits

4.2.1 Trait performance of Recombinant Inbred Lines (RILs) population and its parents

The performance of parents and 222 recombinant inbred lines (RIL) for all the traits studied are presented in Table 15. The phenotypic data was analyzed by employing the SPSS version 16.0 software. The t-test was calculated to determine the significant difference between means of two parents (RHAP 12 and RHAP 15) for agronomic and fibre quality traits (Table 15). In RIL population transgressive segregants were observed in both directions (positive and negative). The normal distribution of individuals within the population for each trait was measured using the kurtosis and skewness (Fig. 5).

Plant height

The genotypes viz., RHAP 12 and RHAP 15 registered a plant height of 124.70 cm and 131.10 cm respectively. The t-test indicated that parents were significantly different from each other for the trait (9.05). The population derived from above genotypes had an average plant height of 116.59 cm with a range of 69.88 cm to 148.40 cm. The population had the kurtosis and skewness of 0.54 and -0.16 respectively for the trait.

Number of monopodia per plant

The t-test value between the parents for the trait was 2.60. An average number of monopodia per plant in the RIL population were 2.40 with a range of 1.30 to 3.80. The population registered positive kurtosis of 0.06 and skewness of 0.25 for the trait.

Table 15: Trait performance of RIL (Recombinant Inbred Line) and its parent's viz., RHAP 12 and RHAP 15 of *G. hirsutum*

Sl. No.	Traits	Parents		t-value	p (two tail)value	RIL population				
		RHAP 12	RHAP 15			Average	Min.	Max.	Kurtosis	Skewness
1	PH	124.70	131.10	9.05*	0.0119*	116.59	69.88	148.40	0.54	-0.16
2	NMP	3	3.65	2.60	0.122	2.40	1.30	3.80	0.06	0.25
3	SNP	10.60	12.90	2.71	0.113	9.76	5.90	14.50	0.31	0.49
4	NBP	25.40	18.50	10.77**	0.009**	21.46	10.90	41.50	0.86	0.94
5	SCYP	70	55	19.20**	0.0027**	60.37	15.70	135.00	0.83	0.47
6	SI	7.40	6.45	3.80	0.063	6.54	4.88	8.90	0.12	0.16
7	BW	3.35	2.64	6.89*	0.0203*	2.85	1.26	4.92	0.01	0.40
8	GOT	38.80	35.85	4.42*	0.0475*	39.26	35.39	42.68	-0.44	-0.14
9	LI	4.69	3.61	5.15	0.0356*	4.24	2.88	6.51	0.76	0.43
10	FS	29.30	22.20	31.75***	0.0004***	25.27	22.33	30.63	0.03	0.67
11	UHML	27.50	25.10	16.97**	0.0034**	24.94	20.40	30.90	0.97	0.34
12	MIC	3.83	3.54	16.36**	0.002**	3.53	2.16	4.68	0.52	-0.26
13	UI	88.80	84.50	30.40**	0.001**	75.67	58.2	94.4	4.92	-0.14
14	MR	0.47	0.55	8.00*	0.0152*	0.57	0.29	0.78	0.35	-0.27
15	FEL	6.40	6.90	12.07	0.07	5.03	4.00	6.60	1.44	1.00

Where,

* = significance at 5 percentage

** = significance at 1 percentage

*** = significance at 0.1 percentage

PH= plant height (cm), NMP= number of monopodia per plant, NSP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value (µg/inch), UI = Uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).

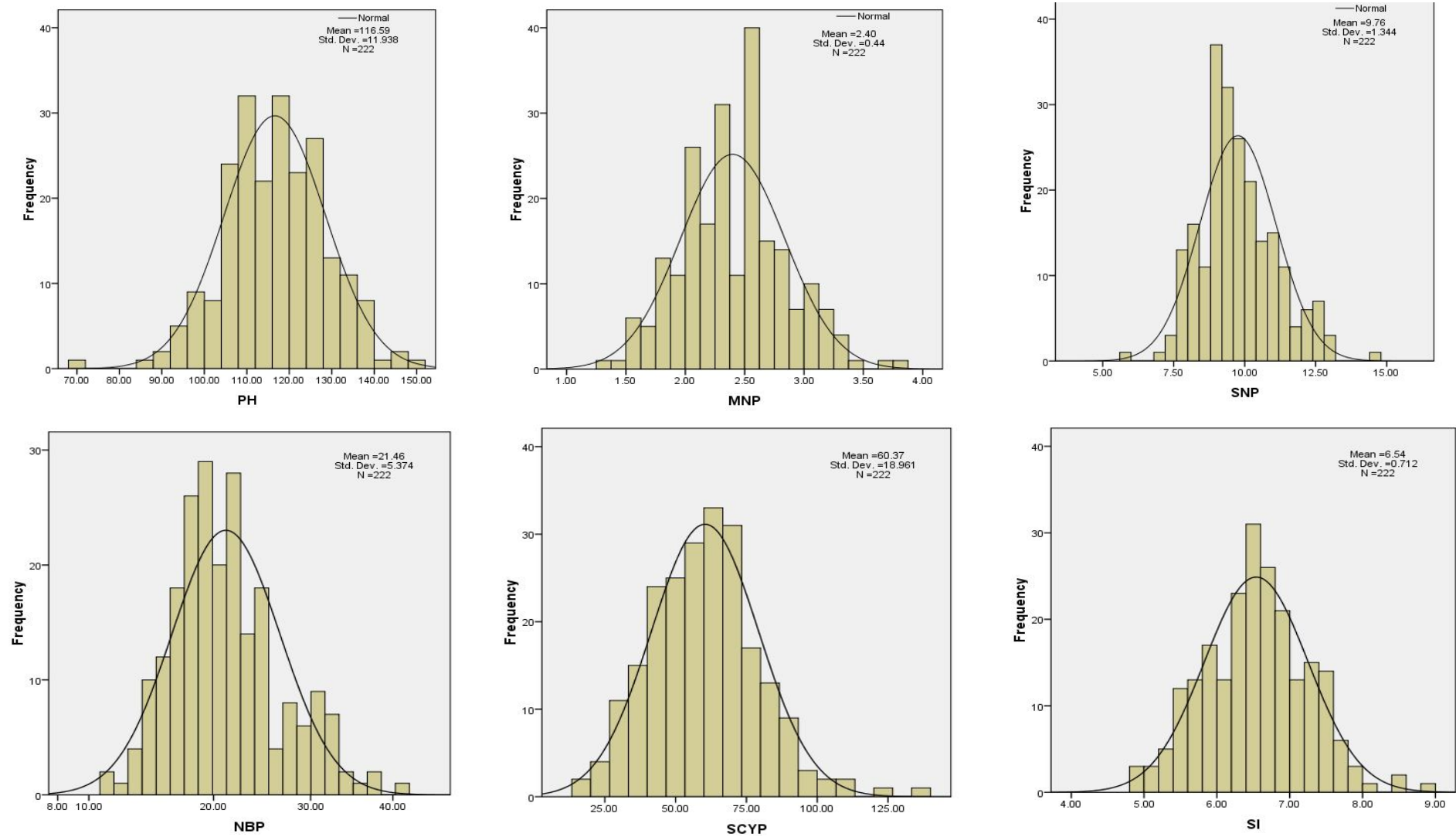
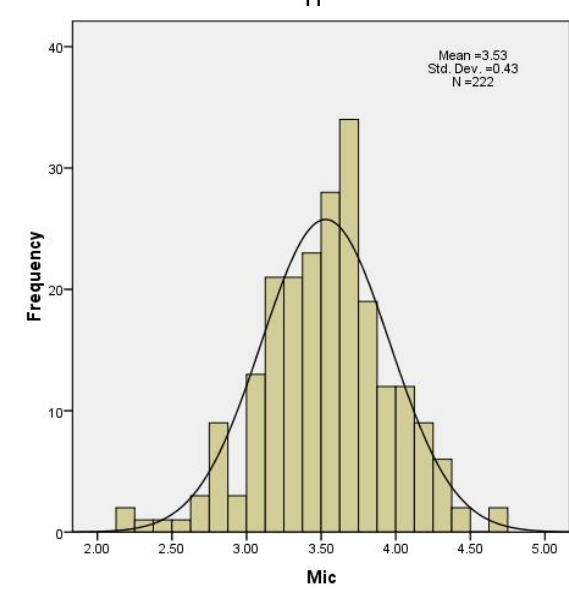
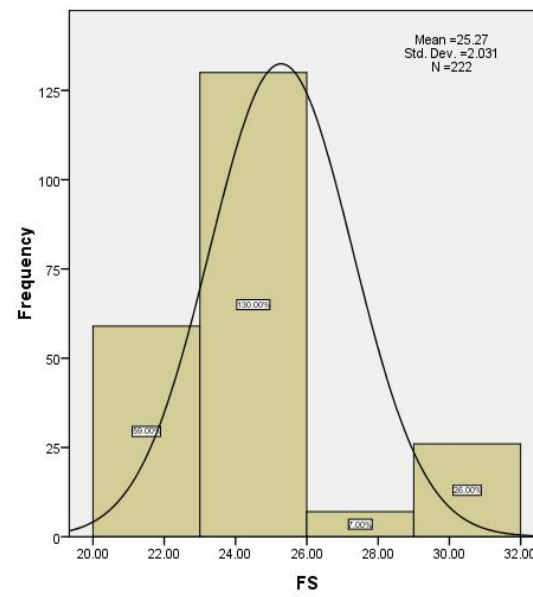
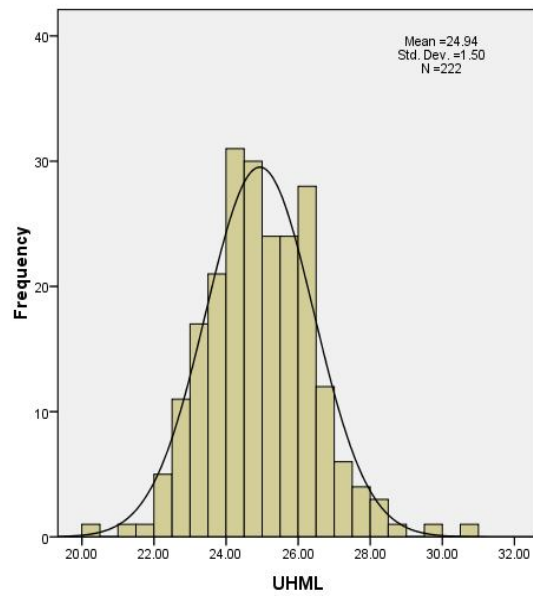
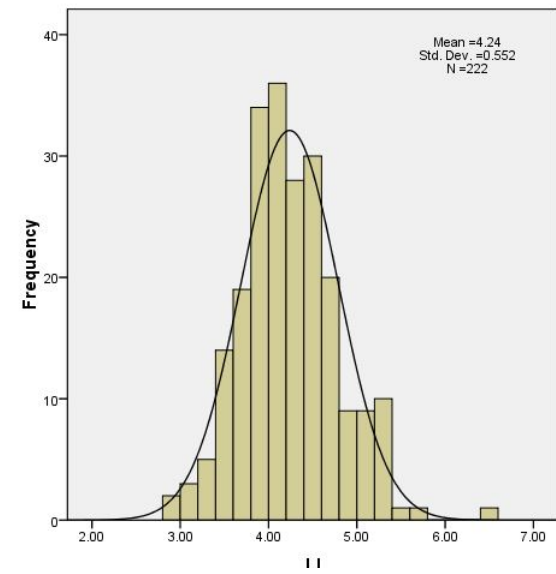
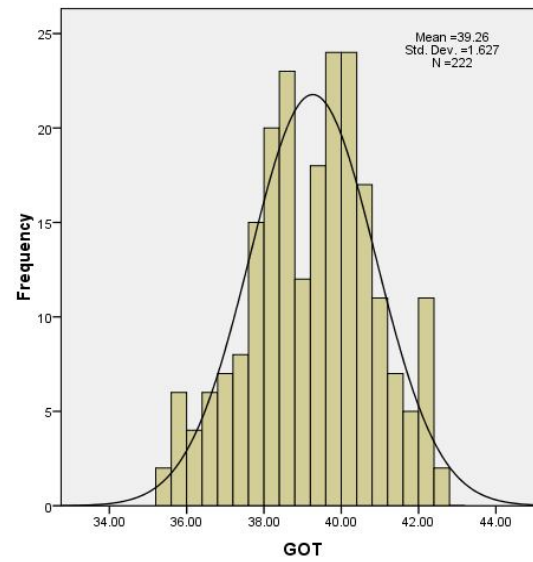
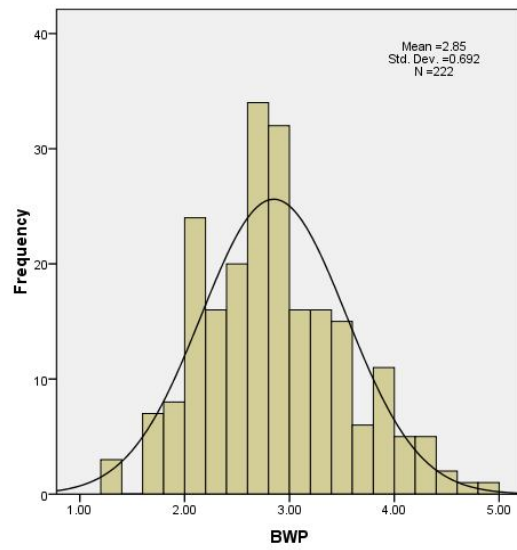
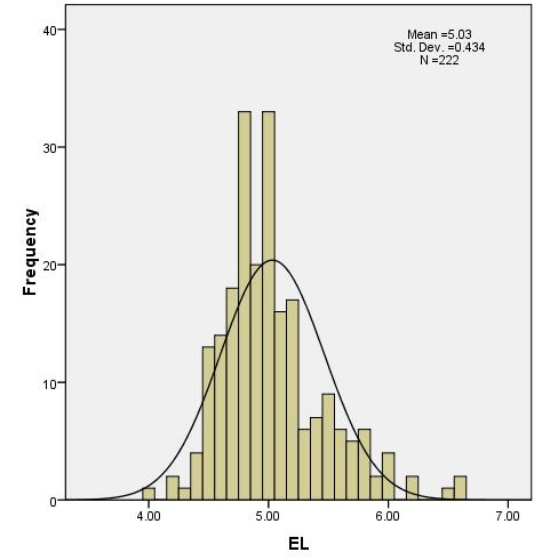
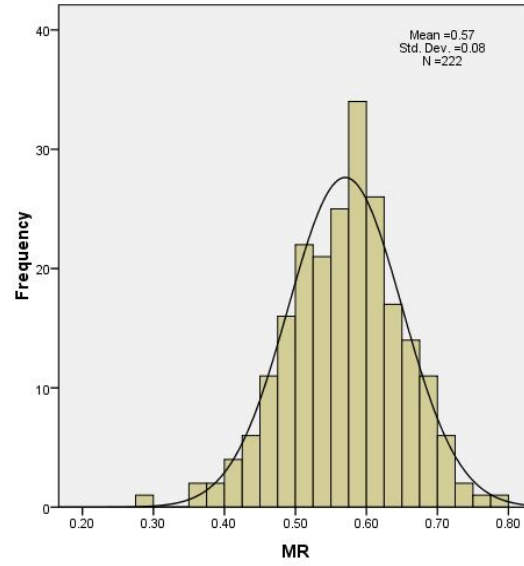
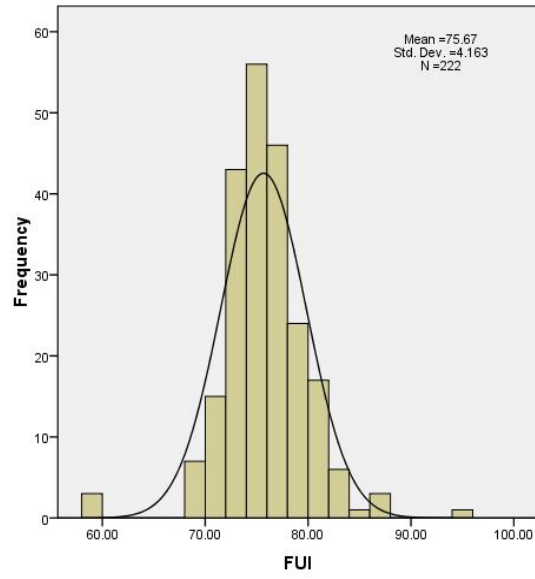


Fig 5: Frequency distribution of agronomic and fibre quality traits in RIL population. Units of X axis are phenotypic values and the units of the Y axis are the number of lines

Contd.....



Contd....



Number of sympodia per plant

The genotypes viz., RHAP 12 and RHAP 15 were hybridized to develop the RIL population which had an average of 9.76 sympodia per plant. The t test indicated that non significant difference between the parents for the trait (2.71). The population had a kurtosis and skewness of 0.31 and 0.49 respectively for the trait.

Number of bolls per plant

The parents RHAP 12 and RHAP 15 recorded an average of 25.40 and 18.50 bolls per plant respectively. An average number of bolls per plant of the RIL population derived from hybridization of above genotypes was 21.46 with a range of 10.90 to 41.50. The kurtosis and skewness value for the trait in the population were 0.86 and 0.94 respectively.

Seed cotton yield per plant

The genotypes namely RHAP 12 and RHAP 15 registered a seed cotton yield per plant of 70 g and 55 g respectively for the trait. The value of t test (19.20) indicated significant difference between the parents for the trait. The population derived from above genotypes had an average of 60.37 g with a range of 15.70g to 135.0 g for the trait. The population had a kurtosis and skewness of 0.83 and 0.47 respectively.

Seed index

The t- test value between the parents for above trait was 3.80. An average seed index in the RIL population was 6.54g with a range of 4.88 g to 8.90 g. The population had a positive and less than one, kurtosis (0.12) and skewness (0.16) value for the trait.

Boll weight

The parents viz., RHAP 12 and RHAP 15 were introgressed to develop the RIL population which had an average boll weight of 2.85 g. The t test indicated the, significance difference between the parents mean for the trait (6.89). The population had a kurtosis and skewness of 0.01 and 0.40 for above trait respectively.

Ginning outturn

The parents, RHAP 12 and RHAP 15 exhibited a ginning outturn of 38.80 and 35.85 per cent respectively for the trait. An average ginning outturn of the RIL population derived from above genotypes was 39.26 per cent with a range of 35.39 to 42.68 per cent. The kurtosis and skewness value for above trait in the population were -0.44 and -0.14 respectively for the trait.

Lint index

The average Lint index of RIL population under present investigation was 4.24 g with the range of 2.88 g to 6.51 g. The parents RHAP 12 and RHAP 15 of the population had a lint index of 4.69 g and 3.61 g respectively. The population had a kurtosis and skewness of 0.76 and 0.43 respectively for the trait.

Fibre strength

The genotypes namely RHAP 12 and RHAP 15 recorded fibre strength of 29.30 g/tex and 22.20 g/tex respectively. The t test value of 31.75 indicated that parents were significantly different from each other for the trait. The population derived from above genotypes had average fibre strength of 25.27 g/tex with a range of 22.33 g/tex and 30.63 g/tex. The population had a kurtosis and skewness of 0.03 and 0.67 respectively for the trait.

Upper half mean length

The maximum and minimum value of upper half mean length in the RIL population were 20.40 mm and 30.90 mm with an average of 24.94 mm. the parents of RIL population viz., RHAP 12 and RHAP 15 recorded upper half mean length of 27.50 and 25.10 respectively. The calculated t test between parents for upper half mean length was 16.97. The kurtosis and skewness for the trait in the population was 0.97 and 0.34 respectively.

Micronaire value

The t- test value between the parents for above trait was 16.36. The average micronaire value in the RIL population was 3.53 µg/inch with a range of 2.16 µg/inch to

4.68 $\mu\text{g}/\text{inch}$. The kurtosis and skewness value for above trait was 0.52 and -0.26 respectively.

Uniformity index

The parents, RHAP 12 and RHAP 15 hybridized to develop the RIL population had fibre uniformity index of 88.80 and 84.50 per cent respectively. The t test indicated the existence of significant difference between the parents for the trait (30.40). An average uniformity index of RIL population was 75.67 per cent. The population had a kurtosis and skewness of 4.92 and -0.14 for the trait respectively.

Maturity ratio

The parent's viz., RHAP 12 and RHAP 15 had a maturity ratio of 0.47 and 0.55 respectively. The average maturity ratio of the RIL population derived from above genotypes was 0.57 with a range of 0.29 and 0.78. The kurtosis and skewness value for the trait in the population were 0.35 and -0.27 respectively.

Fibre elongation length (%)

The genotypes, RHAP 12 and RHAP 15 recorded fibre elongation length of 6.40 and 6.90 per cent respectively. In the present investigation, a t test value of 12.07 indicated that parents were non significantly different from each other for the trait. The population derived from above genotypes had an average fibre elongation length of 5.03 per cent with a range of 4.00 per cent to 6.60 per cent. The population had a kurtosis and skewness of 1.44 and 1.00 respectively for the trait under investigation.

4.2.2 Parental Polymorphism

In the present investigation, Sequence Related Amplified Polymorphism (SRAP) and Target Region Amplified Polymorphism (TRAP) markers were employed to screen the parental polymorphism (RHAP 12 and RHAP 15). To synthesize, SRAP marker system, 153 primer combinations were developed by employing 9 forward primers and 17 reverse primers. Out of 153 SRAP markers, 38 primer combinations generated polymorphic amplicons between the parents. A SRAP marker generates multiple polymorphic loci which ranged from one to four (Plate 5). So in total of 79 polymorphic

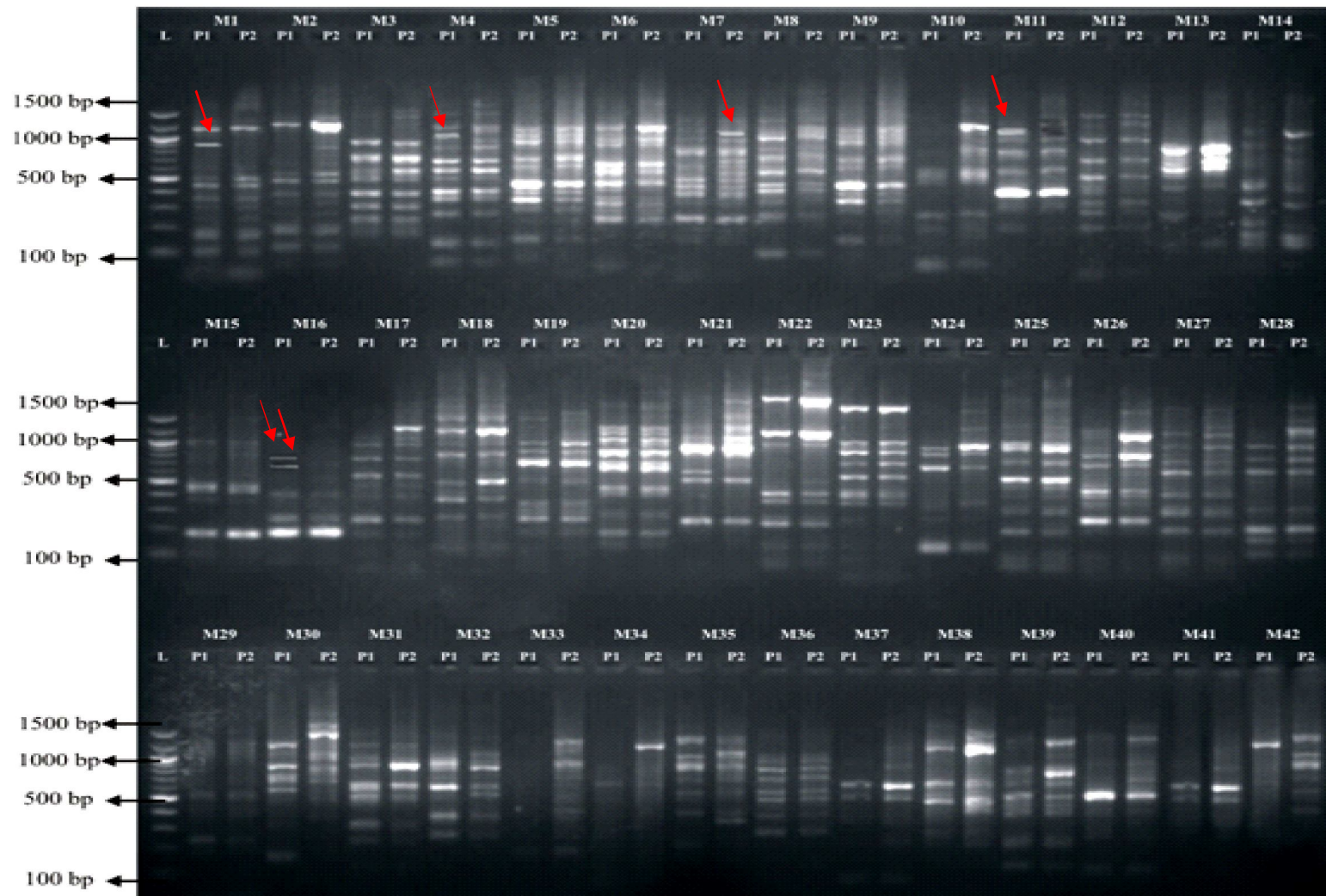


Plate 5: Monomorphic and Polymorphic behavior of Sequence Related Amplified Polymorphism (SRAP) markers between RHAP 12 and RHAP 15 of *G. hirsutum*

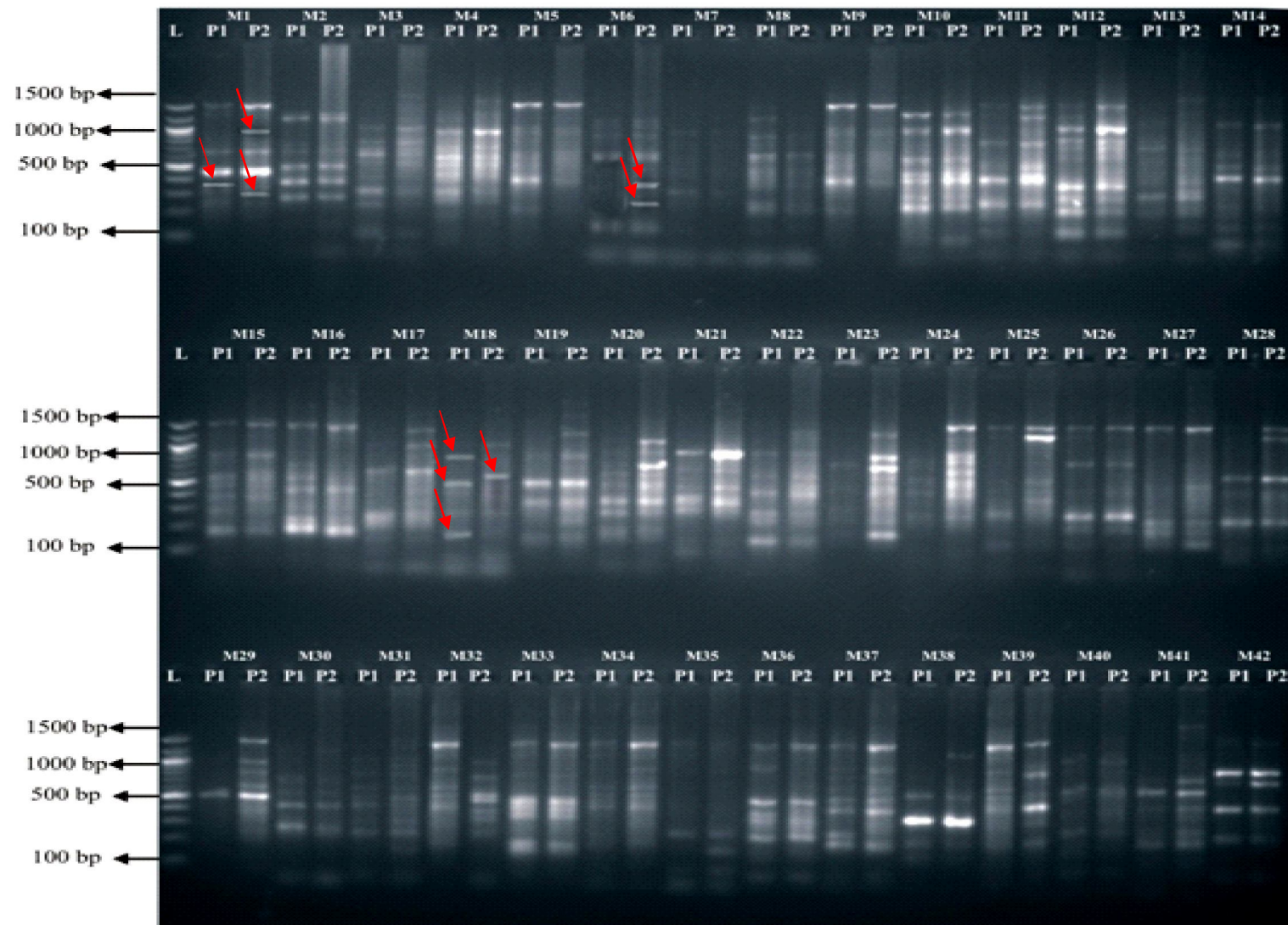


Plate 6: Monomorphic and Polymorphic behavior of Target Region Amplified Polymorphism (TRAP) markers between RHAP 12 and RHAP 15 of *G. hirsutum*

SRAP loci were observed and all considered for genotyping in 222 RIL derived in the present study (Table 16).

Similarly, Target Region Amplified Polymorphism (TRAP) markers were utilized to screen the parent polymorphism (RHAP 12 and RHAP 15). To synthesize TRAP marker system 216 primer combinations were developed by utilizing 24 fixed primers (EST) and 9 reverse primers. Out of 216 TRAP markers, 22 primers generated polymorphic amplicon between the parents. A TRAP marker also generates multiple polymorphic loci which ranges from one to four (Plate 6). A total 67 polymorphic TRAP loci considered for genotyping in 222 RIL (Table 17).

4.2.3 Linkage Analysis and map construction

The primer combinations which generated polymorphic amplicons between the parents were used for genotyping of 222 Recombinant Inbred Lines, derived from intraspecific hybridization between genotypes RHAP 12 and RHAP 15. The calculated recombination frequency (%) between the pair of markers was converted to centimorgan (cM) using Kosambi mapping function. The genotypic data derived from 146 (79 SRAP and 67 TRAP) markers was analysed through *QTL IciMapping software v 4.0* (Wang *et al.*, 2012) for the construction of linkage map. The polymorphic SRAP and TRAP markers harbored on 18 linkage groups at LOD value of 3 (Logarithm of Odds) and with total span length of 2910.8 cM (Table 18 and Fig. 6). An average distance between pair of adjacent markers was 19.94 cM. The 18 linkage group were exhibited the variation with respect to number of markers, map density and genome coverage (Table 18 and Fig. 6).

4.2.3.1 Number of markers on linkage group

A total of 146 markers were employed for construction of linkage map in the present investigation (Table 18 and Fig. 7). Maximum markers were harbored on LG1 (26) followed by LG 4 (18), LG 2 (13), LG 12 (13) LG 3 (11) LG 10 (11) LG 15 (9) LG 5 (8), LG 7 (7), LG 13 (6), LG 16 (6), LG 11 (4), LG 6 (3), LG 8 (3), LG 9 (3), LG 14 (2), LG 17 (2) and LG 18 (1).

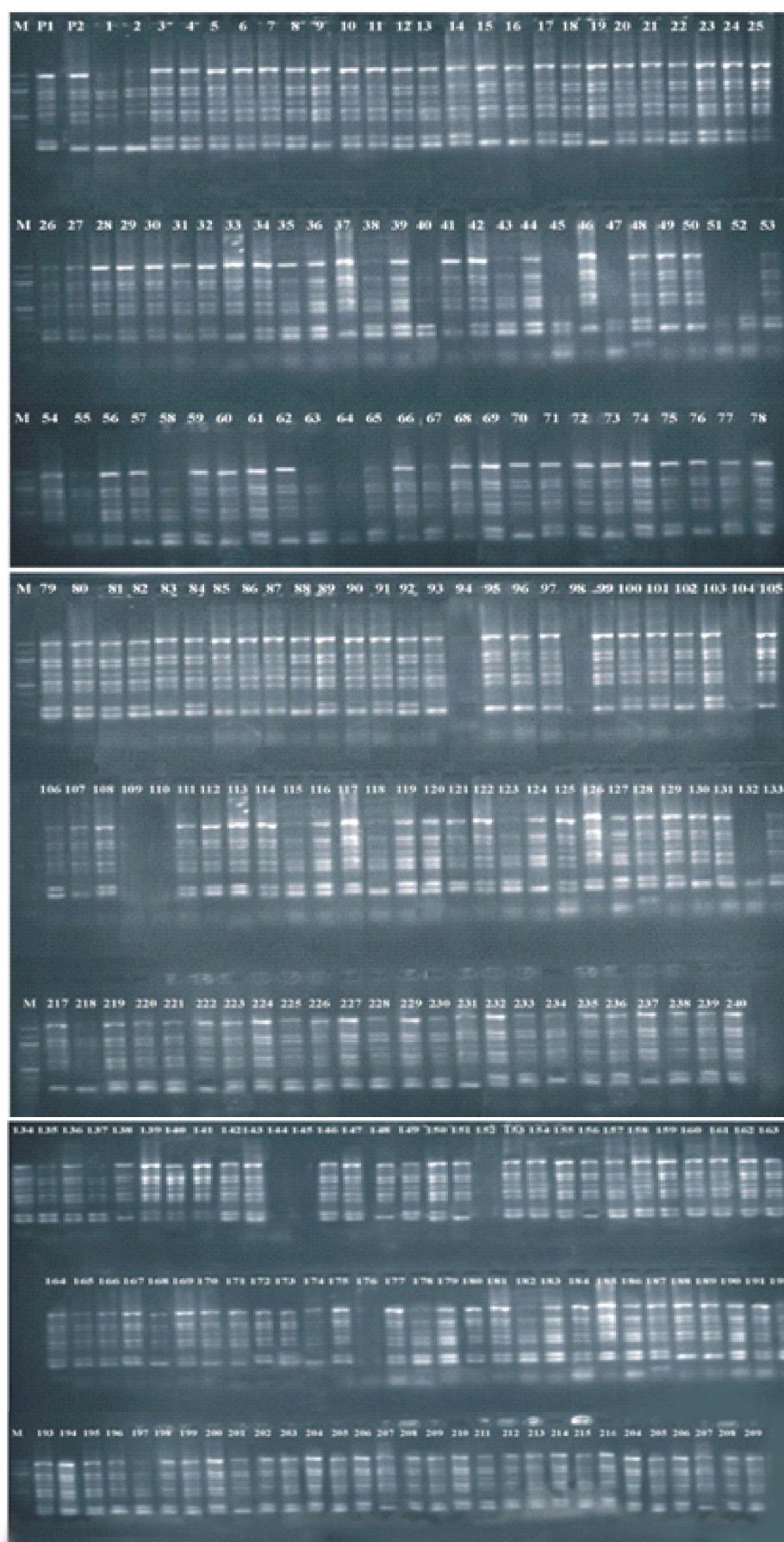


Plate 7: Genotyping the 222 RILs using SRAP marker viz., me8-em8 at 150 bp

Table 16: List of polymorphic Sequence Related Amplified Polymorphic (SRAP) markers identified between the RHAP 12 and RHAP 15 of *G. hirsutum*

Sl. No.	SRAP Marker	Primer combination	No. of loci	Amplicon size	Amplicon contribution	Marker ID
1	1	me3-em5	a	900	A	me3-em5a900A
2	2	me3-em7	a	900	A	me3-em7a900A
3	3	me3-em10	a	900	A	me3-em10a900A
4	4	me3-em15	a	800	A	me3-em15a800A
5	5	me4-em1	a	700	B	me4-em1a700B
6			b	800	A	me4-em1b800A
7	6	me4-em2	a	100	B	me4-em2a100B
8			b	500	A	me4-em2b500A
9			c	900	B	me4-em2c900B
10	7	me4-em4	a	800	B	me4-em4a800B
11			b	600	B	me4-em4b600B
12	8	me4-em7	a	200	B	me4-em7a200B
13			b	400	A	me4-em7b400A
14			c	600	A	me4-em7c600A
15	9	me4-em8	a	300	A	me4-em8a300A
16	10	me4-em13	a	200	A	me4-em13a200A
17			b	400	A	me4-em13b400A
18			c	900	B	me4-em13c900B
19			d	1000	B	me4-em13d1000B
20	11	me4-em17	a	700	A	me4-em17a700A
21			b	800	B	me4-em17b800B
22	12	me5-em3	a	700	A	me5-em3a700A
23			b	800	B	me5-em3b800B
24	13	me5-em6	a	200	B	me5-em6a200B
25			b	600	A	me5-em6b600A
26			c	700	B	me5-em6c700B
27			d	800	B	me5-em6d800B

Contd.....

Sl No.	SRAP Marker	Primer combination	No. of loci	Amplicon size	Amplicon contribution	Marker ID
28	14	me5-em16	a	900	A	me5-em16a900A
29			b	600	A	me5-em1b600A
30	15	me5-em17	a	700	B	me5-em17a700B
31	16	me6-em8	a	500	A	me6-em8a500A
32	17	me7-em1	a	700	B	me7-em1a700B
33	18	me7-em2	a	150	A	me7-em2a150A
34	19	me7-em3	a	250	B	me7-em3a250B
35			b	400	A	me7-em3b400A
36	20	me7-em4	a	400	B	me7-em4a400B
37	21	me7-em5	a	500	A	me7-em5a500A
38			b	600	B	me7-em5b600B
39			c	800	A	me7-em5c800A
40	22	me7-em8	a	300	A	me7-em8a300A
41			b	500	B	me7-em8b500B
42			c	900	A	me7-em8c900A
43			d	1000	B	me7-em8d1000B
44	23	me7-em9	a	400	A	me7-em9a400A
45			b	500	A	me7-em9b500A
46			c	1000	A	me7-em9c1000A
47	24	me7-em10	a	300	B	me7-em10a300B
48			b	400	B	me7-em1b400B
49	25	me7-em14	a	200	B	me7-em14a200B
50			b	600	B	me7-em1b600B
51	26	me7-em16	a	350	A	me7-em16a350A
52	27	me7-em17	a	340	B	me7-em17a340B
53			b	520	A	me7-em17b520A
54			c	950	B	me7-em17c950B
55	28	me8-em1	a	550	A	me8-em1a550A
56			b	600	A	me8-em1b600A
57			c	1000	A	me8-em1c1000A

Contd.....

Sl No.	SRAP Marker	Primer combination	No. of loci	Amplicon size	Amplicon contribution	Marker ID
58	29	me-em2	a	750	B	me8-em2a750B
59			b	1000	B	me8-em2b1000B
60	30	me8-em5	a	250	B	me8-em5a250B
61			b	300	A	me8-em2b300A
62			c	400	A	me8-em2c400A
63	31	me8-em6	a	600	A	me8-em6a600A
64		me8-em7	a	600	B	me8-em7a600B
65			b	840	B	me8-em7b840B
66			c	950	A	me8-em7c950A
67	32	me8-em8	a	300	A	me8-em8a300A
68	33	me8-em9	a	320	A	me8-em9a320A
69	34	me8-em10	a	500	B	me8-em10a500B
70			b	800	A	me8-em10b800A
71			c	950	B	me8-em10c950B
72	35	me8-em12	a	550	A	me8-em12a550A
73			b	900	B	me8-em12b900B
74	36	me8-em13	a	450	A	me8-em13a450A
75		me8-em15	a	450	B	me8-em15a450B
76			b	600	B	me8-em15b600B
77			c	950	A	me8-em15c950A
78	37	me8-em16	a	250	B	me8-em16a250B
79	38	me9-em12	a	200	B	me9-em12a200B

Table 17: List of polymorphic Target Region Polymorphism (TRAP) markers identified between the RHAP 12 and RHAP 15 of *G. hirsutum*

Sl. No.	TRAP Marker	Primer combination	No. of loci	Amplicon size	Amplicon contribution	Marker ID
1	1	2F-me8	a	800	B	2F-me8a800B
2			b	300	A	2F-me8b300A
3			c	200	B	2F-me8c200B
4	2	3F-me3	a	450	B	3F-me3a450B
5			b	350	B	3F-me3b350B
6	3	4F-me7	a	950	A	4F-me7a950A
7			b	700	B	4F-me7b700B
8			c	600	A	4F-me7c600A
9			d	200	A	4F-me7d200A
10	4	5F-me9	a	900	A	5F-me9a900A
11			b	800	B	5F-me9b800B
12			c	700	A	5F-me9c700A
13	5	6F-me3	a	750	B	6F-me3a750B
14			b	500	A	6F-me3b500A
15			c	450	B	6F-me3c450B
16			d	200	A	6F-me3d200A
17	6	7F-me5	a	800	B	7F-me5a800B
18			b	600	B	7F-me5b600B
19			c	200	B	7F-me5c200B
20	7	8F-me7	a	550	B	8F-me7a550B
21			b	300	B	8F-me7b300B
22	8	9F-me3	a	900	B	9F-me3a900B
23			b	850	A	9F-me3b850A
24			c	600	A	9F-me3c600A
25	9	10F-me6	a	800	B	10F-me6a800B
26			b	600	A	10F-me6b600A
27			c	250	A	10F-me6c250A

Contd.....

SL No.	TRAP Marker	Primer combination	No. of loci	Amplicon size	Amplicon contribution	Marker ID
28	10	11F-me1	a	300	B	11F-me1a300B
29	11	12F-me3	a	600	A	12F-me3a600A
30			b	400	A	12F-me3b400A
31			c	250	A	12F-me3c250A
32	12	1R-me3	a	750	B	1R-me3a750B
33			b	600	B	1R-me3b600B
34			c	300	B	1R-me3c300B
35	13	2R-me6	a	800	B	2R-me6a800B
36			b	600	A	2R-me6b600A
37			c	200	A	2R-me6c200A
38	14	3R-me9	a	700	B	3R-me9a700B
39			b	600	B	3R-me9b600B
40			c	300	B	3R-me9c300B
41			d	250	A	3R-me9d250A
42	15	4R-me7	a	700	A	4R-me7a700A
43			b	650	B	4R-me7b650B
44			c	500	A	4R-me7c500A
45	16	5R-me1	a	950	A	5R-me1a950A
46			b	600	B	5R-me1b600B
47			c	500	B	5R-me1c500B
48	17	6R-me5	a	950	A	6R-me5a950A
49			b	700	B	6R-me5b700B
50			c	350	A	6R-me5c350A
51			d	200	B	6R-me5d200B
52	18	8R-me5	a	800	A	8R-me5a800A
53			b	700	A	8R-me5b700A
54			c	500	B	8R-me5c500B
55			d	350	B	8R-me5d350B
56	19	9R-me3	a	800	A	9R-me3a800A
57			b	500	B	9R-me3b500B

Contd.....

SL No.	TRAP Marker	Primer combination	No. of loci	Amplicon size	Amplicon contribution	Marker ID
58			c	600	A	9R-me3c600A
59	20	10R-me9	a	650	B	10R-me9a650B
60			b	200	A	10R-me9b200A
61	21	11R-me6	a	900	A	11R-me6a900A
62			b	750	B	11R-me6b750B
63			c	600	A	11R-me6c600A
64	22	12R-me2	a	850	B	12R-me2a850B
65			b	600	B	12R-me2b600B
66			c	350	B	12R-me2c350B
67			d	200	B	12R-me2d200B

Table 18: Summary of the SRAP and TRAP linkage map of the RHAP 12 × RHAP 15 derived RIL population of *G. hirsutum*

Sl. No.	Linkage Group (LG)	Number of Markers per LG	Number of Markers (%) per LG	Distortion Loci	Length per LG (cM)	Length (%) per LG	Avg. Distance	Max interval	Min. Interval
1	Linkage Group 1	26	17.81	1	461.74	15.86	17.76	60.2	6.39
2	Linkage Group 2	13	8.90	1	229.46	7.88	17.65	46.71	8.15
3	Linkage Group 3	11	7.53	1	128.7	4.42	11.70	43.09	3.58
4	Linkage Group 4	18	12.33	0	414	14.22	23.00	60.48	8.07
5	Linkage Group 5	8	5.48	0	250.81	8.62	31.35	59.94	20.82
6	Linkage Group 6	3	2.05	1	80.51	2.77	26.84	43.85	36.66
7	Linkage Group 7	7	4.79	1	97.22	3.34	13.89	51.84	6.67
8	Linkage Group 8	3	2.05	0	73.48	2.52	24.49	44.33	29.15
9	Linkage Group 9	3	2.05	0	63.66	2.19	21.22	34.66	29
10	Linkage Group 10	11	7.53	0	212.99	7.32	19.36	49.94	3.59
11	Linkage Group 11	4	2.74	0	94	3.23	23.50	48.2	11.65
12	Linkage Group 12	13	8.90	0	298.4	10.25	22.95	49.64	5.02
13	Linkage Group 13	6	4.11	0	97.25	3.34	16.21	29.71	6.12
14	Linkage Group 14	2	1.37	0	53.56	1.84	26.78	0	0
15	Linkage Group 15	9	6.16	0	172.36	5.92	19.15	29.71	6.12
16	Linkage Group 16	6	4.11	0	140.7	4.83	23.45	40.49	14.53
17	Linkage Group 17	2	1.37	0	41.97	1.44	20.99	0	0
18	Linkage Group 18	1	0.68	0	0	0.00	0.00	0	0
	Whole Genome	146			2910.81		19.94		

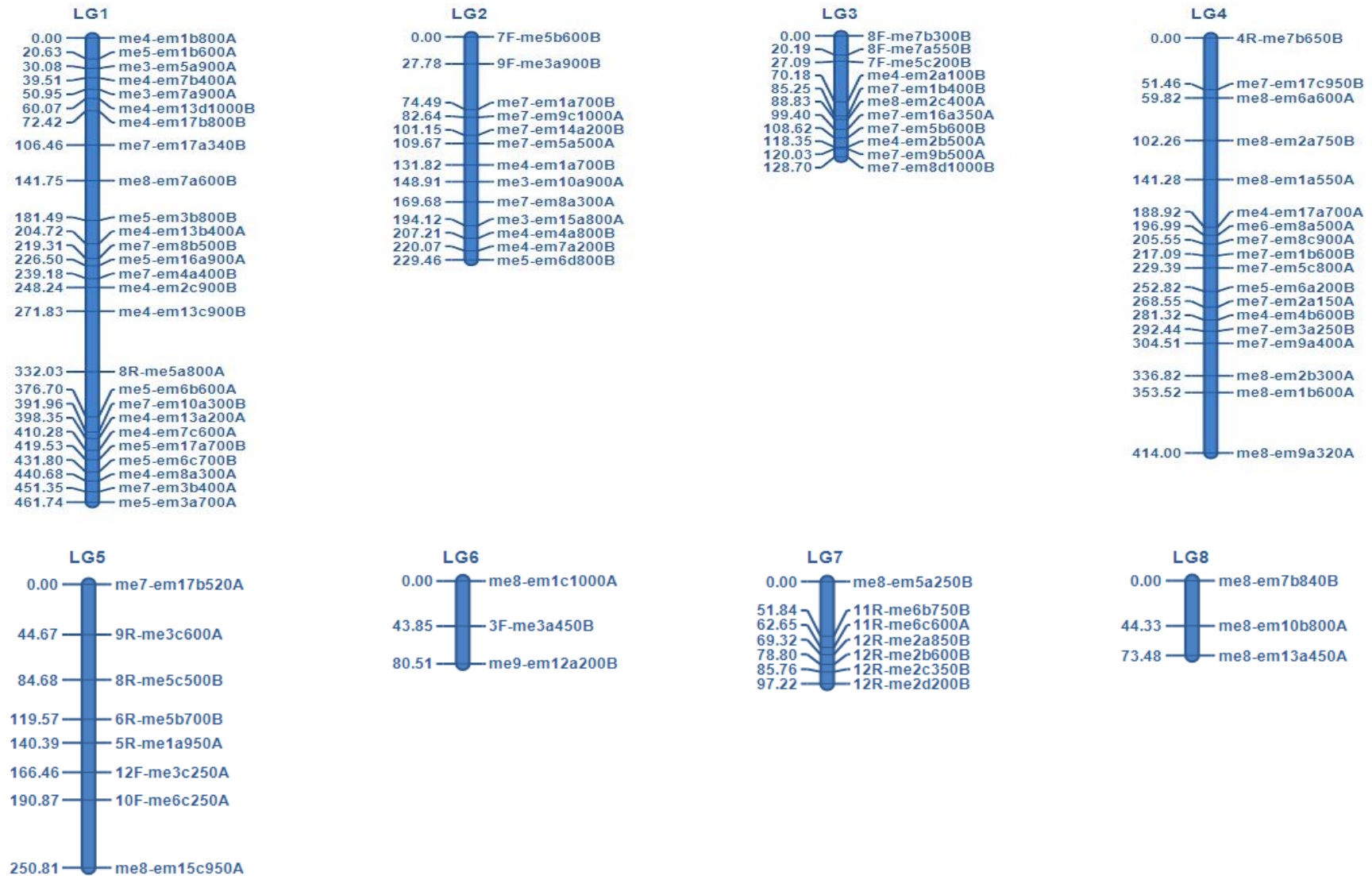
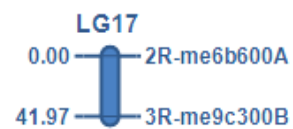
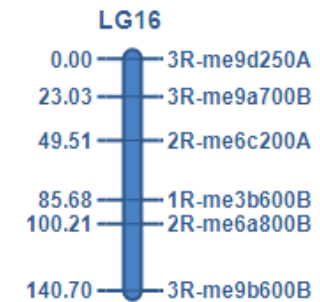
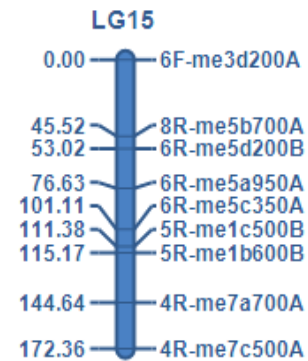
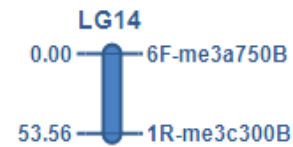
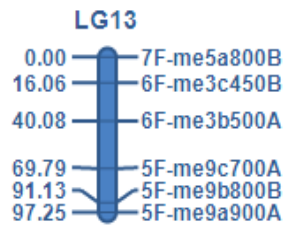
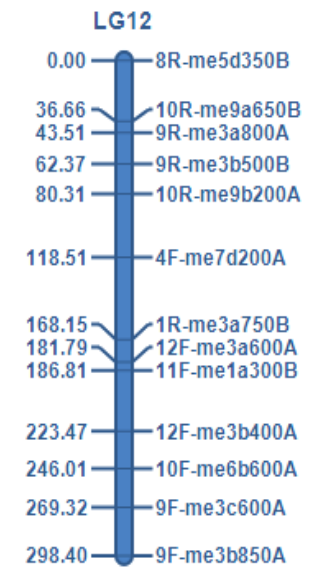
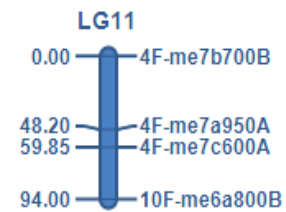
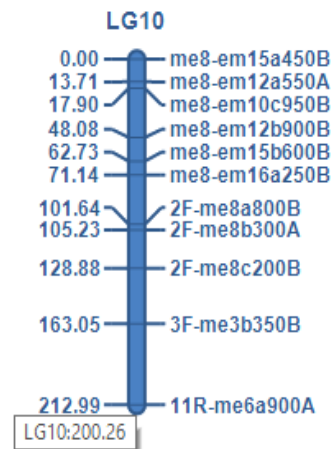
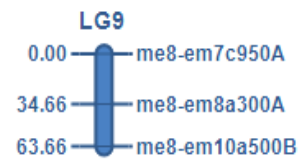


Fig. 6: Construction of linkage map by employing the SRAP and TRAP markers in cotton RIL population. The markers were shown on the right of the linkage group and distance among the marker within the linkage group was indicated in cM on the left.

Contd....



4.2.3.2 Genome coverage

The total genome coverage by 146 markers was 2910.81 cM in the present investigation (Table 18 and Fig. 8). The highest genome coverage was observed in LG 1 (461.74 cM) followed by LG 4 (414 cM), LG 12 (298.4 cM), LG 5 (250.81 cM), LG 2 (229.46 cM), LG 10 (212.99 cM), LG 15 (172.36 cM), LG 16 (140.7 cM), LG 3 (128.7 cM), LG 13 (97.25 cM), LG 7 (97.22 cM), LG 11 (94 cM), LG 6 (80.51 cM), LG 8 (73.48 cM), LG 9 (63.66 cM), LG 14 (53.56 cM), LG 17 (41.97 cM) and LG 18 (0 cM).

4.2.3.3 Marker density on linkage map

The average distance between the adjacent markers assists to know the marker density on linkage group. The linkage group 3 had the least (11.70 cM) distance between the neighboring markers Followed by LG 7 (13.89 cM), LG 13 (16.21 cM), LG 2 (17.65 cM), LG 1 (17.76 cM), LG 15 (19.15 cM), LG 10 (19.36 cM), LG 17 (20.99 cM), LG 9 (21.22 cM), LG 12 (22.95 cM), LG 4 (23 cM), LG 16 (23.45 cM), LG 11 (23.5 cM), LG 8 (24.49 cM), LG 14 (26.78 cM), LG 6 (26.84 cM) and LG 5 (31.35 cM).

4.2.4 Segregation distortion

The markers employed for genotyping in RIL population were tested for expected Mendelian 1:1 segregation ratio through chi square test ($p < 0.05$) (Appendix I). The five loci exhibited the segregation distortion in RIL population, which accounts for 3.42 % per cent (Table 19 and Fig. 9). In the linkage map the distortion loci are indicated by asterisk. The distorted markers belonged to SRAP markers. The distorted loci were distributed on LG1, LG2, LG3, LG 6 and LG 7. Among the distorted loci, two markers me7-em4a400B and me9-em12a200B were contributed from the female parent (RHAP 12) and three loci me7-em1a700B, me7-em16a350A and me8-em5a250B were contributed from the male parent (RHAP 15). Single marker analysis employed for above marker revealed that out of five distorted markers three markers such as me7-em1a700B, me7-em16a350A and me8-em5a250B were significantly distorted (Table 20).

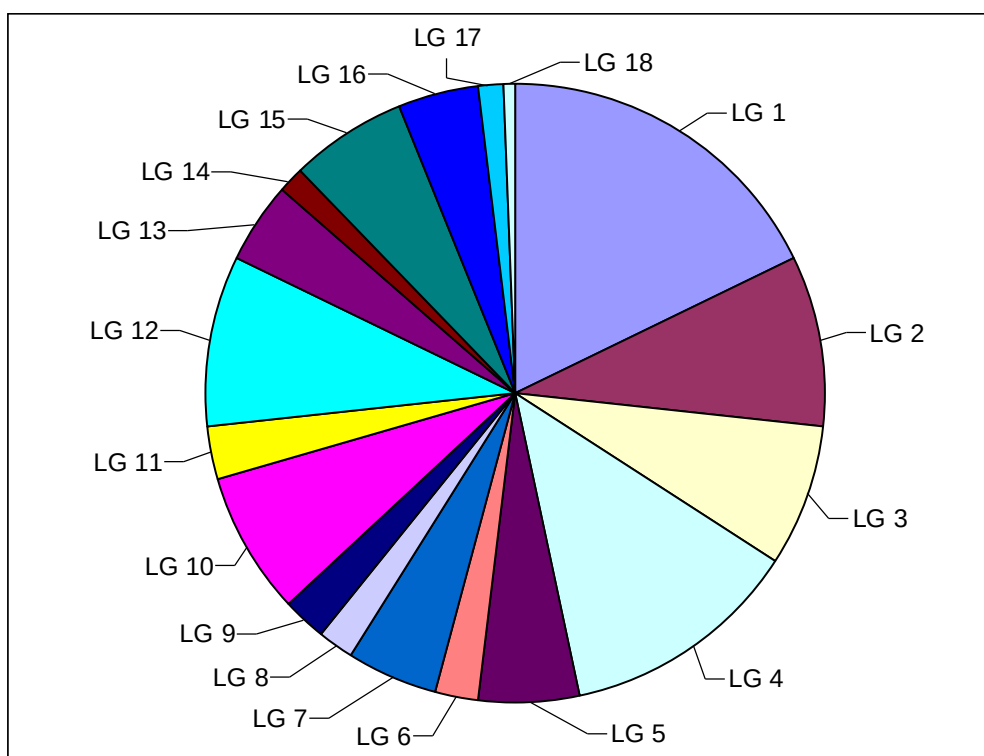


Fig. 7: Number of Markers (%) per linkage group

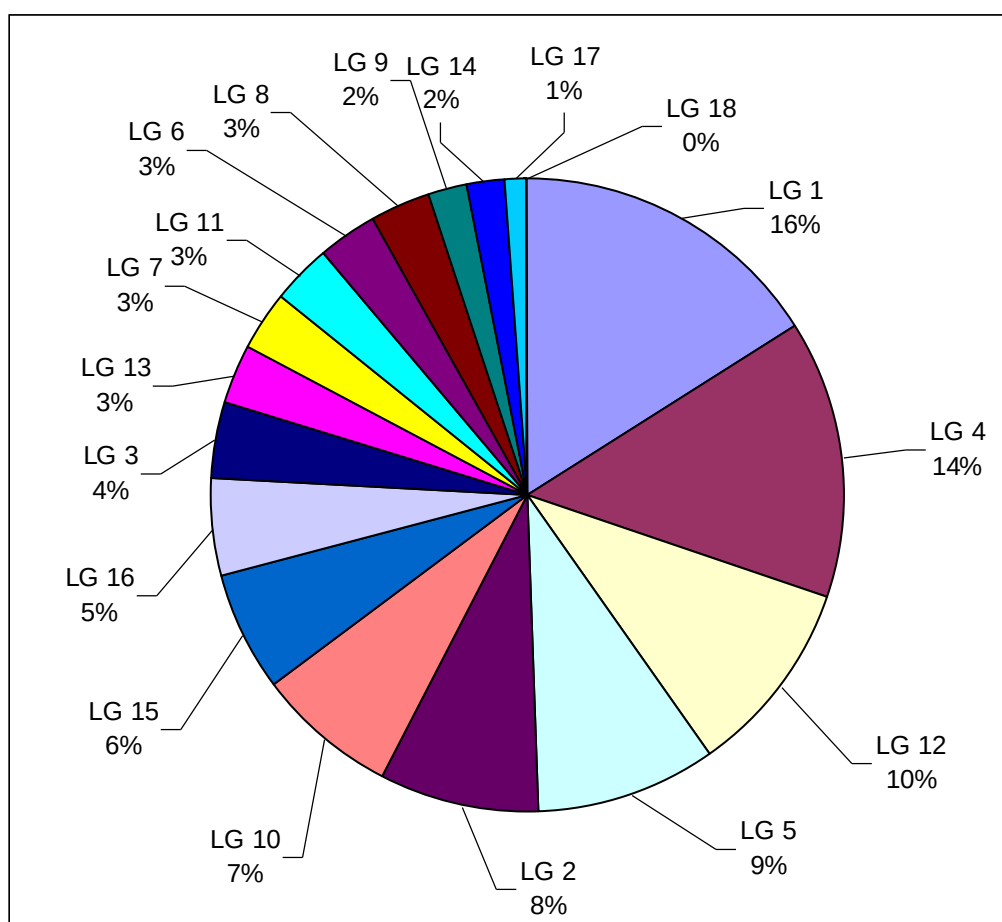


Fig. 8: Genome Cover (%) by each linkage group

Table 19: List of Segregation Distortion loci in the SRAP and TRAP linkage map of the RHAP 12 × RHAP 15 derived RIL population of *G. hirsutum*

Marker Name	Linkage group	Position (cM)	P1	P2	Missing loci	Chi-Square	P value
me7-em4a400B	1	239.18	116	88	18	3.8431	0.05
me7-em1a700B	2	74.49	84	113	25	4.269	0.0388
me7-em16a350A	3	99.4	81	137	4	14.3853	0.0002
me9-em12a200B	6	80.51	135	80	7	14.0698	0.0002
me8-em5a250B	7	0	72	124	26	13.7959	0.0002

Table 20: list of significantly segregation distortion loci in the genetic map of the RHAP 12 × RHAP 15 derived RIL population of *G. hirsutum*

Sl. No.	Marker Name	Linkage group	Position (cM)	LOD
1	me7-em16a350A	3	99.4	2.88
2	me9-em12a200B	6	80.51	3.32
3	me8-em5a250B	7	0	3.10

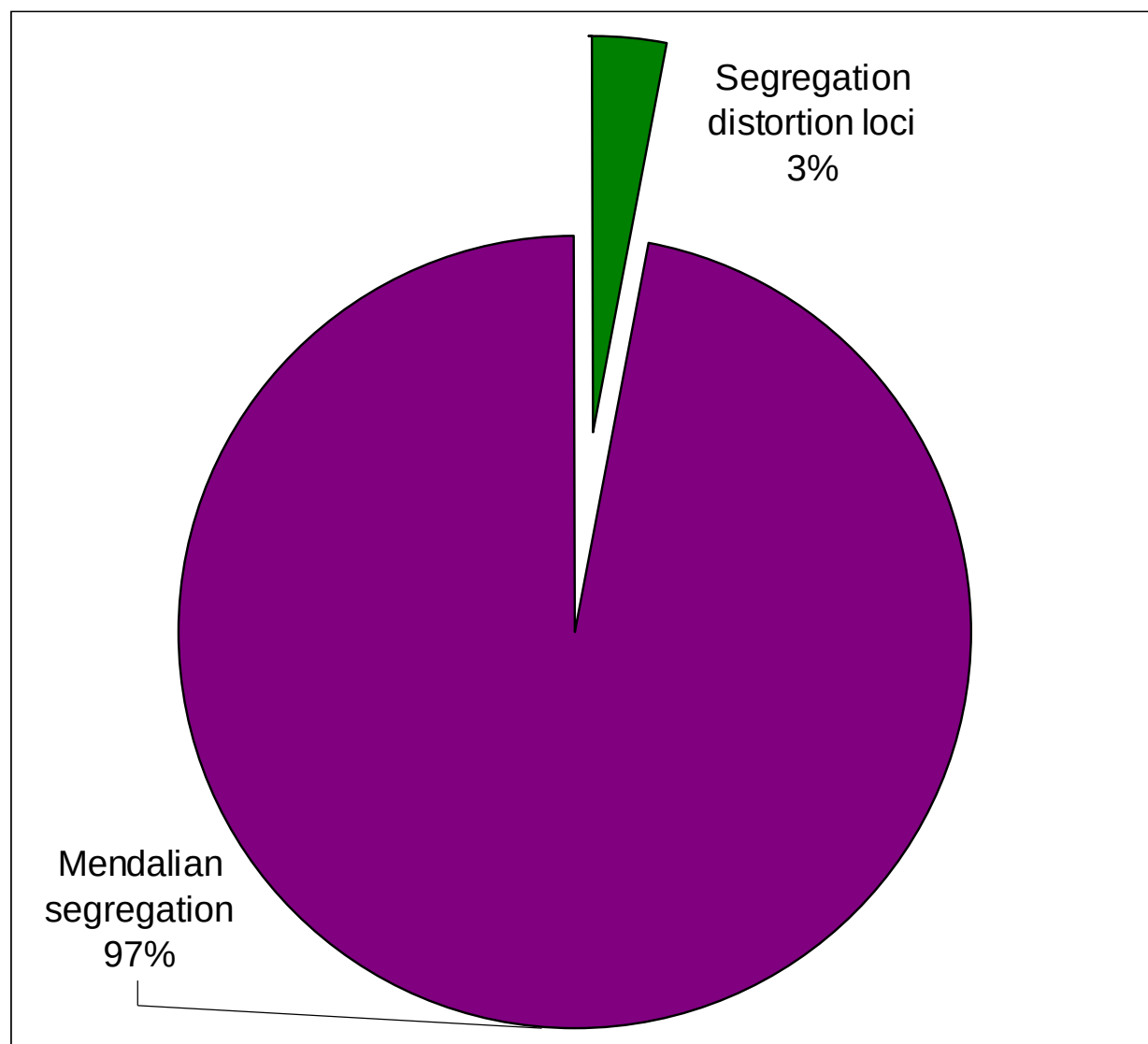


Fig. 9: Percentage of segregation distortion loci in linkage map

4.2.5 QTL mapping for yield and fibre quality traits

By utilizing the genotyping and phenotyping information derived from RIL population. QTLs were identified for various traits (Table 21 and Fig. 10). The QTLs for various characters were identified using the *QTL Ici mapping* software. In the present investigation for QTL analysis, inclusive composite interval mapping method was utilized at a walking speed of 1cM and with a threshold LOD value of 2.5. The results of identified QTLs for yield and quality traits are presented in Table 21 (Fig. 10).

Plant height

A QTL for plant height was identified on linkage group 3 and designated as *qPH-3-1*. The QTL was situated in between the interval of me7-em1b400B and me8-em2c400A markers at 86 cM. The QTL was identified at LOD value of 4.93. The phenotypic variation explained by the QTL was 9.70 per cent to the trait. The QTL derived from male parent *i.e.* RHAP 15 and it had an additive effect of 3.83 cm. The confidence interval for the QTL was 82.5cM to 88.5 cM.

Number of bolls per plant

Two QTLs (Quantitative Trait Locus), referred as *qNBP-1-1* and *qNBP-3-1* were detected and explained a phenotypic variation of 8.94 and 6.53 per cent respectively. The *qNBP-1-1* was in the vicinity of me3-em7a900A and me4-em13d1000B, located on LG 1. The *qNBP-3-1* was in the vicinity of me4-em2b500A and me7-em9b500A, located on LG 3. The *qNBP-1-1* and *qNBP-3-1* were identified at 51 cM and 120 cM on LG 1 and LG 3 respectively. The *qNBP-1-1* was derived from RHAP 15 with an additive effect of 1.44. In contrast, *qNBP-3-1* was derived from RHAP 12 with an additive effect of 1.24.

Seed cotton yield per plant

Two QTLs were identified for seed cotton yield per plant. The QTL was designated as *qSCYP-1-1* and *qSCYP-16-1* which were located on LG 1 (51cM) and LG16 (27 cM) respectively. The *qSCYP-1-1* was identified at LOD value of 7.36; phenotypic variation explained was 9.99 per cent along with contributed by the parent RHAP 15 with an additive effect of 6.64 g. The flanking markers were me3-em7a900A

Table 21: Biometrical parameters of individual QTL affecting the cotton yield and its attributing and fibre quality traits in RIL population derived from intraspecific hybridization between RHAP 12 and RHAP 15 of *G. hirsutum*

SL No	Trait Name ¹	QTL ²	Linkage Group	Position (cM)	Left Marker	Right Marker	LOD	PVE (%)	Add ³	Left CI ⁴	Right CI ⁴
1	PH	<i>qPH-3-1</i>	3	86	me7-em1b400B*	me8-em2c400A*	4.93	9.70	-3.83	82.5	88.5
2	NBP	<i>qNBP-1-1</i>	1	51	me3-em7a900A*	me4-em13d1000B*	3.89	8.94	-1.44	47.5	54.5
3		<i>qNBP-3-1</i>	3	120	me4-em2b500A*	me7-em9b500A*	2.87	6.53	1.24	118.5	123.5
4	SCYP	<i>qSCYP-1-1</i>	1	51	me3-em7a900A*	me4-em13d1000B*	7.36	9.99	-6.64	49.5	52.5
5		<i>qSCYP-16-1</i>	16	27	3R-me9a700B ^Δ	2R-me6c200A ^Δ	7.59	16.79	-8.6	23.5	31.5
6	BW	<i>qBWP-1-1</i>	1	51	me3-em7a900A*	me4-em13d1000B*	3.88	5.39	-0.17	48.5	53.5
7		<i>qBWP-3-1</i>	3	85	me4-em2a100B*	me7-em1b400B*	8.21	12.44	-0.26	81.5	86.5
8		<i>qBWP-16-1</i>	16	29	3R-me9a700B ^Δ	2R-me6c200A ^Δ	4.00	8.82	-0.22	18.5	37.5
9	UHML	<i>qUHML-11-1</i>	11	63	4F-me7c600A ^Δ	10F-me6a800B ^Δ	4.57	8.99	0.50	57.5	73.5
10	FS	<i>qFS-3-1</i>	3	120	me4-em2b500A*	me7-em9b500A*	5.49	8.12	0.58	119.5	122.5
11		<i>qFS-13-1</i>	13	70	5F-me9c700A ^Δ	5F-me9b800B ^Δ	3.13	4.56	0.43	62.5	74.5
12		<i>qFS-16-1</i>	16	43	3R-me9a700B ^Δ	2R-me6c200A ^Δ	7.25	18.44	0.87	36.5	48.5
13	Mic	<i>qMic-13-1</i>	13	58	6F-me3b500A ^Δ	5F-me9c700A ^Δ	3.71	7.57	-0.17	47.5	68.5
14	FUI	<i>qFUI-3-1</i>	3	95	me8-em2c400A*	me7-em16a350A*	2.55	8.28	1.3	91.5	98.5
15		<i>qFUI-3-2</i>	3	121	me7-em9b500A*	me7-em8d1000B*	2.56	5.12	1.03	119.5	124.5
16	MR	<i>qMR-13-1</i>	13	58	6F-me3b500A ^Δ	5F-me9c700A ^Δ	3.69	7.49	-0.03	47.5	68.5

Where,

* = SRAP marker

Δ = TRAP marker

1 = Character name (PH= plant height (cm), NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value (μg/inch), FUI = Fibre uniformity index and MR= Maturity ratio).

2 = QTL of the particular trait (q followed by trait abbreviation then linkage group finally number of particular trait QTL on same linkage group

3 = additive effect or trait value, unit is same as character measurement and + and – indicates the allele derived from RHAP 12 and RHAP 15 respectively.

4= confidence interval

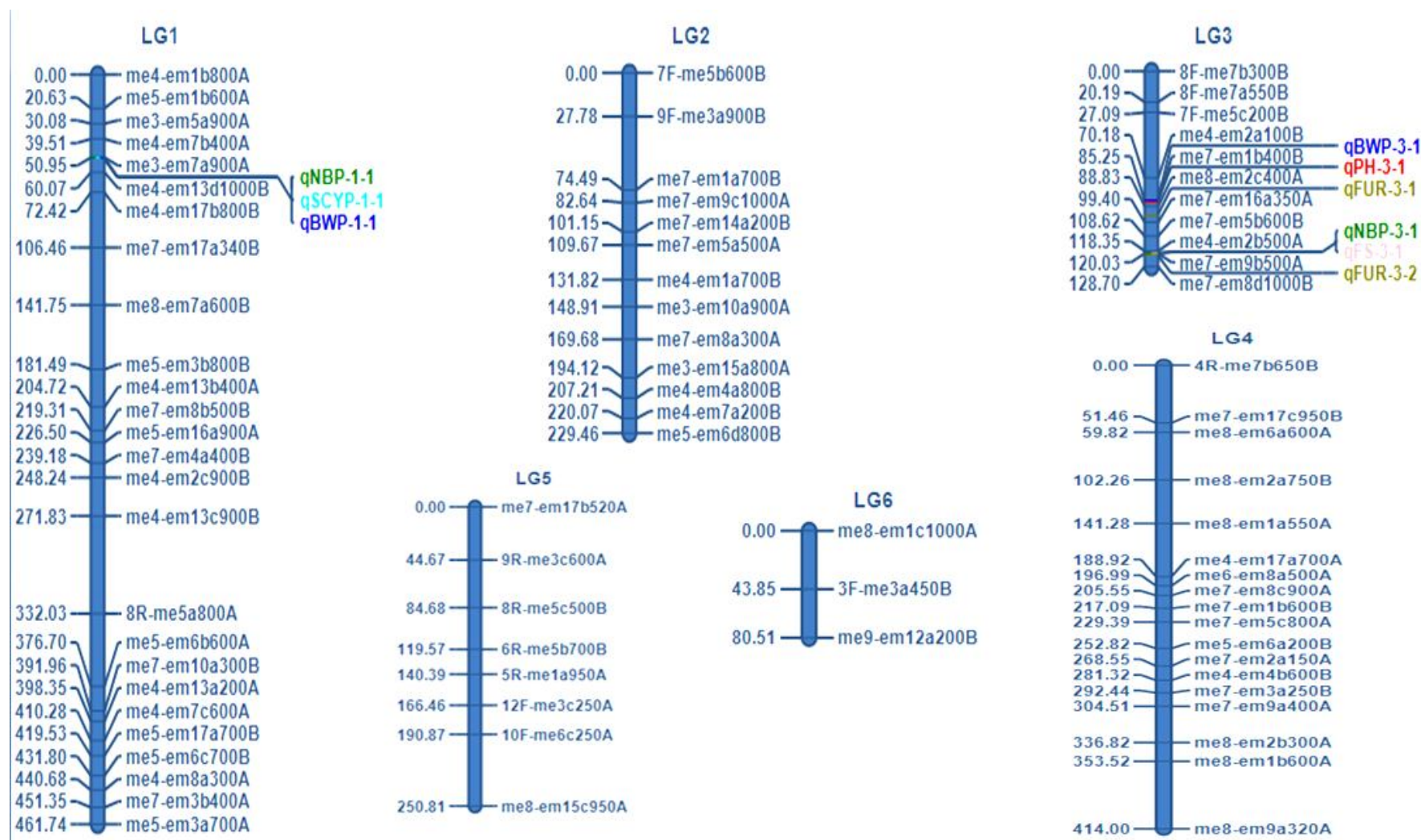
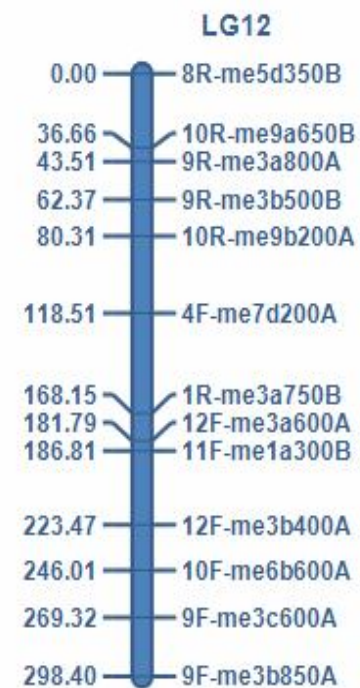
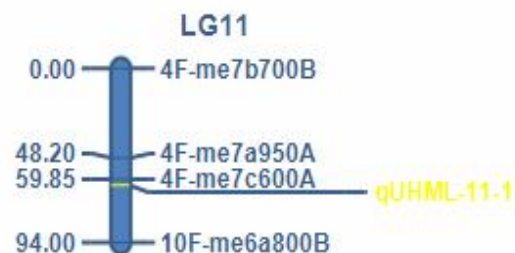
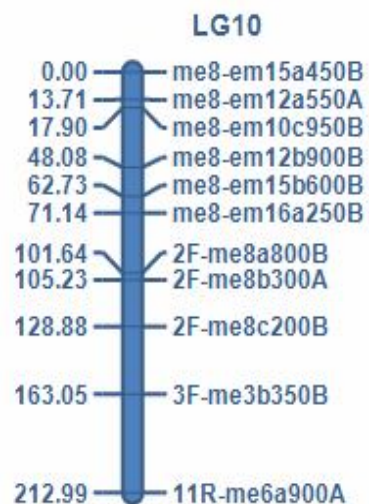
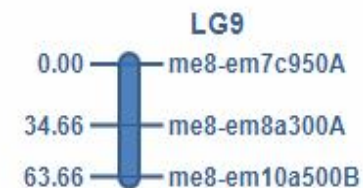
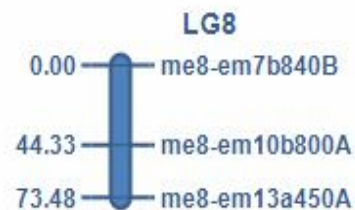
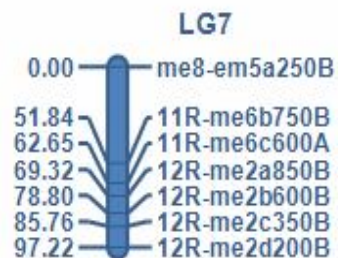
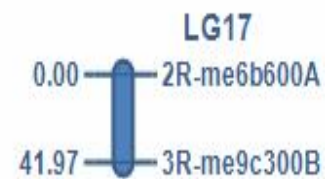
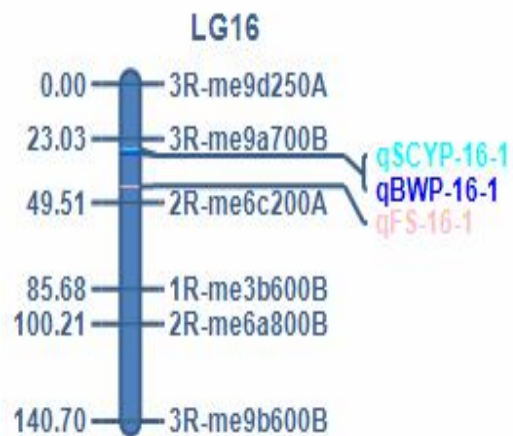
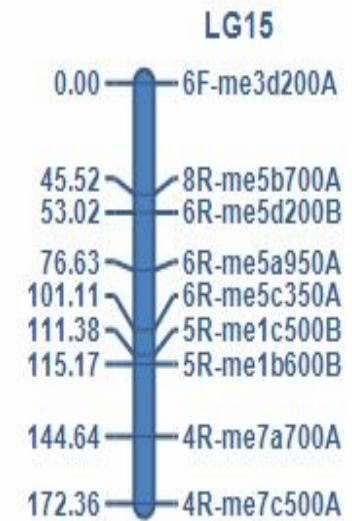
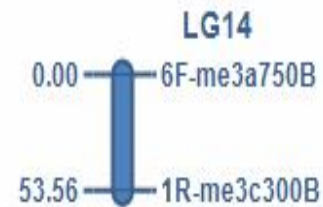
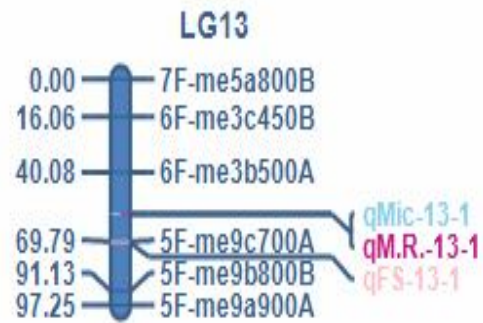


Fig. 10: Genetic linkage map and the location of QTLs for yield and its attributing and fibre quality traits in the intraspecific RIL linkage map. The markers were shown on the right of the linkage group and distance among the marker within the linkage group was indicated in cM on the left. The different trait QTLs were indicated with different colors.

Contd.....



Contd.....



and me4-em13d1000B. In addition, a QTL *qSCYP-16-1* flanked by the markers viz., 3R-me9a700B and 2R-me6c200A explained a phenotypic variation of 16.79 per cent with an additive effect of 8.60 g for the trait.

Boll weight

A total of three QTLs were identified for boll weight and were referred as *qBWP-1-1*, *qBWP-3-1* and *qBWP-16-1*. The QTL, *qBWP-1-1* was located on linkage group 1 at 51 cM, which had the flanking markers viz., me3-em7a900A and me4-em13d1000B. Another QTL, *qBWP-3-1* was located at 85 cM on linkage group 3, flanked by the markers me4-em2a100B and me7-em1b400B. The QTL *qBWP-16-1* was located at 29 cM on linkage group 16 which had the flanking markers 3R-me9a700B and 2R-me6c200A.

The QTL *qBWP-1-1* derived from the parent RHAP 15 was identified at a LOD value of 3.88 and explained a phenotypic variation of 5.39 per cent with an additive effect of 0.17 g for the trait. Another QTL derived from RHAP 15, *qBWP-3-1* was identified at LOD value of 8.21 which explained a phenotypic variation of 12.44 per cent with an additive effect of 0.26 g. The QTL, *qBWP-16-1* was identified at a LOD value of 4.0 which registered a phenotypic variation of 8.82 per cent with an additive effect of 0.22 g.

Upper half mean length

The QTL for UHML identified on linkage group 11 and designated as *qUHML-11-1* and it was situated at 63 cM in the interval of markers, 4F-me7c600A and 10F-me6a800B. The QTL was identified at LOD value of 4.57. The phenotypic variation explained by the locus was 8.99 per cent. The allele was derived from female parent i.e. RHAP 12 which had an additive effect of 0.5 mm. The confidence interval for the QTL was 57.5 to 73.5 cM. for the trait.

Fibre strength

The three QTLs identified for the fibre strength viz., *qFS-3-1*, *qFS-13-1* and *qFS-16-1* and had a explained phenotypic variation of 8.12, 4.56 and 18.44 per cent respectively. The QTL *qFS-3-1*, had a LOD peak value of 5.49 and the neighboring

markers were me4-em2b500A and me7-em9b500A. This QTL was derived from RHAP 12 which had an additive effect of 0.58g/tex. Another QTL viz., *qFS-13-1* was located on linkage group 13 at 70cM and had the flanking markers namely 5F-me9c700A and 5F-me9b800B. In addition, the allele had an additive effect of 0.43g/tex which was derived from RHAP 12 parent. The QTL *qFS-16-1* was considered as major QTL for the trait which had an additive effect of 0.87g/tex. This QTL seemed to arise from parent, RHAP 12 which was located in the interval between the markers 3R-me9a700B and 2R-me6c200A.

Micronaire value

A QTL (quantitative trait locus) was identified for micronaire value, nominated as *qMic-13-1* and explained the phenotypic variation of 7.57 per cent. It was in the vicinity of 6F-me3b500A and 5F-me9c700A markers located on LG 13. The *qMic-13-1* was identified at 3.71 LOD value. The *qMic-13-1* was derived from RHAP 15 with an additive effect of 0.17.

Uniformity index

Two QTLs were identified for uniformity index. The QTLs were designated as *qFUI-3-1* and *qFUI-3-2* which were located on LG 3 at 95 cM and 121 cM respectively. The *qFUI-3-1* was identified at LOD value of 2.55, which was contributed by RHAP 12 parent with an additive effect of 1.30 per cent. It had the flanking markers viz., me8-em2c400A and me7-em16a350A. Another QTL *qFUI-3-2* had the phenotypic variation of 5.12 per cent with an additive effect of 1.03 per cent. The me7-em9b500A and me7-em8d1000B markers flanked the QTL *qFUI-3-2*.

Maturity ratio

A QTL for maturity ratio was identified on linkage group 13 and designated as *qMR13-1*. The QTL situated in the interval of 6F-me3b500A and 5F-me9c700A markers at 58 cM. It was identified at LOD value of 3.69. The phenotypic variation explained by the QTL was 7.49 per cent. The QTL derived from male parent i.e. RHAP 15 had an additive effect of 0.03. The confidence interval for the QTL was 47.5 cM to 68.5 cM.

4.3 Genetic variability parameters for yield and yield attributes and fibre quality traits

The results pertaining to genetic variability parameters viz., range, mean, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability (h^2) and genetic advance over mean (GAM) were estimated to know the extent of genetic variability for characters in RIL population and the values were presented in the Table 22 (Fig. 11). The mean performance of 222 Recombinant Inbred Lines (RILs) for all the characters are presented in Appendix II.

Plant height

The average plant height was 116.59 cm with a range of 69.88 (RIL 25) to 148.40 cm (RIL 53). The genotypic and phenotypic coefficients of variability were low (6.85 %) and moderate (12.76 %) respectively. The heritability in broad sense observed was low (28 %) with a low GAM (7.57 %).

Number of monopodia per plant

The average number of monopodia branches per plant was recorded 2.40 whereas, maximum and minimum monopodials were found in the RIL 40 (3.80) and RIL 211 (1.30) respectively. The population exhibited high PCV (21.65 %), moderate GCV (14.27 %), moderate heritability (43.50 %) and GAM (19.38 %).

Number of sympodia per plant

The average number of sympodia per plant was 9.76 whereas, the observed range of number of sympodia per plant in the population was 5.90 (RIL 22) to 14.50 (RIL 90). The character exhibited the moderate PCV (17.97 %), low GCV (7.48 %), low GAM (6.41) and low heritability (17.30 %).

Number of bolls per plant

The average number of bolls per plant in the population recorded was 21.46 along with line RIL 195 had minimum of 10.90 and the maximum of 41.50 in RIL 54 bolls per plant. The presence of high GCV (21.34 %) and PCV (28.26 %) along with moderate heritability (57.00 %) and high GAM (33.18 %) were observed in the population.

Table 22: Mean, range and components of variance of yield and its component traits and fibre quality traits in recombinant inbred lines of *G. hirsutum*

Sl. No.	Characters	Mean $\pm$ SE	Range Lowest	Range Highest	PCV	GCV	h ² (Broad Sense) (%)	Gen. Adv as % of Mean (5%)
1	PH	116.59 $\pm$ 8.87	69.88	148.40	12.76	6.85	28.00	7.57
2	NMP	2.40 $\pm$ 0.27	1.30	3.80	21.65	14.27	43.50	19.38
3	NSP	9.76 $\pm$ 1.12	5.90	14.50	17.97	7.48	17.30	6.41
4	NBP	21.46 $\pm$ 2.81	10.90	41.50	28.26	21.34	57.00	33.18
5	SCYP	60.37 $\pm$ 8.53	15.70	135.00	34.44	28.05	66.30	47.04
6	SI	6.54 $\pm$ 0.55	4.88	8.90	13.80	6.82	24.40	6.95
7	BW	2.85 $\pm$ 0.39	1.26	4.92	27.89	19.97	51.30	29.47
8	GOT	39.26 $\pm$ 1.06	35.39	42.68	4.96	3.13	40.00	4.08
9	LI	4.24 $\pm$ 0.39	2.88	6.51	16.06	8.99	31.40	10.38
10	FS	25.27 $\pm$ 0.06	22.33	30.63	8.04	8.03	99.80	16.53
11	UHML	24.94 $\pm$ 0.11	20.40	30.90	6.03	6.00	98.90	12.29
12	Mic	3.53 $\pm$ 0.05	2.16	4.68	12.28	12.07	96.70	24.45
13	UI	75.67 $\pm$ 0.66	58.20	94.40	5.57	5.43	95.00	10.90
14	MR	0.57 $\pm$ 0.04	0.29	0.78	16.08	11.68	53.70	17.46
15	FEL	5.03 $\pm$ 0.03	4.00	6.60	8.66	8.60	98.60	17.60

Where, PH= plant height (cm), NMP= number of monopodia per plant, NSP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value (μ g/inch), UI = Uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%). PCV phenotypic coefficient of variation, GCV = genotypic coefficient of variation.

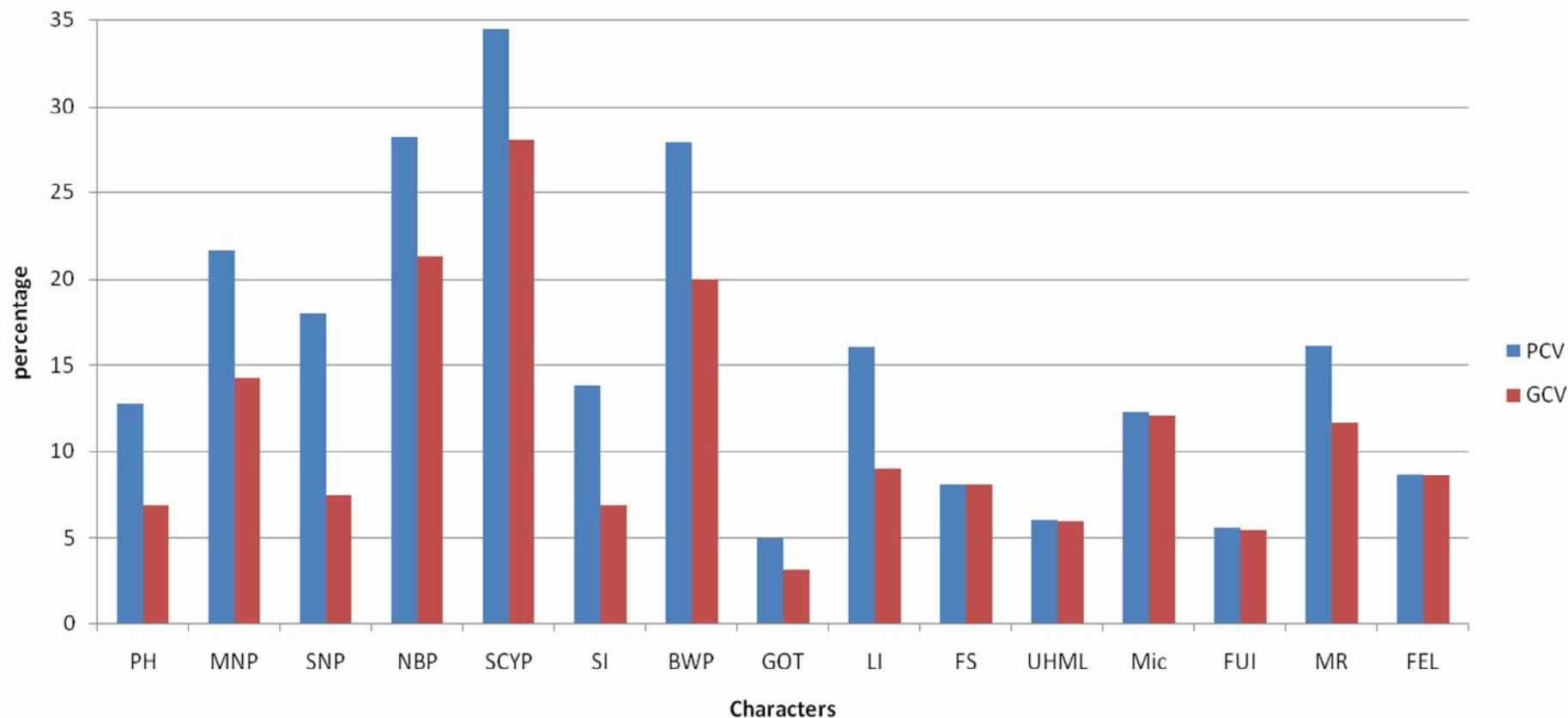


Fig. 11: Graphical representation of phenotypic and genotypic coefficient of variance of yield and fibre quality traits in RIL population of upland cotton

Where,

X axis = characters under investigation

Y axis = percentage

PH= plant height (cm), MNP= number of monopodia per plant, SNP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value ($\mu\text{g}/\text{inch}$), FUI = Fibre uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).

Seed cotton yield per plant

The average seed cotton yield in RIL population was 60.37g with a range of 15.70 g (RIL 144) to 135.00 g (RIL 54). The population revealed high GCV (28.05 %) and PCV (34.44 %) along with observed high heritability of 66.30 per cent and GAM of 47.04 per cent.

Seed index

The average seed index of the population was 6.54 g with a minimum value of 4.88 g (RIL 271) and maximum of 8.90 g (RIL 208). The genotypic and phenotypic variability in the population was low (6.82 %) and moderate (13.80 %) respectively. The trait exhibited a low heritability of 24.4 per cent and GAM of 6.95 per cent.

Boll weight

The average boll weight per plant was 2.85g with a range of 1.26 g (RIL 18) to 4.92 g (RIL 199). The genotypic and phenotypic coefficients of variability were moderate (19.97 %) and high (27.89 %) respectively. The heritability in broad sense was moderate (51.30 %) and GAM was high GAM (29.47 %) for the trait.

Ginning outturn

The RIL 31 showed the maximum (42.68 %) ginning outturn while, the RIL 102 registered a low ginning outturn of 35.39 per cent. The average ginning outturn of the population was 39.26 per cent. A low GCV (3.13 %) and PCV (4.96 %) was observed in the RILs for ginning outturn. In addition, a moderate heritability of 40 *per cent* and a low GAM of 4.08 per cent was observed for the trait.

Lint Index

The mean lint index of the population was 4.24g with the line RIL 101 which registered a minimum of 2.88 g and a maximum of 6.51 g by the RIL 54. While, a low GCV (8.99 %) and moderate PCV (16.06 %) along with a moderate heritability of 31.40 per cent and GAM of 10.38 per cent was observed for the trait.

Fibre strength

The fibre strength in the RIL population varied between 22.33 g/tex (RIL 1) to 30.63 g/tex (RIL 40) with an average of 25.27 g/tex. The trait recorded low GCV (8.03 %) and PCV (8.04 %) with a high heritability (99.80 %) and moderate GAM (16.53 %).

Upper half mean length

The mean UHML of the population was 24.94 mm with a minimum of 20.40 mm (RIL 24) and maximum of 30.90 mm (RIL 3). The UHML recorded a low PCV of 6.03 per cent and GCV of 6.00 per cent in the population along with a high heritability of 98.90 per cent and a moderate GAM of 12.29 per cent.

Micronaire value

The average micronaire value in the population was 3.53 µg/inch with the RILs having minimum of 2.16 µg/inch (RIL 144) and maximum of 4.68 µg/inch (RIL 107). A moderate PCV of 12.28 per cent and GCV of 12.07 per cent were registered for the trait along with a high heritability of 96.70 per cent and a GAM of 24.45 per cent.

Uniformity index

The mean uniformity index of the population was 75.67 per cent with a minimum value of 58.20 per cent (RIL 203) and a maximum of 94.40 per cent (RIL 3). The trait registered a low PCV of 5.57 per cent and a GCV of 5.43 per cent in the population along with a heritability and GAM of 95.00 per cent and 10.90 per cent respectively for the trait.

Maturity ratio

The RIL 107 registered the maximum (0.78) whereas RIL 195 (0.29) was registered lowest maturity ratio with an average of 0.57 in the population. The maturity ratio exhibited a moderate PCV (16.08 %) and GCV (11.68 %) in the RILs the moderate heritability (53.70 %) and GAM (17.46 %) were observed for the trait.

Fibre elongation length

The mean value of fibre elongation length in RIL population was 5.03 per cent with a range of 4.00 per cent (RIL 4) to 6.60 per cent (RIL 26). The PCV and GCV of fibre elongation length were low *i.e.* 8.66 per cent and 8.60 per cent respectively. In addition, heritability (98.60 %) and GAM (17.60 %) were found high and moderate respectively for the trait.

4.4 Character association and path analysis in the RIL population.

4.4.1 Association of seed cotton yield with agronomic and fibre quality traits

In cotton, the associations between various quantitative traits at phenotypic and genotypic level are presented in Table 23 and 24.

Plant height

In the evaluated RIL population, plant height had positive significant association with seed cotton yield per plant at both phenotypic (0.216) and genotypic (0.249) levels. The trait had significant positive correlation with boll weight at phenotypic (0.295) and genotypic level (0.554) respectively.

Number of monopodia per plant

A positive significant positive correlation was evident between the seed cotton yield and number of monopodia per plant in F₆ generation at phenotypic (0.174) and genotypic level (0.198). The trait also exhibited positive significant association with number of bolls per plant at both phenotypic (0.209) and genotypic level (0.211).

Number of sympodia per plant

In the RIL population, the number of sympodia per plant had a positive significant association with seed cotton yield per plant at both phenotypic and genotypic levels of 0.294 and 0.648 respectively. At genotypic level, the trait had significant association with plant height (0.244) and number of bolls per plant (0.987).

Table 23: Phenotypic correlation coefficient between seed cotton yield and its component traits and fibre quality traits in 222 recombinant inbred lines of *G. hirsutum*

Characters	PH	NMP	NSP	NBP	SI	BW	GOT	LI	UHML	FS	Mic	UI	MR	EL	SCYP
PH	1.000	0.042	0.090	-0.011	0.069	0.295**	-0.048	0.041	-0.014	-0.028	0.167**	-0.080	0.076	-0.173**	0.216**
NMP		1.000	0.069	0.209**	0.073	-0.009	0.033	0.082	-0.009	-0.022	0.127**	0.096*	0.098*	-0.046	0.174**
NSP			1.000	0.373**	0.077	-0.029	0.000	0.074	-0.0003	0.026	0.062	0.109	0.052	0.250**	0.294**
NBP				1.000	-0.051	-0.168**	0.102*	0.015	-0.045	-0.028	0.064	0.202**	0.041	0.243**	0.672**
SI					1.000	0.156**	-0.004	0.860**	0.081	0.108*	0.126**	-0.048	0.082	0.032	0.085
BW						1.000	0.108*	0.186**	-0.009	-0.059	0.256**	-0.112*	0.164**	-0.225**	0.593**
GOT							1.000	0.501**	-0.029	0.019	0.173**	0.0008	0.123**	0.018	0.206**
LI								1.000	0.052	0.100*	0.196**	-0.041	0.131**	0.032	0.182**
UHML									1.000	0.640**	-0.176**	0.115*	-0.098*	0.159**	-0.065
FS										1.000	-0.164**	0.182**	-0.131**	0.258**	-0.027
Mic											1.000	-0.079	0.859**	-0.196**	-0.066
UI												1.000	0.036	0.435**	0.060
MR													1.000	-0.125**	0.154**
EL														1.000	0.007
SCYP															1.000

Where,

* = significance at 5% level

** = significance at 1% level

PH= plant height (cm), NMP= number of monopodia per plant, NSP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value (µg/inch), FUI = Fibre uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).

Table 24: Genotypic correlation coefficient between seed cotton yield and its component traits and fibre quality traits in 222 recombinant inbred lines (RILs) of *G. hirsutum*

Characters	PH	NMP	SNP	NBP	SI	BW	GOT	LI	UHML	FS	Mic	UI	MR	EL	SCYP
PH	1.000	0.129**	0.224**	-0.205**	0.315**	0.554**	0.146**	0.338**	-0.003	-0.043	0.358**	-0.103*	0.410**	-0.300**	0.249**
NMP		1.000	0.010	0.211**	0.141**	0.083	0.091	0.172**	-0.012	-0.042	0.198**	0.153**	0.219**	-0.067	0.198**
SNP			1.000	0.987**	0.034	-0.224**	-0.151**	-0.044	-0.009	0.060	0.137**	0.249**	0.098*	0.593**	0.648**
NBP				1.000	-0.064	0.027	0.232**	0.081	-0.056	-0.036	0.092*	0.281**	0.100*	0.325**	0.759**
SI					1.000	0.250**	0.081	0.825**	0.160**	0.216**	0.248**	-0.113*	0.173**	0.049	0.119**
BW						1.000	0.167**	0.285**	-0.015	-0.083	0.359**	-0.167**	0.290**	-0.321**	0.662**
GOT							1.000	0.628**	-0.040	0.032	0.287**	0.013	0.317**	0.027	0.329**
LI								1.000	0.092	0.179**	0.355**	-0.076	0.135**	0.046	0.278**
UHML									1.000	0.639**	-0.200**	0.094*	-0.236**	0.151**	-0.031
FS										1.000	-0.176**	0.176**	-0.225**	0.256**	-0.080
Mic											1.000	-0.125**	0.988**	-0.219**	0.308**
UI												1.000	-0.167*	0.427**	0.080
MR													1.000	-0.264**	0.278**
EL														1.000	0.009
SCYP															1.000

Where,

* = significance at 5% level

** = significance at 1% level

PH= plant height (cm), NMP= number of monopodia per plant, SNP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value (µg/inch), FUI = Fibre uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).

Number of bolls per plant

The number of bolls per plant and seed cotton yield per plant had significant positive association at both phenotypic (0.672) and genotypic (0.759) level. Number of bolls per plant trait had negative significant association with boll weight (-0.168) at phenotypic level.

Seed index

The seed index showed non significant positive association with seed cotton yield per plant at phenotypic level (0.085) but at the genotypic level it registered positive significant association (0.119).

Boll weight

The boll weight had significant positive correlation with seed cotton yield per plant at phenotypic and genotypic level in RIL population (0.593, 0.662 respectively). The boll weight registered positive significant association at both phenotypic and genotypic level with seed index (0.156, 0.250 respectively) and lint index (0.186, 0.285 respectively) in the RIL population.

Ginning outturn

At phenotypic and genotypic levels, ginning outturn and seed cotton yield per plant had significant positive correlation (0.206, 0.329 respectively) in the RIL population. The GOT also registered significant positive association with lint index (0.501, 0.628 respectively) and boll weight (0.108, 0.167 respectively) at the phenotypic and genotypic level.

Lint index

The RIL populations lint index had significant positive association with seed cotton yield per plant at phenotypic (0.182) and genotypic (0.278) level.

Upper half mean length

Upper half mean length had non significant negative association with seed cotton yield per plant (-0.065, -0.031 respectively) in the RIL population at phenotypic

and genotypic level. At phenotypic and genotypic levels the trait also had positive significant association with fibre strength (0.640, 0.639 respectively), uniformity index (0.115, 0.094 respectively) and fibre elongation (0.159, 0.151 respectively) whereas, with micronaire value (-0.176, -0.200 respectively) and maturity ratio (-0.098, -0.236 respectively) on the exhibited significant negative association.

Fibre strength

The non significant negative association was found between the fibre strength and seed cotton yield in population at phenotypic (-0.027) and genotypic (-0.080) level. Considering the association with other quality trait at both phenotypic and genotypic level except micronaire value (-0.164, -0.176 respectively) and maturity ratio (-0.131, -0.225 respectively) other quality traits viz., UHML (0.640, 0.639 respectively) uniformity index (0.182, 0.176 respectively) and fibre elongation length (0.258, 0.256 respectively) had significant positive association.

Micronaire value

In the RIL population fibre micronaire value had significant association with seed cotton yield per plant at genotypic level (0.308). At phenotypic and genotypic level this trait had significant positive association with maturity ratio (0.859, 0.988 respectively) and significant negative association with uniformity index (-0.079, -0.125 respectively) and elongation length (-0.196, -0.219 respectively).

Uniformity index

The uniformity index had non significant positive association with seed cotton yield per plant at both phenotypic (0.060) and genotypic (0.080) level. This character exhibited the significant negative association with maturity ratio (-0.167) and fibre elongation length (0.427) at genotypic level in RIL population.

Maturity ratio

The significant positive correlation was observed between maturity ratio and seed cotton yield per plant in F₆ generation at phenotypic (0.154) and genotypic (0.278) levels. Whereas, the trait had significant negative correlation with fibre elongation length at phenotypic (0.125) and genotypic (-0.264) level in RIL population.

Fibre elongation length

The fibre elongation length had non significant association with seed cotton yield per plant at both phenotypic (0.007) and genotypic (0.009) levels.

4.4.2 Path analysis of seed cotton yield with agronomic and fibre quality traits

Path analysis was employed to study the extent and nature of direct and indirect effects of various characters on seed cotton yield per plant. The result of path analysis in RIL population is presented in Tables 25 and 26 (Fig. 12). The Residual effect indicated the number of traits observed in the experiment had considerable influence on yield. The Residual effect at phenotypic and genotypic level was 0.175 and 0.0796 respectively.

Plant height

Plant height had negligible positive direct effect on seed cotton yield per plant at both phenotypic (0.009) and genotypic (0.021) level. At phenotypic level the positive indirect effect of plant height were exerted on seed cotton yield per plant via number of sympodia per plant, boll weight, micronaire value where as the negative indirect effects were exerted through uniformity index. At the genotypic level the positive indirect effect of plant height on seed cotton yield per plant were exerted via number of monopodia per plant, number of sympodia per plant, seed index, boll weight, ginning outturn, lint index, micronaire value and maturity ratio.

Number of monopodia per plant

Considering number of monopodia per plant, The trait had recorded direct effect of 0.013 and -0.010 at phenotypic and genotypic respectively on seed cotton yield. At phenotypic level, number of monopodia per plant had the indirect effect on yield via plant height, number of sympodia per plant, number of bolls per plant, seed index, lint index, micronaire value, uniformity index, maturity ratio and fibre elongation length. At genotypic level number of monopodia per plant had the indirect effect on yield via plant height, number of bolls per plant, seed index, boll weight, ginning outturn, lint index, micronaire value, uniformity index, maturity ratio and fibre elongation length.

Table 25: Phenotypic path coefficient among seed cotton yield and its component traits and fibre quality traits in 222 recombinant inbred lines of *G. hirsutum*

Characters	PH	NMP	SNP	NBP	SI	BW	GOT	LI	UHML	FS	Mic	UI	MR	EL	SCYP
PH	0.009	0.000	0.001	0.000	0.001	0.003	0.000	0.000	0.000	0.000	0.002	-0.001	0.001	-0.002	0.216**
NMP	0.001	0.013	0.001	0.003	0.001	0.000	0.000	0.001	0.000	0.000	0.002	0.001	0.001	-0.001	0.174**
SNP	0.002	0.002	0.027	0.010	0.002	-0.001	0.000	0.002	0.000	0.001	0.002	0.003	0.001	0.007	0.294**
NBP	-0.009	0.163	0.292	0.782	-0.040	-0.131	0.080	0.012	-0.035	-0.022	0.051	0.159	0.033	0.190	0.672**
SI	-0.013	-0.014	-0.015	0.010	-0.189	-0.030	0.001	-0.163	-0.016	-0.021	-0.024	0.009	-0.015	-0.006	0.085
BW	0.209	-0.006	-0.020	-0.119	0.111	0.710	0.077	0.133	-0.006	-0.042	0.183	-0.080	0.117	-0.160	0.593**
GOT	0.003	-0.002	0.000	-0.007	0.000	-0.007	-0.064	-0.032	0.002	-0.001	-0.011	0.000	-0.008	-0.001	0.206**
LI	0.010	0.019	0.017	0.003	0.199	0.043	0.116	0.231	0.012	0.023	0.046	-0.009	0.030	0.007	0.182**
UHML	0.000	0.000	0.000	-0.001	0.003	0.000	-0.001	0.002	0.030	0.020	-0.005	0.004	-0.003	0.005	-0.027
FS	0.001	0.000	0.000	0.000	-0.002	0.001	0.000	-0.002	-0.010	-0.016	0.003	-0.003	0.002	-0.004	-0.066
Mic	-0.001	-0.001	0.000	0.000	-0.001	-0.001	-0.001	-0.001	0.001	0.001	-0.005	0.000	-0.004	0.001	0.244**
UI	0.001	-0.001	-0.001	-0.003	0.001	0.001	0.000	0.001	-0.001	-0.002	0.001	-0.012	0.000	-0.005	0.06
MR	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	-0.002	0.000	-0.003	0.000	0.154**
EL	0.004	0.001	-0.006	-0.006	-0.001	0.005	0.000	-0.001	-0.004	-0.006	0.005	-0.010	0.003	-0.024	0.008

Residual effect = 0.175

Where,

* = significance at 5% level, ** = significance at 1% level

PH= plant height (cm), NMP= number of monopodia per plant, SNP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value (µg/inch), FUI = Fibre uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).

Table 26: Genotypic path coefficient among seed cotton yield and its component traits and fibre quality traits in 222 recombinant inbred lines of *G. hirsutum*

Characters	PH	NMP	SNP	NBP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL	SCYP
PH	0.021	0.003	0.005	-0.004	0.007	0.011	0.003	0.007	0.000	-0.001	0.007	-0.002	0.009	-0.006	0.249
NMP	-0.001	-0.010	0.000	-0.002	-0.001	-0.001	-0.001	-0.002	0.000	0.000	-0.002	-0.002	-0.002	0.001	0.198
NSP	0.012	0.001	0.051	0.057	0.002	-0.012	-0.008	-0.002	-0.001	0.003	0.007	0.013	0.005	0.031	0.648
NBP	-0.142	0.146	0.770	0.694	-0.044	0.018	0.161	0.057	-0.039	-0.025	0.064	0.195	0.070	0.226	0.759
SI	-0.062	-0.028	-0.007	0.012	-0.195	-0.049	-0.016	-0.161	-0.031	-0.042	-0.049	0.022	-0.034	-0.010	0.119
BWP	0.342	0.051	-0.138	0.016	0.155	0.618	0.103	0.177	-0.010	-0.052	0.222	-0.103	0.179	-0.198	0.662
GOT	-0.008	-0.005	0.008	-0.013	-0.005	-0.009	-0.056	-0.035	0.002	-0.002	-0.016	-0.001	-0.018	-0.002	0.329
LI	0.082	0.042	-0.010	0.020	0.200	0.070	0.153	0.243	0.023	0.044	0.086	-0.019	0.077	0.011	0.278
UHML	0.000	-0.001	0.000	-0.002	0.007	-0.001	-0.002	0.004	0.043	0.028	-0.009	0.004	-0.010	0.007	-0.031
FS	0.001	0.001	-0.002	0.001	-0.006	0.002	-0.001	-0.005	-0.017	-0.026	0.005	-0.005	0.006	-0.007	-0.08
Mic	0.015	0.008	0.006	0.004	0.011	0.015	0.012	0.015	-0.009	-0.007	0.042	-0.005	0.044	-0.009	0.308
UI	0.001	-0.001	-0.002	-0.003	0.001	0.002	0.000	0.001	-0.001	-0.002	0.001	-0.009	0.002	-0.004	0.08
MR	-0.025	-0.013	-0.006	-0.006	-0.010	-0.017	-0.019	-0.019	0.014	0.014	-0.062	0.010	-0.060	0.016	0.279
EL	0.014	0.003	-0.027	-0.015	-0.002	0.015	-0.001	-0.002	-0.007	-0.012	0.010	-0.020	0.012	-0.046	0.01

Residual effect = 0.0796

Where,

* = significance at 5% level, ** = significance at 1% level

PH= plant height (cm), NMP= number of monopodia per plant, NSP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value (µg/inch), FUI = Fibre uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).

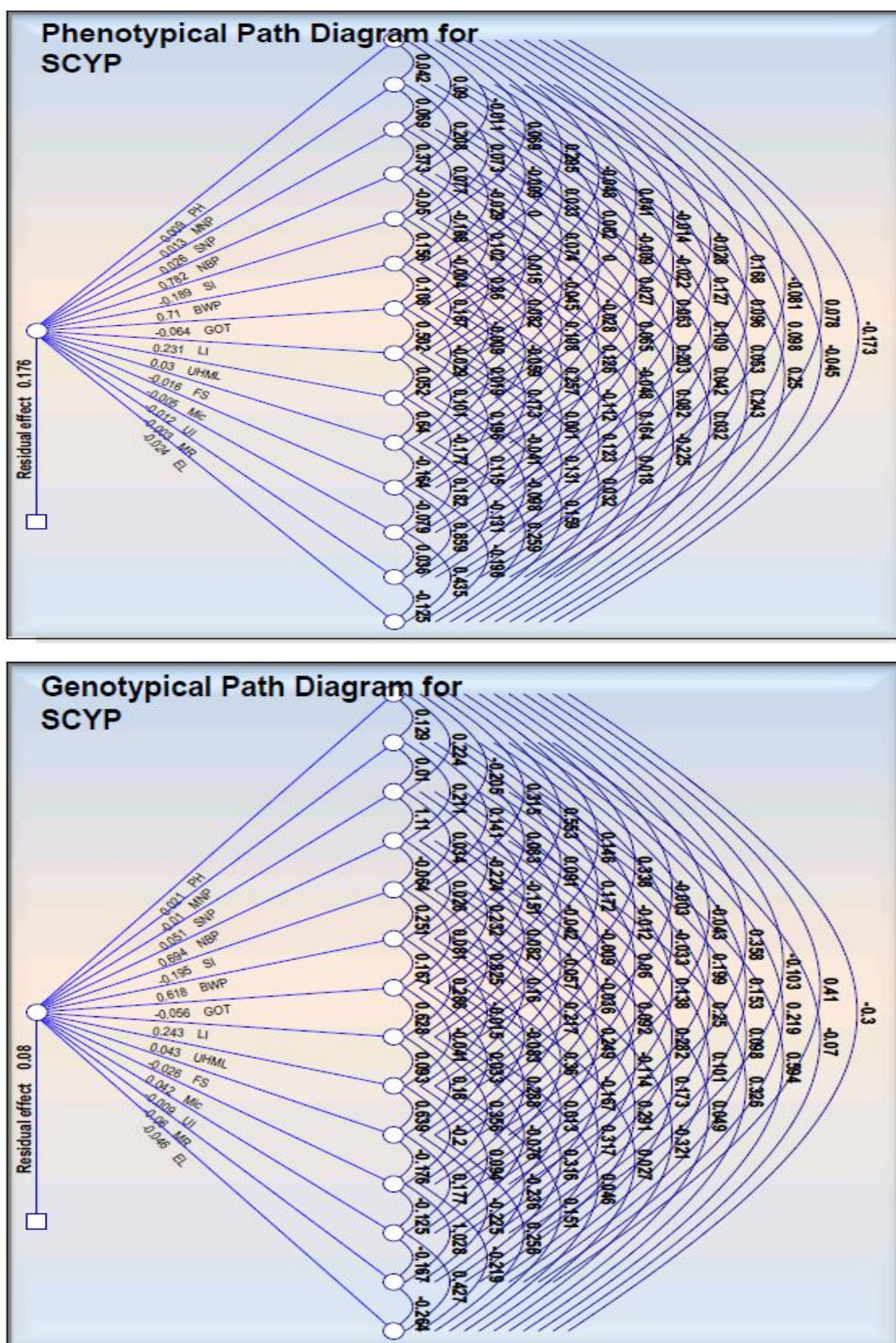


Fig. 12: Path analysis of seed cotton yield per plant in 222 recombinant inbred lines derived from RHAP 12 and RHAP 15 genotypes

Number of sympodia per plant

Number of sympodia per plant had 0.027 and 0.051 direct effect on seed cotton yield per plant at both phenotypic and genotypic level respectively. The number of sympodia per plant had positive indirect effect on seed cotton yield per plant via plant height, number of monopodia per plant, number of bolls per plant, seed index, fibre strength, micronaire value, uniformity index, maturity ratio and fibre elongation length at both genotypic and phenotypic level where as negative indirect effect through boll weight at both levels.

Number of bolls per plant

The number of bolls per plant had direct effect of 0.782 at phenotypic and 0.694 at genotypic level on seed cotton yield per plant. The number of bolls per plant had positive indirect effect on seed cotton yield per plant via number of monopodia per plant, number of sympodia per plant, ginning outturn, lint index, micronaire value, uniformity index, maturity ratio and fibre elongation length at both phenotypic and genotypic level. On the contrary negative indirect effect at both levels through plant height, seed index, upper half mean length, and fibre strength were exerted.

Seed index

Seed index had negative indirect effect on seed cotton yield at phenotypic (-0.189) and genotypic (-0.195) level. The trait had positive indirect effect on seed cotton yield per plant through number of bolls per plant and uniformity index whereas, negative indirect effect via plant height, number of monopodia per plant, number of sympodia per plant, boll weight, lint index, upper half mean length, fibre strength, micronaire value, maturity ratio and fibre elongation length at both phenotypic and genotypic levels.

Boll weight

The direct effect of boll weight on seed cotton yield per plant was 0.710 and 0.618 at phenotypic and genotypic level respectively. The boll weight had positive indirect effect on yield via plant height, seed index, ginning outturn, lint index, micronaire value and maturity ratio whereas negative indirect effect through number of

sympodia per plant, upper half mean length, fibre strength, uniformity index and fibre elongation length at both phenotypic and genotypic levels.

Ginning outturn

Ginning outturn had negative direct on seed cotton yield per plant at phenotypic and genotypic level *i.e.* -0.064 and -0.056 respectively. At phenotypic level ginning outturn had indirect effect through plant height, number of monopodia per plant, number of bolls per plant, boll weight, lint index, upper half mean length, fibre strength, micronaire value, maturity ratio and fibre elongation length. At genotypic level ginning outturn had indirect effect on seed cotton yield per plant via number of sympodia per plant, seed index and uniformity index.

Lint index

Lint index had high direct effect on seed cotton yield per plant at phenotypic (0.231) and genotypic (0.243) level. It had positive indirect effect on seed cotton yield per plant through all the observed traits *viz.*, plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, seed index, boll weight, ginning outturn, upper half mean length, fibre strength, micronaire value, maturity ratio and fibre elongation length except uniformity index, which had negative indirect effect at both phenotypic and genotypic levels on seed cotton yield.

Upper half mean length

The trait exerted direct effect of 0.030 and 0.043 on seed cotton yield at phenotypic and genotypic levels respectively. The upper half mean length had positive indirect on seed cotton yield per plant via seed index, lint index, fibre strength, uniformity index and fibre elongation length, where as negative indirect effect on seed cotton yield per plant via number of bolls per plant, ginning outturn, micronaire value and maturity ratio at both phenotypic and genotypic levels were observed.

Fibre strength

The fibre strength had negative direct effect on seed cotton yield per plant at both phenotypic (-0.016) and genotypic (-0.026) levels. Indirect positive effect of fibre

strength on seed cotton yield via plant height, boll weight, micronaire value and maturity ratio were registered whereas, negative indirect effect via seed index, lint index, upper half mean length, uniformity index and fibre elongation length were observed.

Micronaire value

The direct effect of micronaire value on seed cotton yield per plant was -0.005 and 0.042 at genotypic and phenotypic levels respectively. The micronaire value had positive indirect effect on seed cotton yield per plant via plant height, number of monopodia per plant, seed index, boll weight, ginning outturn, lint index and maturity ratio at genotypic level but negative indirect effects were observed at phenotypic level for the characters mentioned. At phenotypic level the micronaire value had positive indirect effect on seed cotton yield per plant via upper half mean length, fibre strength and fibre elongation length.

Uniformity index

The uniformity index had negative direct effect on seed cotton yield per plant at phenotypic (-0.012) and genotypic (-0.009) level. The uniformity index had positive indirect effect on seed cotton yield per plant via plant height, seed index, boll weight, lint index and micronaire value whereas negative indirect effect through monopodia branches per plant, number of sympodia per plant, upper half mean length, fibre strength and fibre elongation length at both phenotypic and genotypic levels.

Maturity ratio

Maturity ratio had negative direct effect of -0.003 and -0.060 at phenotypic and genotypic levels respectively on seed cotton yield per plant. The indirect effect of maturity ratio on seed cotton yield per plant via various trait was nil except micronaire value at phenotypic level. However, at the genotypic level maturity ratio had negative indirect effect on seed cotton yield per plant via plant height, monopodia branches per plant, number of sympodia per plant, number of bolls per plant, seed index, boll weight, ginning outturn, lint index and micronaire value.

Elongation length

A negative direct effect of fibre elongation length on seed cotton yield per plant at phenotypic (-0.024) and genotypic (-0.046) levels were registered. The fibre elongation length had positive indirect effect on seed cotton yield per plant via plant height, monopodia branches per plant, boll weight, micronaire value and maturity ratio whereas, negative indirect effect via number of sympodia per plant, number of bolls per plant, seed index, lint index, upper half mean length and fibre strength at both phenotypic and genotypic level was observed.

4.5 Intergeneration correlation and regression between the F₄ Vs F₅ and F₅ Vs F₆ generation.

4.5.1 Intergeneration correlation and regression between the F₄ Vs F₅ and F₅ Vs F₆ generation for yield and yield attributes

The correlation coefficient and simple linear regression were analyzed for yield and its components across the segregating generation viz., F₄, F₅ and F₆ derived from crossing RHAP 12 and RHAP 15 parent (Table 27 and Fig. 13) (Appendix IIIa).

Plant height

The plant height had positive and significant correlation coefficient between F₄ and F₅ generation (0.901). A similar trend was observed between F₅ and F₆ generation with a positive and significant correlation coefficient of 0.982. The intergeneration regression for plant height was found positive and significant between F₄ and F₅ generation of 0.918 and also between F₅ and F₆ of 0.959.

Number of sympodia per plant

The sympodia per plant in F₄ generation had significant positive correlation (0.247) and significant regression coefficient (0.201) with number of sympodia performance in F₅ lines. The intergeneration correlation (0.947) and regression (0.869) recorded a positive significant for the number of sympodia per plant between the F₅ and F₆ generation also.

Table 27: Intergeneration correlation and regression between the F₄ Vs F₅ and F₅ Vs F₆ generations of segregating population derived from hybridization of RHAP 12 and RHAP 15 of *G. hirsutum*

Characters	F ₄ and F ₅		F ₅ and F ₆	
	Correlation	Regression	Correlation	Regression
Yield and yield attributing traits				
PH	0.901**	0.918**	0.982**	0.959**
NSP	0.247**	0.201**	0.947**	0.869**
NMP	0.091	0.086	0.968**	0.898**
NBP	0.314**	0.304**	0.921**	0.824**
BW	0.004	0.004	0.936**	0.948**
SCYP	0.270**	0.110**	0.992**	0.981**
SI	0.144*	0.108*	0.908**	0.845**
GOT	0.123	0.096	0.870**	0.887**
LI	0.155*	0.118*	0.907**	0.884**
Fibre quality traits				
UHML	-	-	0.920**	0.830**
FS	-	-	0.945**	0.880**
Mic	-	-	0.871**	0.830**
UI	-	-	0.800**	0.750**
MR	-	-	0.884**	0.840**
FEL	-	-	0.943**	0.860**

Where,

PH= plant height (cm), NMP= number of monopodia per plant, NSP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value (µg/inch), UI = Uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).

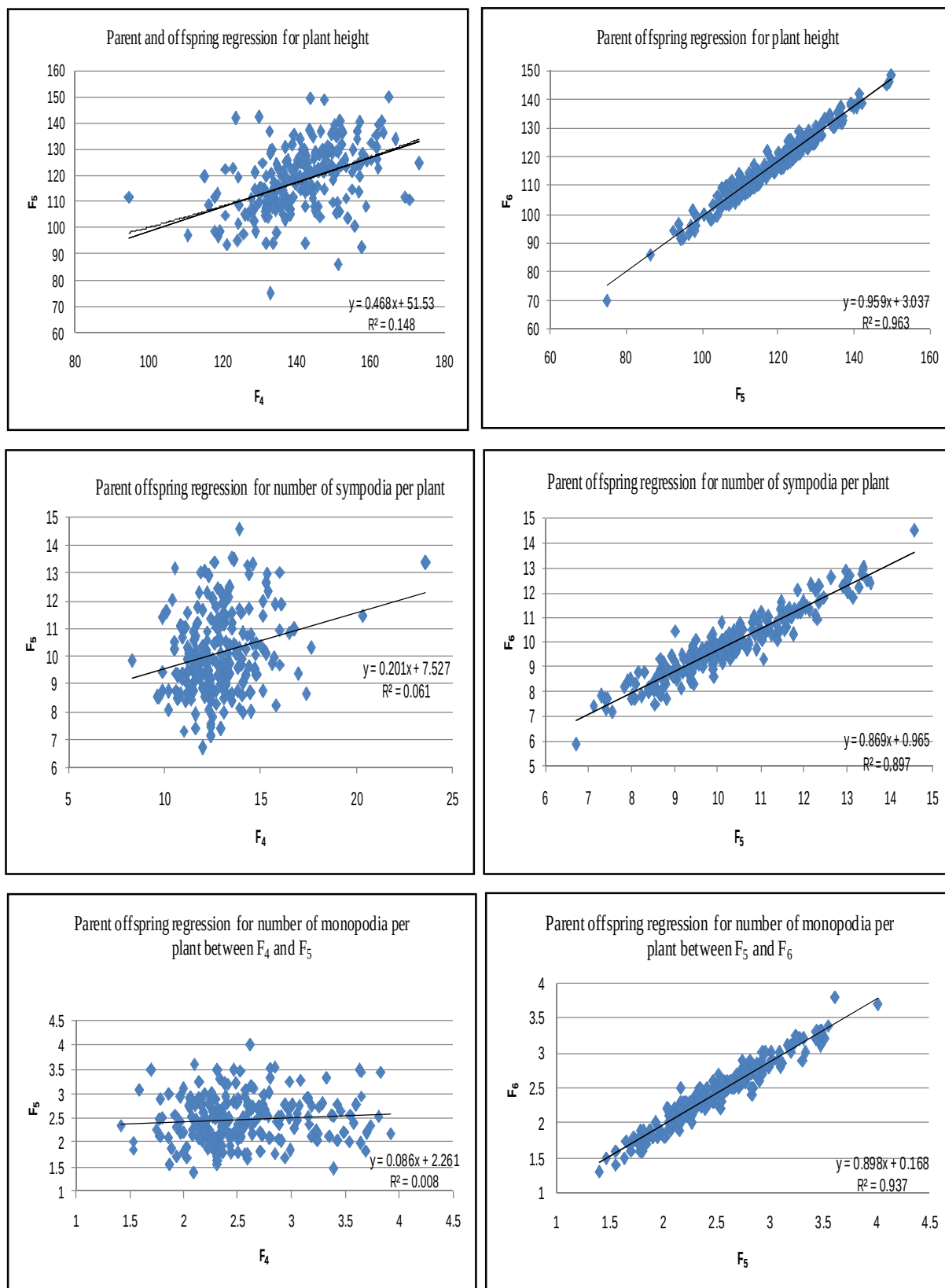
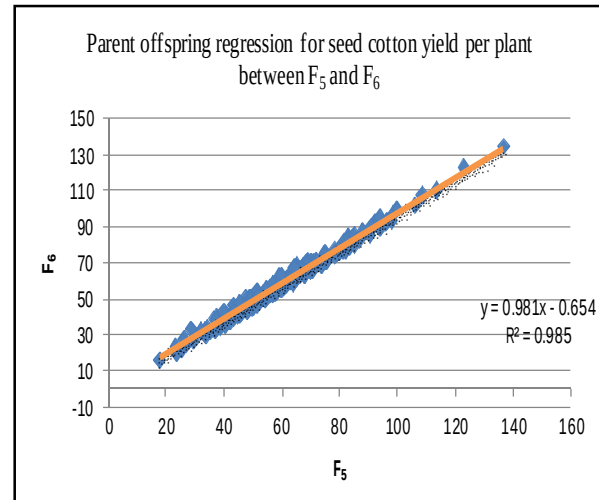
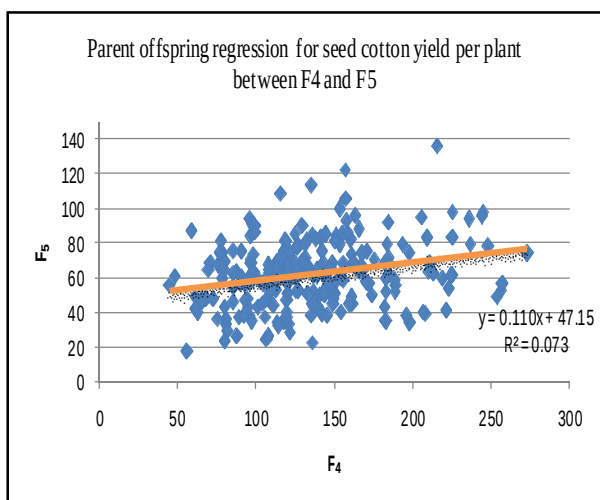
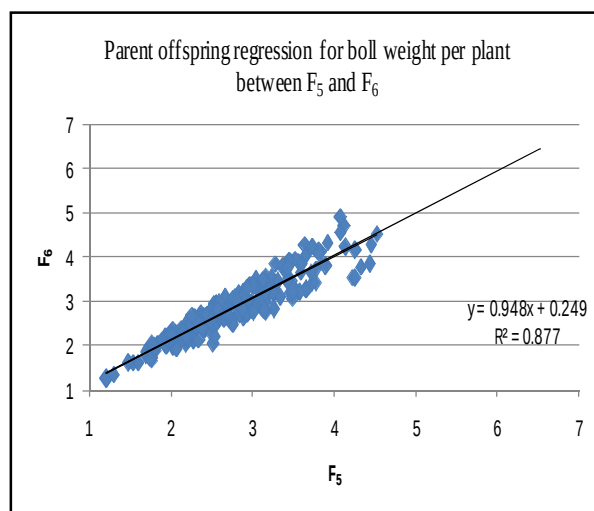
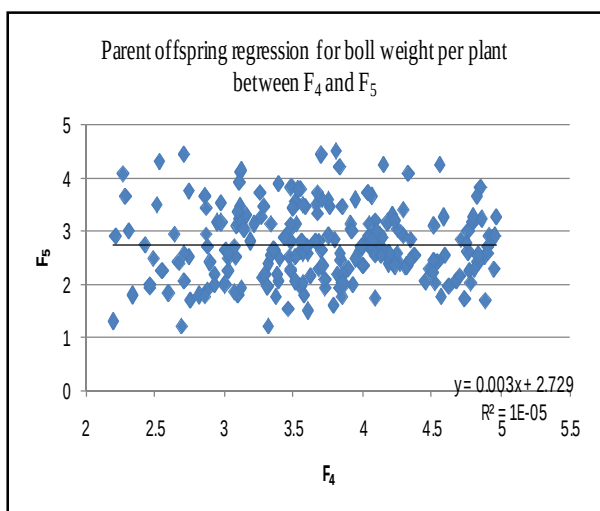
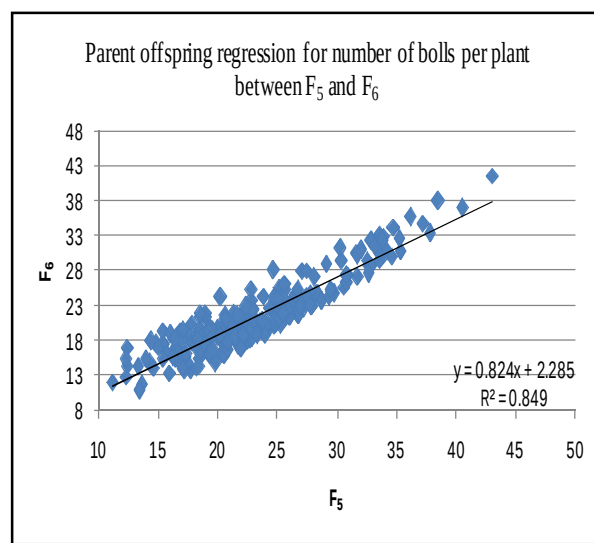
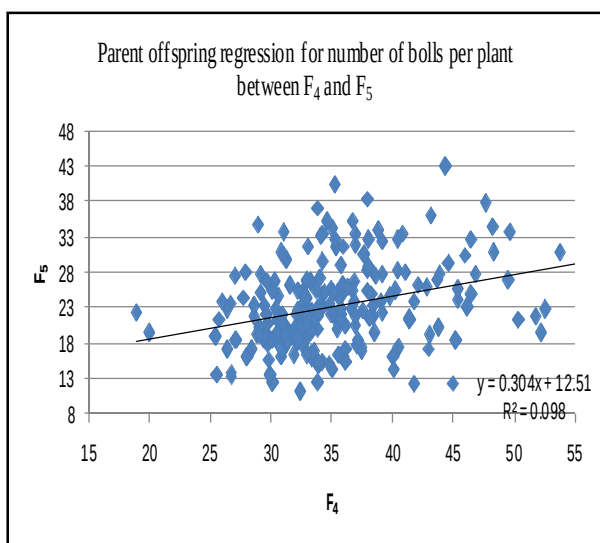
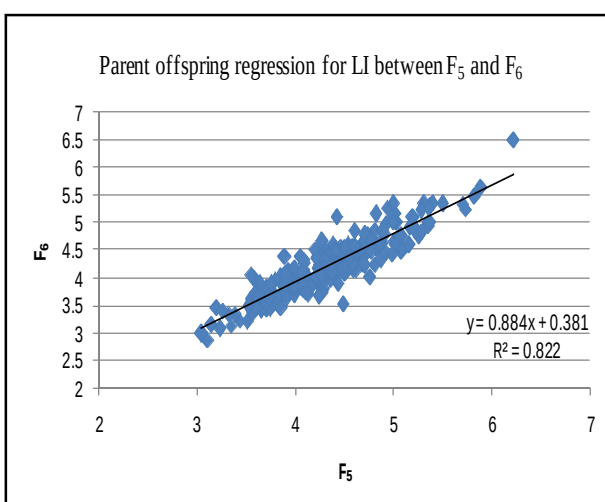
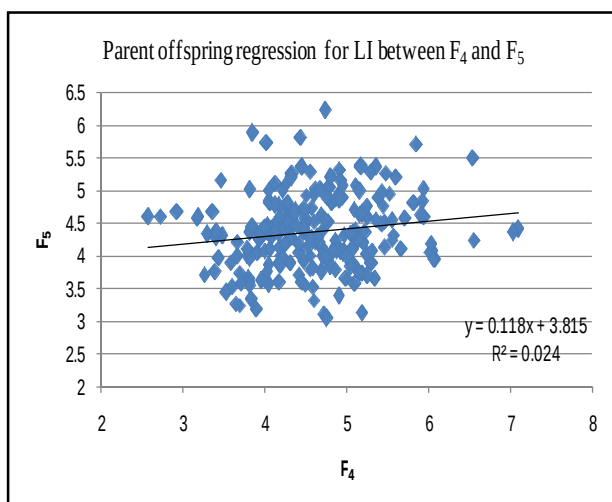
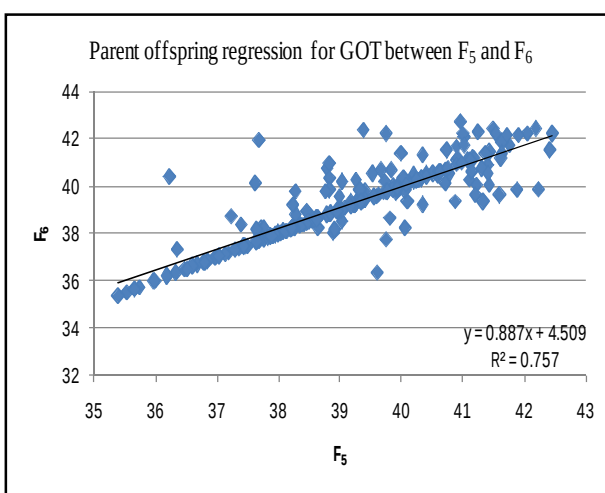
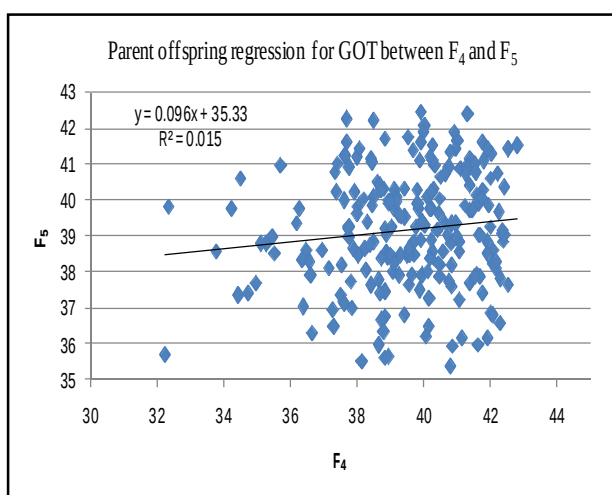
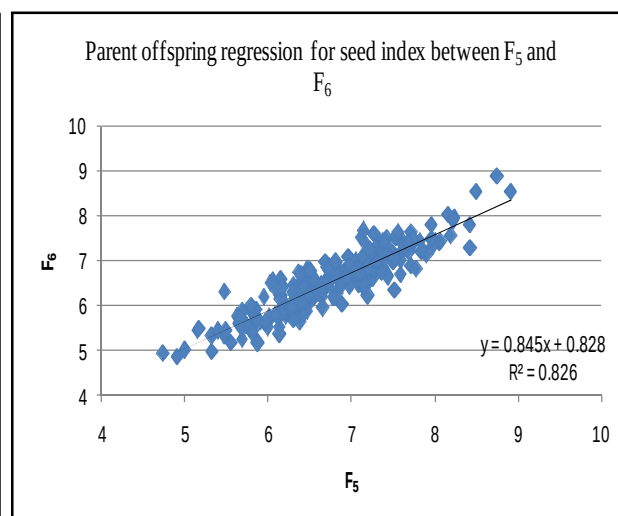
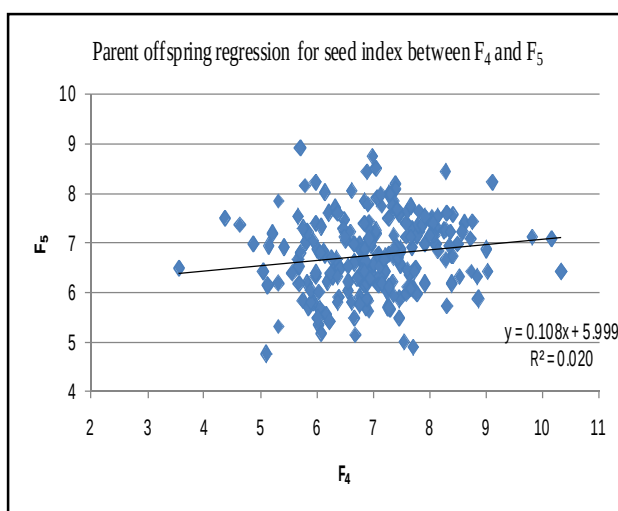


Fig. 13: Parent offspring linear regression graph for the yield and its attributing traits and fibre quality traits across the segregating generation

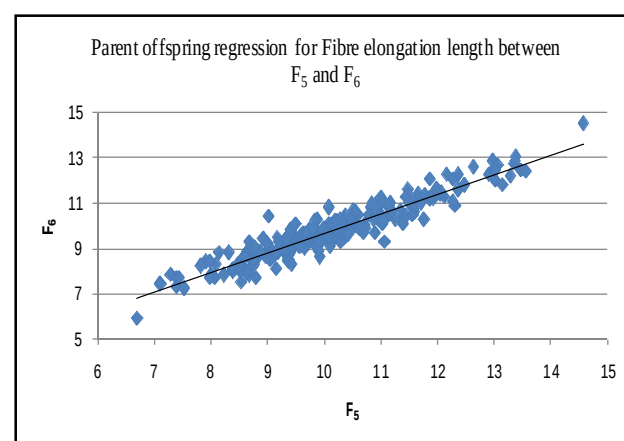
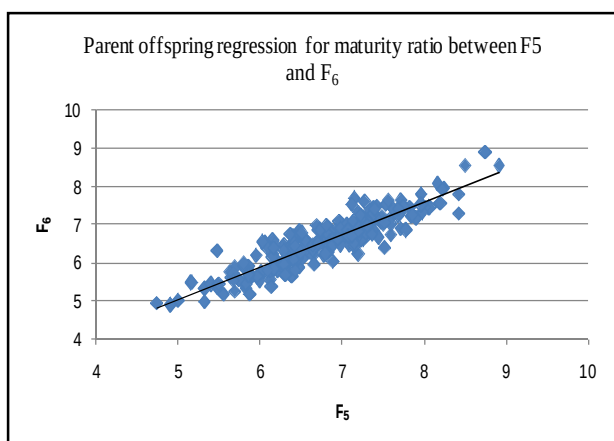
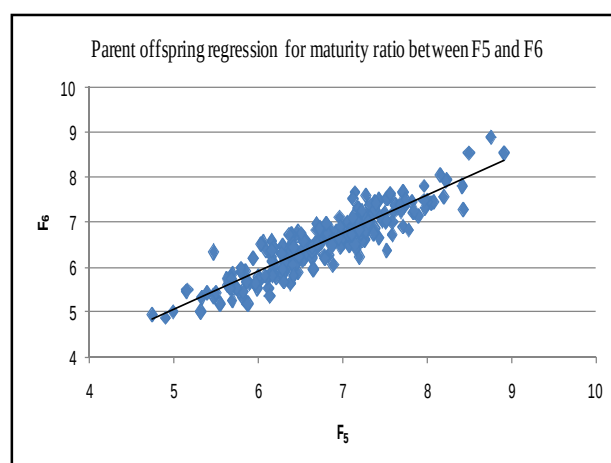
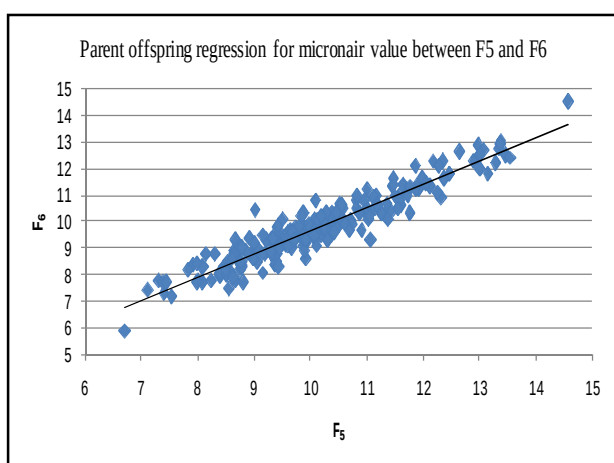
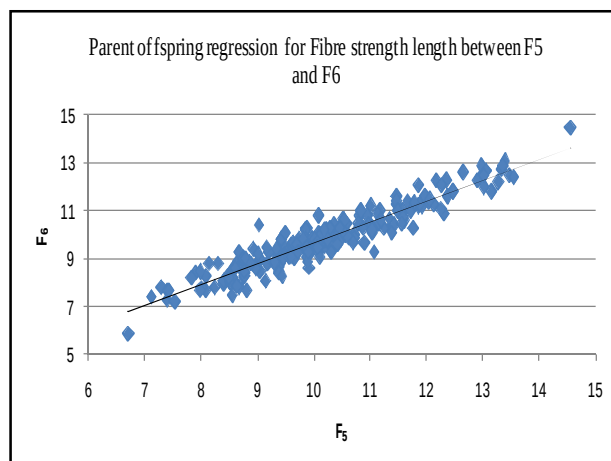
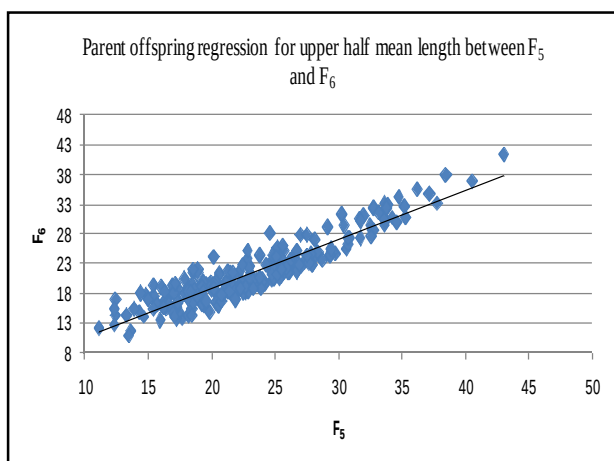
Contd.....



Contd.....



Contd.....



Number of monopodia per plant

The F_4 generation number of monopodia per plant had non significant association (0.091) with F_5 generation for the trait. The similar relationship had find in simple linear regression (0.086). This non significant association turned into significant between F_5 and F_6 generation ($r=0.968$ and $b=0.898$) for the trait.

Number of bolls per plant

The number of bolls per plant had a positive and significant correlation coefficient of 0.314 between the F_4 and F_5 generations. The regression coefficient between the F_4 and F_5 for the trait was found positive and significant (0.304). The intergeneration correlation and regression coefficients between F_5 and F_6 were 0.921 and 0.824 respectively for the trait.

Boll weight

The boll weight of F_4 generation parental line had non significant positive association (0.004) with boll weight of F_5 progeny lines and similar trend was observed for linear regression analysis (0.004). However, the significant intergeneration correlation of 0.936 and regression analysis of 0.948 g for boll weight was observed between F_5 and F_6 generations.

Seed cotton yield per plant

The seed cotton yield per plant of F_4 generation parental lines had a significant positive association of 0.27 with F_5 progeny lines. A similar positive significant association value of 0.992 was observed in between the F_5 and F_6 generations for trait. The regression coefficient also showed positive and significant association of 0.110 and 0.981 between F_4 Vs F_5 and F_5 Vs F_6 generations respectively for the trait.

Seed index

Considering seed index, a positive and significant correlation coefficient of 0.144 was found between the generations F_4 and F_5 . The regression coefficient between the F_4 and F_5 for the trait was found positive and significant (0.108). While the intergeneration correlation and regression between F_5 and F_6 recorded were 0.908 and 0.845 respectively for the trait.

Ginning outturn

The intergeneration correlation coefficient between F_4 and F_5 generations for the trait was positive and non significant (0.123). A similar trend was observed for linear regression (0.096). Whereas, intergeneration correlation and regression were positive and significant between the F_5 and F_6 generation ($r=0.870$ and $b=0.887$) for the trait

Lint index

The lint index of F_4 generation parental line had a significant positive association (0.155) with F_5 progeny lines for trait. A similar trend was observed between the F_5 and F_6 generation for the trait (0.907). The regression coefficient was found positive and significant for lint index (0.118) between the F_4 and F_5 generation and between F_5 and F_6 generation (0.884).

4.5.2 Intergeneration correlation and regression between the F_5 and F_6 generation for fibre quality traits.

The inter generation correlation and regression analysis for fibre quality traits were assessed between the F_5 and F_6 generation (Table 27 and Fig. 13) (Appendix IIIb).

Upper half mean length

The upper half mean length had a positive significant correlation of 0.920 between F_5 and F_6 generation. The intergeneration regression was also found positive and significant between F_5 and F_6 (0.830) for the trait.

Fibre strength

The F_5 generation fibre strength had positive and significant correlation coefficient of 0.945 and regression coefficient of 0.880 with fibre strength of F_6 lines.

Micronaire value

The intergeneration correlation coefficient of 0.871 and simple linear regression of 0.830 was observed between F_5 and F_6 generations for the trait.

Uniformity index

The uniformity index had positive significant correlation of 0.800 between F_5 and F_6 generation. The intergeneration regression was found positive and significant between F_5 and F_6 (0.750) for the trait.

Maturity ratio

The F_5 generation maturity ratio had positive and significant correlation coefficient of 0.884 and a significant regression coefficient of 0.840 with maturity ratio of F_6 lines.

Fibre elongation length

The intergeneration correlation coefficient of 0.943 and simple linear regression of 0.860 was observed between F_5 and F_6 generations for the trait.

4.6 Identification of transgressive segregants in RIL population

In present investigation, transgressive segregants were identified on either sides of superiority or inferiority of the parents for all the considered traits. The parent's performance, population mean, number of transgressive segregants, frequency of segregants, range and per cent of change with respect to parents were assessed for all traits and results are presented in Table 28.

Plant height

Among 222 RILs, 26 transgressive segregants (0.12) were found superior to RHAP 15 (131.1 cm) for the trait. These transgressive lines registered a height in the range of 131.6 to 148.1 cm. Out of 26 transgressive lines for plant height 23 lines showed superiority of 10 per cent and 3 lines were 10-20 per cent advantageous over the superior parent (RHAP 15) for the trait.

The female parent RHAP 12 had a height of 124.7 cm. Out of 222 RILs 163 lines were transgressive segregants over RHAP 12. The frequency of transgressive segregants was 0.73. These transgressive lines had plant height in the range of 69.87 to 124.60 cm. out of 163 transgressive lines 78, 67 and 18 lines were in the superiority

Table 28: Identification of Transgressive Segregants (TS) in the RIL population derived from hybridization between RHAP 12 and RHAP 15 of *G.hirsutum*

Sl. No	Character	Parent	parent Performance	Population mean	No. of TS individuals	Frequency	Direction of action ¹	Range	Per cent change		
									<10%	10-20%	>20%
1	PH	RHAP15	131.1	116.58 ± 8.87	26	0.12	+	131.6 to 148.1	23	3	-
		RHAP 12	124.7		163	0.73	-	69.87 to 124.6	78	67	18
2	NMP	RHAP15	3.65	2.39 ± 0.27	2	0.01	+	3.75 to 3.8	-	-	2
		RHAP 12	3		198	0.89	-	2.9 to 1.3	34	53	111
3	NSP	RHAP15	12.9	9.76 ± 1.12	2	0.01	+	13.05 to 14.5	2	-	-
		RHAP 12	10.6		168	0.76	-	5.9 to 10.5	60	73	35
4	NBP	RHAP 12	25.4	21.46 ± 2.81	39	0.18	+	25.7 to 41.5	8	12	19
		RHAP15	18.5		70	0.32	-	10.9 to 18.4	34	23	13
5	SCYP	RHAP 12	70	60.37 ± 8.53	61	0.27	+	70.4 to 135	24	16	21
		RHAP15	55		85	0.38	-	15.7 to 54.8	21	19	45
6	SI	RHAP 12	7.4	6.54 ± 0.55	27	0.12	+	7.41 to 8.90	24	3	-
		RHAP15	6.45		92	0.41	-	4.88 to 6.43	56	32	4
7	BWP	RHAP 12	3.35	2.85 ± 0.39	37	0.17	+	3.50 to 4.92	7	16	14
		RHAP15	2.64		83	0.37	-	1.26 to 2.63	27	27	29
8	GOT	RHAP 12	38.80	39.26 ± 1.06	131	0.59	+	38.2 to 42.68	131	-	-
		RHAP15	35.85		4	0.02	-	35.39 to 35.72	4	-	-
9	LI	RHAP 12	4.69	4.23 ± 0.39	38	0.17	+	4.70 to 6.51	23	13	2
		RHAP15	3.61		24	0.11	-	2.88 to 3.56	17	6	1

Contd.....

Sl. No	Character	Parent	parent Performance	Population mean	No. of TS individuals	Frequency	Direction of action ¹	Range	Per cent change		
									<10%	10-20%	>20%
10	UHML	RHAP 12	27.5	24.93 ± 0.11	9	0.04	+	27.75 to 30.9	9	-	-
		RHAP15	25.1		123	0.55	-	20.4 to 25.05	113	10	
11	FS	RHAP 12	29.3	25.27 ± 0.06	8	0.04	+	29.40 to 30.62	8	-	-
		RHAP15	22.2		0	0	-	-	-	-	-
12	Mic	RHAP 12	3.54	3.52 ± 0.05	110	0.5	+	2.16 to 3.53	64	33	13
		RHAP15	3.83		48	0.22	-	3.84 to 4.68	35	11	2
13	UI	RHAP 12	88.8	75.66 ± 0.66	1	0	+	94.4	1	-	-
		RHAP15	84.5		217	0.98	-	58.2 to 83.6	86	128	3
14	MR	RHAP 12	0.47	0.57 ± 0.04	18	0.08	+	0.29 to 0.46	9	6	3
		RHAP15	0.55		138	0.62	-	0.56 to 0.78		138	-
15	FEL	RHAP 12	6	5.03 ± 0.03	5	0.02	+	6.2 to 6.6	5	-	-
		RHAP15	4.8		53	0.24	-	4 to 4.7	49	4	-

Where,

1 = Direction of action where +ve indicate the desirable direction and – indicate non desirable direction

PH= plant height (cm), NMP= number of monopodia per plant, NSP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value (µg/inch), FUI = Fibre uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).

range of 10 per cent, 10-20 per cent and more than 20 per cent respectively over the inferior parent, RHAP 12.

Number of monopodia per plant

Two lines (RIL 40 and RIL 110) with a frequency of 0.01 possessed more number of monopodia over the superior parent *i.e.* RHAP 15 (3.65) with an advantage of more than 20 per cent over the parent for the trait.

The female parent RHAP 12 produced three monopodia branches. In population, 198 lines were transgressive segregants (0.89) over the inferior parent for the trait. These lines had monopodia in a range of 1.3 to 2.9. Out of 198 lines 34, 53 and 111 lines had less monopodia over parent (RHAP 12) where all are in range of 10 per cent, 10-20 per cent and more than 20 per cent respectively.

Number of sympodia per plant

The RIL 90 (14.5) and RIL 14 (13.05) lines were the only transgressive segregants in the population with respect to superior parent RHAP 15 (12.9). Out of these two lines the RIL 90 was 12.40 per cent superior over parent RHAP 15

In RILs population, 168 lines segregants transgressively (0.76) with respect to inferior parent RHAP 12 (10.6) for the trait. The numbers of sympodia per plant observed were in the range of 5.9 to 10.5. Out of 168 lines 60, 73 and 35 lines showed less than 10 per cent, 10-20 per cent and more than 20 per cent reduction over the parent.

Number of bolls per plant

In population 39 lines were superior over the superior parent RHAP 12 for the trait which recorded of 25.4 bolls per plant. Out of 39 RILs 8, 12 and 19 lines had more number of bolls in a range of less than 10 per cent, 10-20 per cent and more than 20 per cent respectively over the best parent.

Among 222 RILs, 70 transgressive segregants (0.32) had less bolls as compared to inferior parent RHAP 15 (18.5). The lines had a range of 10.90 to 18.40 for the trait.

Out of 70 transgressive 34, 23 and 13 lines expressed less than 10 per cent, 10-20 per cent and more than 20 per cent reduction respectively over the parent (RHAP 15).

Seed cotton yield per plant

Out of 222 RILs, 61 lines were identified as transgressive segregants (0.27) for seed cotton yield per plant with respect to superior parent RHAP 12 which recorded of 70 g per plant. The yield of transgressive segregants ranged between 70.4 g to 135g. Out of 61 lines 24, 16, 21 lines registered more than 10 per cent, 10-20 per cent and more than 20 per cent increase in yield over better parent, RHAP12 respectively.

The male parent RHAP 15 recorded 55 g seed cotton yield per plant. In population, observed the 85 lines were transgressive segregants (0.38) with respect to inferior parent RHAP 15 for the trait. These lines ranged between 15.7 g to 54.8 g. The 21, 19 and 45 lines out of 85 were inferior over the parent RHAP 15 with less than 10 per cent, 10-20 per cent and more than 20 per cent level regressed respectively for the trait.

Seed index

Out of 222 lines, 27 lines transgressed over the superior parent *i.e.* RHAP 12. The frequency of transgression was 0.12 in which 24 and 3 lines showed less than 10 per cent and 10-20 per cent advantage respectively over the parent.

In the population 92 transgressive were identified over the inferior parent RHAP 15 for seed index with frequency of 0.41. Out of 92 lines 56, 32 and 4 lines had less seed index over the parent RHAP 15 at less than 10 per cent, 10-20 per cent and more than 20 per cent level respectively.

Boll weight

Transgressive segregants numbering 37 with the frequency of 0.17 were observed over the superior parent RHAP 12 (3.35g). Out of 37 lines 7, 16 and 14 lines were superior over the parent RHAP 12 at less than 10 per cent, 10-20 per cent and more than 20 per cent level respectively.

Among 222 RILs, 83 transgressives (0.37) were found inferior over the inferior parent RHAP 15 (2.64 g) for the trait. These transgressives ranged from 1.26 to 2.63g. Out of 83 transgressive for trait, 29 lines had 20 per cent over more boll weight than RHAP 15.

Ginning outturn

In the population, 131 transgressives were identified over the superior parent RHAP 12 (38.80 per cent) for ginning outturn with a frequency of 0.59. The transgressive lines recorded ginning outturn of 38.20 to 42.68 per cent which showed a ginning outturn lesser than 10per cent superiority over the parent.

A total of four transgressives observed with a range of 35.39 to 35.72 per cent ginning outturn and these were inferior over parent RHAP 15 at less than 10 per cent.

Lint index

Out of 222 lines, 38 lines were transgressive segregants with a frequency of 0.17 over the superior parent RHAP 12 (4.69) for the trait. The minimum and maximum lint index of transgressives was 4.70 g and 6.51 g respectively. Out of 38 lines 23, 13 and 2 lines had more seed index over the parent RHAP 12 of less than 10 per cent, 10-20 per cent and more than 20 per cent level respectively.

Among 222 RILs, 24 transgressive segregants (0.11) with a range of 2.88 to 3.56 were found inferior to parent RHAP 15 (3.61 g) for the trait. Out of 24 transgressive lines 17, 6 and one lines were of less than 10 per cent, 10-20 per cent and more than 20 per cent respectively reduction over the inferior parent (RHAP 15).

Upper half mean length

A total of 9 lines with a range of 27.75 mm to 30.9 mm transgressed superiorly over the superior parent RHAP 12 (27.5mm) in a range of 0 to 10 per cent.

The 123 transgressives were found inferior over the least parent RHAP 15 with a frequency of 0.55. Out of 123 transgressive lines 113 and 10 lines had less upper half mean length over the parent RHAP 15 of less than 10 per cent and 10-20 per cent level respectively.

Fibre strength

In comparison with superior parent RHAP 12 (29.30 g/tex), eight lines (0.04) of the 222 RILs were transgressed for fibre strength. The fibre strength of transgressive ranged from 29.40 g / tex to 30.62 g / tex. All the lines of transgressive segregants are modified by less than 10 per cent over the parent RHAP 12. No transgressive segregants for the trait were identified with regard to the inferior parent RHAP 15.

Micronaire value

A total of 110 transgressive segregants (0.5) have been reported for the trait in the population, referring to better parent RHAP 12 (3.54). When taking into account the percentage of change over the parent, 13 lines are higher than 20 per cent.

For the phenotype, 48 transgressive segregants (0.22) were found among the RIL population, taking into account the inferior parent RHAP 15 (3.83). The micronaire value of these transgressives was 3.84 to 4.68. Of the 48 transgressives, the 35, 11 and two lines were less than 10 per cent, 10-20 per cent and more than 20 per cent disadvantage over the parent (RHAP 15).

Uniformity index

Only one line of 222 RILs was transgressed for the trait against superior parent RHAP 12 (88.8 %). The transgressive segregants (RIL 3) had a 94.4 % uniformity index.

With respect to inferior parent RHAP 15, 217 transgressive segregants were reported for trait with a frequency of 0.98 in the population. Of the 217 lines 86, 128 and 3 lines had a disadvantage of less than 10 % and 10-20 % and more than 20 % respectively compare to RHAP 15 parent.

Maturity ratio

In the RIL population, 18 lines with respect to superior parent RHAP 12 (0.47), was found to be transgressive segregants (0.08). Out of 18 lines 9, 6 and 3 lines were additional benefit over the better parent RHAP 12 at less than 10 per cent and 10-20 per cent and more than 20 per cent level respectively.

As regards inferior RHAP 15 (0.55) for the trait, a total of 138 lines were observed as transgressive. The registered maturity ratio of the transgressive lines was between 0.56 and 0.78. All 138 lines were 10-20 per cent change over the parent RHAP 15.

Fibre elongation length

Out of 222 lines five lines were transgressive segregants over the superior parent *i.e.* RHAP 12 (6 per cent). All 5 lines had a change of less than 10 per cent over the parent.

A total of 53 lines were identified as transgressive segregants (0.24) for fibre elongation length with reference to inferior parent RHAP 15 (4.8 per cent). The fibre elongation length of transgressive segregants diversified between 4 and 4.7 per cent. Of the 53 lines 49 and four lines, registered at less than 10 per cent and 10-20 per cent respectively, changed over parent RHAP 15.

4.7 Identification of superior recombinant inbred lines based on *per se* performance

The mean performance recombinant inbred lines for yield and yield attributes and quality traits are presented in Appendix II. The superior RILs for the each traits studied in the present investigation are presented in the Table 29.

Plant height

The average plant height of population was 116.59 cm with a range of 69.88 cm (RIL 25) to 148.40 cm (RIL 53). The RIL53 (148.4 cm), RIL104 (145.9 cm), RIL146 (144.7 cm), RIL140 (142 cm), RIL122 (138.8 cm), RIL214 (138.6 cm), RIL80 (138.4 cm), RIL54 (137.7 cm), RIL171 (137.4 cm) and RIL208 (137.1 cm) of the population generated were found superior for the trait.

Number of monopodia per plant

The lines *viz.*, RIL 40 (3.8), RIL110 (3.7), RIL62 (3.3), RIL77 (3.3), RIL114 (3.3), RIL208 (3.3), RIL39 (3.25), RIL41 (3.2), RIL51 (3.2) and RIL61 (3.2) were

Table 29: List of top 20 superior lines based on *per se* performance for each trait in RIL population of *G. hirsutum*

RILs	PH	RILs	NMP	RILs	NSP	RILs	NBP	RILs	SCYP	RILs	SI	RILs	BWP	RILs	GOT	RILs	LI	RILs	UHML	RILs	FS	RILs	Mic	RILs	UI	RILs	MR	RILs	EL
53	148.4	40	3.8	90	14.5	54	41.5	54	135	208	8.9	199	4.92	31	42.68	208	6.51	3	30.9	40	30.63	144	2.16	3	94.4	107	0.78	26	6.6
104	145.9	110	3.7	16	13.05	90	38	90	122.5	163	8.55	79	4.73	54	42.45	203	5.64	13	29.6	23	30	195	2.21	1	87.6	155	0.77	28	6.6
146	144.7	62	3.375	41	12.9	207	37	207	110	203	8.54	213	4.58	108	42.4	52	5.5	67	28.5	3	29.9	141	2.27	20	87.3	53	0.73	1	6.5
140	142	77	3.325	54	12.85	11	35.7	92	107.2	179	8.05	176	4.51	186	42.38	169	5.36	90	28.4	90	29.9	13	2.41	5	87.1	178	0.73	3	6.2
122	138.8	114	3.3	26	12.75	16	34.7	108	101.6	52	7.95	216	4.34	43	42.3	161	5.35	101	28.3	101	29.8	15	2.57	15	85.3	156	0.72	13	6.2
214	138.6	208	3.3	98	12.7	15	34.25	138	100.2	194	7.91	146	4.29	207	42.25	109	5.35	218	28.1	47	29.43	78	2.72	24	83.6	184	0.72	12	6
80	138.4	39	3.25	11	12.6	43	33.3	53	96.7	53	7.81	50	4.29	208	42.25	194	5.35	206	27.95	13	29.4	73	2.73	11	83.1	36	0.71	15	6
54	137.7	41	3.2	1	12.5	10	33.1	39	94.75	76	7.8	180	4.26	15	42.22	53	5.34	145	27.9	35	29.4	206	2.74	17	83	39	0.71	22	6
171	137.4	51	3.2	104	12.5	12	32.9	43	93.4	87	7.67	139	4.23	90	42.2	76	5.32	17	27.75	52	29.3	142	2.77	21	82.9	90	0.71	25	6
208	137.1	61	3.2	100	12.4	98	32.7	109	92.8	169	7.66	164	4.18	35	42.18	213	5.28	97	27.5	63	29.3	64	2.78	27	82.6	167	0.71	9	5.9
48	137	102	3.2	4	12.4	41	32.3	10	92.7	171	7.64	138	4.15	92	42.15	35	5.28	86	27.4	67	29.3	187	2.8	40	82.1	43	0.7	93	5.9
213	137	109	3.2	10	12.3	53	32.3	104	92.4	8	7.61	112	4.14	138	42.15	179	5.25	35	27.3	27	29.2	29	2.82	152	81.7	148	0.7	17	5.8
121	135.6	115	3.2	103	12.275	47	31.7	11	91.7	161	7.6	169	4.1	109	42.1	171	5.23	49	27.2	28	29.2	20	2.83	13	81.6	126	0.69	5	5.8
161	135.4	97	3.15	14	12.25	39	31.25	194	91.5	24	7.57	194	4.07	107	41.95	8	5.19	63	27.2	111	29.2	125	2.84	8	81.5	160	0.69	19	5.8
175	134.2	36	3.1	6	12.2	29	31	139	90.4	167	7.54	130	3.97	39	41.85	87	5.17	176	27	145	29.2	18	2.85	14	81.5	196	0.69	21	5.8
216	134	70	3.1	92	12.1	108	30.8	107	89.4	153	7.53	179	3.95	36	41.75	90	5.13	197	27	173	29.2	22	2.86	12	81.4	37	0.68	100	5.8
139	133.1	181	3.1	9	12.1	44	30.7	98	87.8	48	7.52	58	3.91	213	41.71	186	5.12	195	26.95	15	29.1	17	2.87	138	81.3	66	0.68	202	5.8
41	133	192	3.1	102	12	14	30.6	12	86.8	205	7.5	64	3.88	190	41.68	72	5.07	23	26.9	42	29.1	74	2.89	162	81	115	0.68	4	5.7
120	132.8	50	3	3	11.8	26	30.53	179	85.7	37	7.48	118	3.87	38	41.5	210	5.03	42	26.9	49	29.1	190	2.92	6	80.8	209	0.68	8	5.7
114	132.6	67	3	101	11.8	17	30.2	93	84.9	210	7.48	178	3.86	161	41.49	163	5.03	56	26.9	140	29.1	25	2.99	16	80.8	210	0.68	11	5.7

Where,

PH= Plant height (cm), NMP= Number of monopodia per plant, NSP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value ($\mu\text{g/inch}$), UI = Uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).

found superior for the character. The average number of monopodia branch per plant in the evaluated RILs was 2.40. The maximum and minimum monopodia were found in the RIL 40 (3.8) and RIL11 (1.3) in the present study.

Number of sympodia per plant

The average number of sympodia per plant was 9.76. The observed range of sympodia per plant in the population were 5.90 (RIL 22) and 14.50 (RIL 90). The lines viz., RIL90 (14.5), RIL16 (13.05), RIL41 (12.9), RIL54 (12.85), RIL26 (12.75), RIL98 (12.7), RIL 11 (12.6), RIL1 (12.5), RIL104 (12.5), RIL100 (12.4) seemed promising for the trait.

Number of bolls per plant

The RIL54 (41.5), RIL90 (38), RIL207 (37), RIL11 (35.7), RIL16 (34.7), RIL15 (34.25), RIL43 (33.3), RIL10 (33.1), RIL12 (32.9) and RIL98 (32.7) registered maximum number of bolls per plant. The average number of bolls per plant in the population was 21.46. The RIL 195 (10.90) showed the least number of bolls per plant.

Seed cotton yield per plant

The average seed cotton yield per plant of RIL population was 60.37g with a range of 15.70 g (RIL 144) and 135.00 g (RIL 54). The top RILs with more seed cotton yield per plant were RIL54 (135 g), RIL90 (122.5 g), RIL207 (110 g), RIL92 (107.2 g), RIL108 (101.6 g), RIL138 (100.2 g), RIL53 (96.7 g), RIL39 (94.75 g), RIL43 (93.4 g) and RIL109 (92.8 g) for the trait.

Seed index

Some of promising lines for seed index were RIL208 (8.9 g), RIL163 (8.55 g), RIL203 (8.54 g), RIL179 (8.05 g), RIL52 (7.95 g), RIL194 (7.91 g), RIL53 (7.81 g), RIL76 (7.8 g), RIL87 (7.67 g) and RIL169 (7.66 g). The average seed index of the population was 6.54 g with a minimum value of 4.88g (RIL 271) and maximum of 8.90 g (RIL 208).

Boll weight

The average boll weight was 2.85g with a range of 1.26 g (RIL18) to 4.92 g (RIL 199). The lines such as RIL199 (4.92 g), RIL79 (4.73 g), RIL213 (4.58 g), RIL176 (4.51 g), RIL216 (4.34 g), RIL146 (4.29 g), RIL50 (4.29 g), RIL180 (4.26 g), RIL139 (4.23 g) and RIL164 (4.18 g) exhibited maximum boll weight.

Ginning outturn (%)

The genotypes viz., RIL31 (42.67), RIL54 (42.45), RIL108 (42.4), RIL186 (42.38), RIL43 (42.3), RIL207 (42.25), RIL208 (42.25), RIL15 (42.22), RIL90 (42.2) and RIL35 (42.18) showed higher ginning outturn in the RIL population evaluated. The RIL 31 had maximum (42.68 %) GOT on contrary to RIL 102 (35.39 %) with an average of 39.26 per cent in population.

Lint index (g)

The average lint index of the population was 4.24g with the line having the minimum of 2.87 g (RIL 101) and the maximum of 6.51 (RIL 54). In the population some of the lines had better lint index namely RIL208 (6.51), RIL203 (5.64), RIL52 (5.5), RIL169 (5.36), RIL161 (5.35), RIL109 (5.35), RIL194 (5.35), RIL53 (5.34), RIL76 (5.32) and RIL213 (5.28)

Upper half mean length

The highest fibre length was recorded by RIL3 (30.9 mm), RIL13 (29.6 mm), RIL67 (28.5 mm), RIL90 (28.4 mm), RIL101 (28.3 mm), RIL218 (28.1 mm), RIL206 (27.95 mm), RIL145 (27.9 mm), RIL17 (27.75 mm) and RIL97 (27.5 mm). The mean UHML of the population was 24.94 mm with the minimum length of 20.40 mm (RIL 24) and maximum of 30.90 mm (RIL 3).

Fibre strength (g/tex)

The value for fibre strength in RIL population varied between 22.33 g/tex (RIL 1) to 30.63 g/tex (RIL 40) with an average of 25.27 g/tex. The lines found promising for fibre strength were RIL40 (30.63 g/tex), RIL23 (30 g/tex), RIL3 (29.9 g/tex), RIL90 (29.9 g/tex), RIL101 (29.8 g/tex), RIL47 (29.43 g/tex), RIL13 (29.4 g/tex), RIL35 (29.4 g/tex), RIL52 (29.3 g/tex) and RIL63 (29.3 g/tex).

Micronaire value ($\mu\text{g}/\text{inch}$)

The average micronaire value in the population was $3.53 \mu\text{g}/\text{inch}$ with RIL 144 which registered minimum of $2.16 \mu\text{g}/\text{inch}$ and maximum of $4.68 \mu\text{g}/\text{inch}$ by RIL 107. The RILs 144 ($2.16 \mu\text{g}/\text{inch}$), RIL195 ($2.21 \mu\text{g}/\text{inch}$), RIL141 ($2.27 \mu\text{g}/\text{inch}$), RIL13 ($2.41 \mu\text{g}/\text{inch}$), RIL15 ($2.57 \mu\text{g}/\text{inch}$), RIL78 ($2.72 \mu\text{g}/\text{inch}$), RIL73 ($2.73 \mu\text{g}/\text{inch}$), RIL206 ($2.74 \mu\text{g}/\text{inch}$), RIL142 ($2.77 \mu\text{g}/\text{inch}$), RIL64 ($2.78 \mu\text{g}/\text{inch}$) also furnished better micronaire value.

Uniformity index

The lines like RIL3 (94.4 %), RIL1 (87.6 %), RIL20 (87.3 %), RIL5 (87.1 %), RIL15 (85.3 %), RIL24 (83.6 %), RIL11 (83.1 %), RIL17 (83 %), RIL21 (82.9 %), RIL27 (82.6 %) had better UI in the population. The average uniformity index of the population was 75.67 per cent with minimum value of 58.20 per cent (RIL 203) and maximum of 94.40 per cent (RIL 3).

Maturity ratio

The RIL 107 exhibited maximum (0.78) maturity ratio while, RIL 195 (0.29) showed minimum maturity ratio. The average performance of population was 0.57. The RIL107 (0.78), RIL155 (0.77), RIL53 (0.73), RIL178 (0.73), RIL156 (0.72), RIL184 (0.72), RIL36 (0.71), RIL39 (0.71), RIL90 (0.71) and RIL167 (0.71) had better performers *w.r.t* traits.

Fibre elongation length

The mean value of FEL in RIL population was 5.03 % with a range of 4.00 % (RIL 4) to 6.60 % (RIL 26). Some of the lines like RIL26 (6.6 %), RIL28 (6.6 %), RIL1 (6.5 %), RIL3 (6.2 %), RIL13 (6.2 %), RIL12 (6 %), RIL15 (6 %), RIL22 (6 %), RIL25 (6 %) and RIL9 (5.9 %) had better fibre elongation length.

4.8 Identification of superior recombinant inbred lines (RIL) over the check varieties

The trait performance of seed cotton yield per plant, ginning outturn, upper half mean length and fibre strength, production and processing point were considered for

identification of superior RILs in the population over the commercial check varieties MCU 5 and Sahana employed in the present study.

Seed cotton yield per plant (g)

The seed cotton yield per plant of the superior lines was in the range of 81.1 g to 135gm. A total of 31 RILs (Table 30) were found significantly superior over the best commercial check Sahana (80gm/plant). RIL54 (135 g), RIL90 (122.5 g), RIL207 (110 g), RIL92 (107.2 g), RIL108 (101.6 g), RIL138 (100.2 g), RIL53 (96.7 g), RIL39 (94.75 g), RIL43 (93.4 g) and RIL109 (92.8 g) were some of significant RILs evaluated in the present study.

Ginning outturn (%)

The ginning outturn of the superior lines diverged between 41.07 and 42.65 per cent. A total of 32 RILs (Table 31) were found significantly superior over the best commercial check MCU 5 (40.2 %) variety. The RIL 31 (42.68%), RIL 54 (42.45 %), RIL 108 (42.40%), RIL 186 (42.38%), RIL 43 (42.30%) and RIL 207 (42.25%) were promising lines for ginning outturn (Table 31).

Upper half mean length

The variety MCU 5 (29.10mm) was considered the check line. Here only two lines were superior over the check variety viz., RIL 3 and RIL 13 lines had the upper half mean length of 30.9mm and 29.60 mm respectively. The rest of listed lines were non significant with check variety but promising lines (Table 32).

Fibre strength

Out of 222 lines 33 lines were superior over the check MCU 5 variety (28.10 g/tex). The line RIL 40 (30.63 g/tex) had the highest fibre strength. The recombinant inbred lines like RIL40 (30.63 g/tex), RIL23 (30 g/tex), RIL3 (29.9 g/tex), RIL90 (29.9 g/tex), RIL101 (29.8 g/tex), RIL47 (29.43 g/tex), RIL13 (29.4 g/tex), RIL35 (29.4 g/tex), RIL52 (29.3 g/tex) and RIL63 (29.3 g/tex) were some of significant lines for fibre strength (Table 33).

Table 30: List of significantly superior lines over check variety for seed cotton yield per plant in RIL population of *G. hirsutum*

RIL	PH	NMP	NSP	NBP	SCYP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL
54	137.70	2.60	12.85	41.50	135.00	5.61	3.27	42.45	4.13	26.40	25.90	3.12	78.80	0.52	4.60
90	104.00	3.00	14.50	38.00	122.50	7.02	3.22	42.20	5.13	28.40	29.90	4.26	77.00	0.71	4.80
207	122.50	3.00	8.50	37.00	110.00	5.67	2.99	42.25	4.15	26.40	25.80	3.44	76.80	0.57	4.90
92	126.90	2.10	12.10	30.20	107.20	6.90	3.54	42.15	5.03	24.90	25.10	3.54	72.50	0.59	5.10
108	110.30	2.60	11.00	30.80	101.60	6.29	3.34	42.40	4.63	23.55	24.93	4.21	75.00	0.62	5.20
138	128.60	2.10	9.40	24.30	100.20	6.59	4.16	42.15	4.80	24.80	25.10	3.69	81.30	0.61	4.50
53	148.40	2.30	10.80	32.30	96.70	7.82	2.98	40.45	5.34	26.10	25.70	4.39	78.60	0.73	5.50
39	99.38	3.25	9.63	31.25	94.75	6.79	3.03	41.85	4.88	23.80	22.80	4.26	77.70	0.71	4.90
43	108.30	2.10	9.85	33.30	93.40	6.65	2.82	42.30	4.87	24.30	25.40	4.19	78.70	0.70	5.00
109	110.00	3.20	10.00	24.90	92.80	7.36	3.73	42.10	5.35	24.55	25.23	4.22	72.60	0.62	5.00
10	110.60	2.60	12.30	33.10	92.70	5.82	2.81	41.40	4.11	23.85	25.13	3.29	58.40	0.47	5.70
104	145.90	1.90	12.50	27.40	92.40	6.92	3.37	40.74	4.77	25.25	25.73	3.64	73.80	0.52	5.00
11	114.10	2.90	12.60	35.70	91.70	6.72	2.57	41.16	4.70	22.80	22.90	3.47	83.10	0.58	5.70
194	125.90	2.70	9.70	22.40	91.50	7.92	4.07	40.30	5.35	26.00	25.80	3.91	76.20	0.65	4.60
139	133.10	2.50	11.00	21.70	90.40	6.46	4.24	41.16	4.51	23.55	25.33	3.70	80.70	0.53	5.50
107	118.10	2.80	11.30	30.10	89.40	6.09	2.98	41.95	4.40	23.50	22.70	4.68	75.80	0.78	5.20
98	114.60	2.60	12.70	32.70	87.80	7.14	2.70	40.13	4.80	24.75	25.33	3.55	72.80	0.51	5.10
12	103.90	2.50	10.80	32.90	86.80	6.67	2.62	40.12	4.53	22.30	22.80	3.17	81.40	0.53	6.00

Contd.....

RIL	PH	NMP	NSP	NBP	SCYP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL
179	130.20	2.60	10.30	21.60	85.70	8.06	3.96	39.33	5.25	25.90	25.90	3.71	77.90	0.62	4.90
93	108.10	2.70	11.40	29.10	84.90	6.38	2.94	40.45	4.34	26.05	28.83	3.96	75.90	0.58	5.90
213	137.00	2.40	8.20	18.40	84.20	7.41	4.58	41.71	5.28	24.90	25.60	3.39	78.30	0.56	4.80
8	130.90	2.60	11.60	28.00	83.90	7.62	2.98	40.21	5.19	22.90	25.00	3.55	81.50	0.59	5.70
91	106.80	2.20	10.20	26.13	83.70	6.60	3.21	39.91	4.38	26.10	25.20	3.61	75.00	0.60	5.00
210	112.20	2.50	9.50	24.50	83.40	7.48	3.47	40.15	5.03	23.30	22.90	4.11	76.00	0.68	4.80
29	110.25	2.60	9.60	31.00	83.05	6.65	2.69	36.48	3.84	25.60	25.30	2.82	80.30	0.47	5.10
16	126.50	2.30	13.05	34.70	82.70	7.22	2.37	38.24	4.39	22.70	25.40	3.68	80.80	0.61	5.50
64	116.00	2.20	9.30	22.20	82.50	6.60	3.89	39.45	4.31	26.40	25.90	2.78	69.60	0.46	4.70
182	132.50	2.60	10.60	26.30	82.10	6.07	3.10	37.75	3.68	26.10	25.60	3.74	78.00	0.62	5.00
14	96.00	2.85	12.25	30.60	82.05	6.83	2.66	38.75	4.33	24.40	25.20	3.05	81.50	0.51	5.50
15	85.75	2.75	10.50	34.25	81.20	5.32	2.38	42.23	3.89	26.20	29.10	2.57	85.30	0.43	6.00
79	114.40	2.70	9.80	17.10	81.10	6.57	4.74	39.60	4.32	23.80	22.80	3.62	71.70	0.60	4.80
MCU 5	120.40	2.60	10.40	20.60	75.00	6.50	3.75	40.20	4.36	29.10	28.10	3.78	83.45	0.59	5.81
SAHA NA	118.40	2.40	10.80	22.00	80.00	6.80	4.20	39.60	4.45	27.10	27.10	4.49	82.87	0.56	8.80

Where, PH= plant height (cm), NMP= number of monopodia per plant, NSP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value ($\mu\text{g}/\text{inch}$), FUI = Fibre uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).

Table 31: List of significantly superior lines over check variety for ginning outturn in RIL population of *G. hirsutum*

RIL	PH	NMP	NSP	NBP	SCYP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL
31	109.17	1.83	8.83	21.58	46.58	5.93	2.16	42.68	4.41	23.40	25.10	3.24	77.20	0.54	4.90
54	137.70	2.60	12.85	41.50	135.00	5.61	3.27	42.45	4.13	26.40	25.90	3.12	78.80	0.52	4.60
108	110.30	2.60	11.00	30.80	101.60	6.29	3.34	42.40	4.63	23.55	24.93	4.21	75.00	0.62	5.20
186	107.50	2.30	9.00	12.10	27.10	6.97	2.22	42.38	5.12	25.50	25.50	3.30	74.90	0.55	5.10
43	108.30	2.10	9.85	33.30	93.40	6.65	2.82	42.30	4.87	24.30	25.40	4.19	78.70	0.70	5.00
207	122.50	3.00	8.50	37.00	110.00	5.67	2.99	42.25	4.15	26.40	25.80	3.44	76.80	0.57	4.90
208	137.10	3.30	9.30	27.30	76.30	8.90	2.78	42.25	6.51	25.05	25.63	3.37	77.60	0.48	5.30
15	85.75	2.75	10.50	34.25	81.20	5.32	2.38	42.23	3.89	26.20	29.10	2.57	85.30	0.43	6.00
90	104.00	3.00	14.50	38.00	122.50	7.02	3.22	42.20	5.13	28.40	29.90	4.26	77.00	0.71	4.80
35	113.20	2.30	11.00	19.40	40.40	7.22	2.04	42.19	5.28	27.30	29.40	3.52	73.30	0.58	4.90
92	126.90	2.10	12.10	30.20	107.20	6.90	3.54	42.15	5.03	24.90	25.10	3.54	72.50	0.59	5.10
138	128.60	2.10	9.40	24.30	100.20	6.59	4.16	42.15	4.80	24.80	25.10	3.69	81.30	0.61	4.50
109	110.00	3.20	10.00	24.90	92.80	7.36	3.73	42.10	5.35	24.55	25.23	4.22	72.60	0.62	5.00
107	118.10	2.80	11.30	30.10	89.40	6.09	2.98	41.95	4.40	23.50	22.70	4.68	75.80	0.78	5.20
39	99.38	3.25	9.63	31.25	94.75	6.79	3.03	41.85	4.88	23.80	22.80	4.26	77.70	0.71	4.90
36	93.80	3.10	8.10	24.30	52.40	5.56	2.12	41.75	3.98	24.80	22.70	4.29	75.80	0.71	4.80
213	137.00	2.40	8.20	18.40	84.20	7.41	4.58	41.71	5.28	24.90	25.60	3.39	78.30	0.56	4.80
190	105.70	1.80	8.60	17.40	45.70	6.57	2.58	41.69	4.67	24.05	22.63	2.92	68.80	0.40	4.00

Contd.....

RIL	PH	NMP	NSP	NBP	SCYP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL
38	117.70	2.50	10.50	19.50	42.10	6.73	2.13	41.50	4.77	24.60	25.50	3.78	75.80	0.63	4.90
161	135.40	2.60	10.90	21.30	77.70	7.61	3.66	41.49	5.35	24.05	22.73	4.25	71.00	0.63	5.00
105	119.00	2.60	11.60	20.40	69.70	5.93	3.41	41.43	4.19	22.60	22.70	3.52	75.50	0.58	5.10
10	110.60	2.60	12.30	33.10	92.70	5.82	2.81	41.40	4.11	23.85	25.13	3.29	58.40	0.47	5.70
159	113.70	2.50	10.10	24.20	68.30	5.51	2.80	41.37	3.89	23.90	22.80	3.92	74.50	0.65	4.60
83	125.30	2.50	7.80	20.33	39.10	6.57	1.94	41.35	4.63	22.90	22.80	3.74	72.00	0.62	4.80
72	112.20	2.10	8.60	16.20	38.30	7.19	2.47	41.34	5.07	24.90	25.00	3.36	75.00	0.56	4.80
88	111.50	2.20	8.90	15.40	50.70	6.48	3.29	41.18	4.54	25.90	25.90	3.78	76.30	0.63	5.20
11	114.10	2.90	12.60	35.70	91.70	6.72	2.57	41.16	4.70	22.80	22.90	3.47	83.10	0.58	5.70
139	133.10	2.50	11.00	21.70	90.40	6.46	4.24	41.16	4.51	23.55	25.33	3.70	80.70	0.53	5.50
116	131.60	2.80	11.80	21.40	75.20	6.63	3.57	41.15	4.66	24.90	25.20	3.90	74.80	0.65	4.70
169	130.40	2.30	9.80	16.30	64.90	7.66	4.11	41.11	5.36	25.90	25.60	3.72	72.10	0.62	4.50
21	116.50	2.30	10.70	21.80	58.60	6.60	2.79	41.10	4.61	25.20	25.60	4.05	82.90	0.67	5.80
157	128.60	2.20	10.80	15.30	43.10	6.53	2.83	41.08	4.54	25.10	25.40	3.83	73.90	0.64	4.90
MCU 5	120.40	2.60	10.40	20.60	75.00	6.50	3.75	40.20	4.36	29.10	28.10	3.78	83.45	0.59	5.81
SAHAN A	118.40	2.40	10.80	22.00	80.00	6.80	4.20	39.60	4.45	27.10	27.10	4.49	82.87	0.56	8.80

Where, PH= plant height (cm), NMP= number of monopodia per plant, NSP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value (µg/inch), FUI = Fibre uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).

Table 32: List of significantly superior lines over check variety for fibre strength in RIL population of *G. hirsutum*

RIL	PH	NMP	NSP	NBP	SCYP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL
40	94.40	3.80	9.40	14.40	39.60	6.81	2.75	40.65	4.67	26.55	30.63	3.52	82.10	0.50	5.40
23	107.00	2.10	8.80	24.80	52.30	5.00	2.12	39.26	3.23	26.90	30.00	3.66	78.00	0.61	5.00
90	104.00	3.00	14.50	38.00	122.5	7.02	3.22	42.20	5.13	28.40	29.90	4.26	77.00	0.71	4.80
3	122.30	2.30	11.80	29.60	77.00	5.72	2.66	40.20	3.85	30.90	29.90	3.19	94.40	0.54	6.20
101	119.60	2.60	11.80	18.30	39.00	6.65	2.13	35.72	3.70	28.30	29.80	3.22	74.00	0.53	5.50
47	129.10	2.70	9.70	31.70	70.40	6.55	2.23	35.98	3.69	24.35	29.43	3.35	78.20	0.48	5.00
35	113.20	2.30	11.00	19.40	40.40	7.22	2.04	42.19	5.28	27.30	29.40	3.52	73.30	0.58	4.90
13	102.63	2.37	9.25	24.67	61.93	7.01	2.51	38.46	4.38	29.60	29.40	2.41	81.60	0.40	6.20
52	123.50	2.60	9.30	20.20	51.30	7.95	2.53	40.90	5.50	26.00	29.30	3.40	74.00	0.56	5.20
63	109.20	2.60	8.80	24.00	75.70	6.62	3.17	38.62	4.16	27.20	29.30	3.16	78.80	0.52	5.20
67	125.00	3.00	8.80	18.70	51.70	6.75	2.79	38.13	4.15	28.50	29.30	3.58	75.40	0.59	5.30
111	118.17	1.97	10.77	15.47	40.53	7.45	2.63	39.58	4.94	25.40	29.20	3.51	78.80	0.58	5.60
173	122.40	1.68	10.20	18.60	54.80	5.44	3.05	39.01	3.48	26.30	29.20	3.32	74.90	0.55	5.10
27	103.00	2.60	11.20	28.80	60.40	5.62	2.14	38.55	3.52	24.40	29.20	3.04	82.60	0.50	5.00
145	108.40	1.90	9.90	21.20	52.30	7.00	2.48	37.43	4.20	27.90	29.20	3.16	73.50	0.52	5.00
28	113.50	2.10	11.40	22.50	46.40	6.89	2.06	36.67	3.99	26.10	29.20	3.13	80.30	0.52	6.60
15	85.75	2.75	10.50	34.25	81.20	5.32	2.38	42.23	3.89	26.20	29.10	2.57	85.30	0.43	6.00
199	117.00	2.40	7.80	14.40	70.90	5.65	4.92	40.63	3.87	24.80	29.10	3.54	76.00	0.59	5.00

Contd.....

RIL	PH	NMP	NSP	NBP	SCYP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL
140	142.00	2.35	9.90	19.90	56.30	6.59	2.84	40.61	4.50	25.90	29.10	3.07	76.00	0.51	5.50
49	121.83	2.57	8.93	19.93	38.90	5.88	2.03	39.85	3.89	27.20	29.10	3.85	75.50	0.64	5.50
183	118.70	2.10	10.10	22.05	42.40	7.32	1.91	39.85	4.84	26.10	29.10	3.36	75.30	0.56	5.20
203	112.30	2.40	9.10	19.20	64.80	8.55	3.37	39.76	5.64	22.70	29.10	3.64	58.20	0.60	5.20
200	111.60	2.20	7.90	16.20	33.30	6.22	1.98	39.23	4.02	25.70	29.10	3.21	76.50	0.53	5.00
42	116.20	1.80	10.90	19.70	37.10	6.73	1.85	38.22	4.16	26.90	29.10	3.81	73.10	0.63	5.00
222	117.10	2.90	8.45	17.90	63.10	6.74	3.54	39.17	4.34	24.40	29.00	3.50	79.40	0.58	5.60
100	106.90	1.90	12.40	21.00	52.30	6.49	2.47	37.44	3.88	25.90	29.00	3.24	78.40	0.54	5.80
195	126.10	2.80	9.30	10.90	24.30	5.81	2.27	39.78	3.85	26.95	28.93	2.21	72.30	0.29	4.70
65	105.20	2.30	8.50	17.30	45.00	5.89	2.64	39.77	3.90	26.55	28.93	4.14	75.50	0.61	5.10
50	124.60	3.00	8.90	17.75	75.90	7.33	4.29	38.34	4.56	26.75	28.93	3.50	75.40	0.50	4.90
206	116.30	2.00	8.30	18.90	37.20	6.84	2.00	36.32	3.90	27.95	28.93	2.74	74.40	0.38	4.80
93	108.10	2.70	11.40	29.10	84.90	6.38	2.94	40.45	4.34	26.05	28.83	3.96	75.90	0.58	5.90
216	134.00	2.00	8.90	16.60	71.00	6.64	4.35	39.93	4.36	26.75	28.83	3.47	73.50	0.50	5.30
57	107.50	2.80	8.20	20.20	70.70	6.23	3.50	39.23	4.02	24.65	28.83	3.89	79.70	0.57	5.20
MCU 5	120.4	2.6	10.4	20.6	75	6.5	3.75	40.2	4.36	29.10	28.1	3.78	83.45	0.59	5.81
SAHANA	118.4	2.4	10.8	22	80	6.8	4.2	39.6	4.45	27.10	27.1	4.49	82.873	0.56	8.8

Where, PH= plant height (cm), NMP= number of monopodia per plant, NSP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value (µg/inch), FUI = Fibre uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).

Table 33: List of superior lines over check variety for upper half mean length (UHML) in RIL population of *G. hirsutum*

	PH	NMP	NSP	NBP	SCYP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL
3*	122.30	2.30	11.80	29.60	77.00	5.72	2.66	40.20	3.85	30.90	29.90	3.19	94.40	0.54	6.20
13*	102.63	2.37	9.25	24.67	61.93	7.01	2.51	38.46	4.38	29.60	29.40	2.41	81.60	0.40	6.20
67	125.00	3.00	8.80	18.70	51.70	6.75	2.79	38.13	4.15	28.50	29.30	3.58	75.40	0.59	5.30
90	104.00	3.00	14.50	38.00	122.5	7.02	3.22	42.20	5.13	28.40	29.90	4.26	77.00	0.71	4.80
101	119.60	2.60	11.80	18.30	39.00	6.65	2.13	35.72	3.70	28.30	29.80	3.22	74.00	0.53	5.50
218	120.50	1.80	8.60	15.70	58.10	6.30	3.69	39.33	4.08	28.10	25.40	3.13	73.90	0.52	4.80
206	116.30	2.00	8.30	18.90	37.20	6.84	2.00	36.32	3.90	27.95	28.93	2.74	74.40	0.38	4.80
145	108.40	1.90	9.90	21.20	52.30	7.00	2.48	37.43	4.20	27.90	29.20	3.16	73.50	0.52	5.00
17	108.10	2.80	10.00	30.20	57.70	7.06	1.90	38.82	4.47	27.75	25.53	2.87	83.00	0.40	5.80
97	130.50	3.15	11.10	18.00	43.60	7.16	2.41	38.40	4.46	27.50	25.70	3.50	75.10	0.58	5.00
86	96.30	2.20	9.10	19.40	62.40	6.20	3.31	39.39	4.01	27.40	25.40	3.38	76.50	0.56	4.60
35	113.20	2.30	11.00	19.40	40.40	7.22	2.04	42.19	5.28	27.30	29.40	3.52	73.30	0.58	4.90
63	109.20	2.60	8.80	24.00	75.70	6.62	3.17	38.62	4.16	27.20	29.30	3.16	78.80	0.52	5.20
49	121.83	2.57	8.93	19.93	38.90	5.88	2.03	39.85	3.89	27.20	29.10	3.85	75.50	0.64	5.50
197	118.20	2.40	8.30	23.20	78.70	5.95	3.40	40.43	4.06	27.00	25.90	3.64	75.30	0.60	4.80
176	131.60	2.10	9.40	15.40	69.70	7.42	4.51	36.85	4.32	27.00	25.60	4.02	75.40	0.67	4.50
MCU 5	120.4	2.6	10.4	20.6	75	6.5	3.75	40.2	4.36	29.10	28.1	3.78	83.45	0.59	5.81
SAHANA	118.4	2.4	10.8	22	80	6.8	4.2	39.6	4.45	27.10	27.1	4.49	82.87	0.56	8.8

Where, * - significant superior RIL, PH= plant height (cm), NMP= number of monopodia per plant, NSP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value ($\mu\text{g}/\text{inch}$), FUI = Fibre uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).

5. DISCUSSION

In this section, the results obtained from the present study are discussed under various headings as follows.

- 5.1 Analysis of variance
- 5.2 Identification of QTLs for yield and fibre quality traits
 - 5.2.1 Trait performance of RIL population and its parents
 - 5.2.2 Parental polymorphism
 - 5.2.3 Linkage Analysis and map construction
 - 5.2.4 Segregation distortion
 - 5.2.5 QTL mapping for yield and fibre quality traits
- 5.3 Genetic variability parameters for yield and yield attributes and fibre quality traits
- 5.4 Character association and path analysis in the RIL population
- 5.5 Intergeneration correlation and regression between the F_4 vs F_5 and F_5 Vs F_6 generation
- 5.6 Identification of transgressive segregants in RIL population
- 5.7 Identification superior lines over the commercial variety
- 5.8 Identification of superior recombinant inbred lines based on *per se* performance

5.1 Analysis of variance

All the Recombinant Inbred Lines (RILs) displayed considerable differences in the mean performance for all the observed characters viz., plant height (cm), number of monopodia branches per plant, number of sympodia branches per plant, number of bolls per plant, seed cotton yield per plant (g), seed index (g), boll weight (g), lint index (g), ginning outturn (%), fibre strength (g/tex), fibre length (mm), micronaire value ($\mu\text{g}/\text{inch}$), maturity ratio (%), fibre elongation length (%) and fibre uniformity index (%). The genotypic mean sum of square exhibited significant difference for all traits in

the present study (Table 14), which suggested that the derived RILs from RHAP 12 and RHAP 15 possessed considerable amount of variation among them.

5.2 Identification of QTLs for yield, yield attributes and fibre quality traits

A lot of research attention is paid to improve the fibres quality and yield improvement to *G.hirsutum* (Wakelyn and Chaudhry, 2010). The genetic mapping and identification of Quantitative Trait Loci (QTL) for complex traits could lay the solid foundation for marker-assisted breeding and map-based cloning (Wakelyn and Chaudhry, 2010). In the present study, an effort has been made to construct linkage map employing Sequence Related Amplified Polymorphism (SRAP) and Target Region Amplified Polymorphism (TRAP) markers in the intraspecific cotton (*G. hirsutum* × *G. hirsutum*)

5.2.1 Trait performance in the parents and RIL population

Through intraspecific hybridization between the two upland cotton lines viz., RHAP 12 and RHAP 15, a maximum of 222 recombinant inbred lines were generated. The single boll descent method from F₂ onwards was employed to produce the RIL population (Schneider, 2005). The Recombinant inbred lines (RILs) are set of homozygous lines produced by continuous inbreeding/selfing of individual F₂ plants (Burr *et al.*, 1988). Continuous selfing leads to development of RILs which achieve homozygousness so that they can be maintained indefinitely (Darvasi and Soller, 1995) and hence, RILs are essentially a perpetual or permanent mapping population. The term perpetual population is preferable over immortal population as biological entity is not indeed immortal (Burr *et al.*, 1988). The RIL population assists in understanding the additive and additive×additive gene action. The cotton crop is an essentially a self pollinated crop and shows very marginal inbreeding depression which is an open the gate for development of RIL population in cotton (<http://www.ncagr.gov/pollinators/documents/DominicReisigNCPollinatorProtectionPlanCotton.pdf>).

The agronomic and fibre quality characters like plant height (cm), number of monopodia per plant, number of sympodia per plant, number of bolls per plant, seed cotton yield per plant (g), seed index (g), boll weight (g), lint index (g), ginning out turn

(%), fibre strength (g/text), fibre length (mm), micronaire value ($\mu\text{g}/\text{inch}$), maturity ratio (%), fibre elongation length (%) and fibre uniformity ratio (%) were assessed in parents and its derived RILs population (Table 15). The parent should be contrastingly different to each other for the trait of interest which is the first basic rule in the development of mapping population (McDonald, J. H., 2008). Hence, a t-test was conducted to determine the significant difference between the means of two parents (RHAP 12 and RHAP 15) for agronomic and quality traits. All the characters considered in the present study showed significant difference between the parents except number of monopodia per plant, number of sympodia per plant and fibre elongation length. The parents were highly contrasting for seed cotton yield per plant and fibre strength. Hence, in the present investigation, for QTL mapping, all traits which showed significant difference between the parents were considered.

The average performance of agronomic and fibre quality of the RIL population was intermediate between parental performances (Table 15). Based on the maximum and minimum value, the population registered transgressive segregants on both sides *i.e.* either superiority or inferiority. The heritability and correlation of various traits in the population discussed under the sections 5.3 and 5.4 respectively (Tables 22 and 23) (Yu *et al.*, 2013). The traits exhibited high heritability and possessed high precision in QTL identification (Viana *et al.*, 2016). The correlation assists to know clustering nature of QTLs. Before considering a trait's phenotypic value for QTL mapping, there should exist normal distribution for the trait and hence, the kurtosis and skewness for each trait in the population are calculated to determine whether the normal distribution exists for the traits. These two statistical tests provide an insight into the distribution of recombinant inbred lines in the population (Groeneveld and Meeden, 1984). All the characteristics were fairly (0 to -0.5 or 0 to 0.5) and slightly (-0.5 to -1 or 0.5 to < 1) symmetrical depending on the skewedness value except fibre elongation length (Table 15 and Fig.5). The negative skewness value was shown to skew data to the left and positive sign was shown to skew data to the right of the mean of the population (Groeneveld and Meeden, 1984). The kurtosis shows the degree of normal curve peakness. Except fibre uniformity index, all the traits had kurtosis value of less than 3 which indicated that the maximum value of the curve was less than normal distribution along with the positive sign which indicated that curve was tall and thin. While

population fibre uniformity index follows the platy kurtosis *i.e.* flat curve (Groeneveld and Meeden, 1984). Therefore, on the basis of t test and skewness test, 12 traits were considered for the present QTL analysis of the RILs population generated.

There are numerous studies in cotton using the RIL population to identify QTLs of fibre quality, yield and its components (Wang *et al.*, 2006; Shen *et al.*, 2007; Wang *et al.*, 2007; Lacape *et al.*, 2009; Zhang *et al.*, 2009; Tan *et al.*, 2014; Liu *et al.*, 2015; Wang, *et al.*, 2015; Shang *et al.*, 2015; Zhang *et al.*, 2015; Hantao *et al.*, 2015; Jamshed *et al.*, 2016; Li *et al.*, 2016; Jia *et al.*, 2016; Zhang *et al.*, 2017). They concluded that the RIL population assists to build fine QTL mapping along with the major and minor QTLs determination.

5.2.2 Parent polymorphism

It is difficult to identify polymorphism in intra-specific hybridization as the presence of fixed homozygous blocks and parents by descent was identical (Fang *et al.*, 2014). The new marker systems such as Sequence Related Amplified Polymorphism (SRAP) and Target Region Amplified Polymorphism (TRAP) were employed to ameliorate the problem. A total of 153 SRAP and 263 TRAP markers were engaged to identify the polymorphism in the parents (RHAP 12 and RHAP 15). The SRAP and TRAP markers generate multiple bands ranging from one to four (Plate 5 and 6). The Sequence Related Amplified Polymorphism (SRAP) and Target Region Amplified Polymorphism (TRAP) markers produced 79 and 67 polymorphic loci respectively in the present investigation (Tables 16 and 17). On an average of 0.51 and 0.31 polymorphic loci per primer combination were observed by employment of SRAP and TRAP markers respectively. Similarly Yu *et al.* (2007) constructed a high-density linkage map of cultivated allotetraploid cotton based on SSR, TRAP, SRAP and AFLP markers. He observed that per pair of SSR produced 0.32 polymorphism where as SRAP and TRAP procuced 0.98 and 2.1 polymorphic loci between the parents. Hence SRAP and TRAP marker yields high polymorphism as compared to other markers (Guo *et al.*, 2014).

Lin *et al.*, 2005, Wang *et al.*, 2006, He *et al.*, 2007 and Zhang *et al.*, 2009 employed either SRAP or TRAP markers for linkage mapping and QTL identification in cotton. This was the first attempt to combine the SRAP and TRAP marker to build

the linkage map in the RIL population of cotton. Li and Quiros (2001), Jin *et al.* (2007), Li *et al.* (2007), Jin *et al.* (2007), Chu *et al.* (2008), Shridar *et al.* (2008), Yue, *et al.* (2008), Menzo *et al.* (2013), Guo *et al.* (2014), Guo *et al.* (2014), Ashok and Gerald, (2015) Guindon *et al.* (2016) used either SRAP or TRAP markers in isolation for construction of linkage map of various crops other than cotton and concluded that SRAP and TRAP markers yield high polymorphism as compared to other marker systems.

5.2.3 Linkage Analysis and map construction

A genetic map was established by a set of 146 polymorphic markers by genotyping in 222 RILs (Plate 7). A linkage map was constructed by using *QTL IciMapping* v. 3.2 software (<https://www.integratedbreeding.net>) in which linkage groups were created at a threshold LOD (Logarithm of Odds) score of 3 and the marker order was determined by maximum likelihood mapping algorithm (Fig. 6). The Kosambi mapping function measured the recombination fraction which was converted to centimorgan. (Lander *et al.*, 1987).

The number of markers harbored on linkage groups varied from 1 (LG 18) to 26 (LG1). The 146 marker were anchored on 18 linkage groups with genome coverage of 2910.81 cM (Table 18 and Fig. 6). In the present investigation, only 18 linkage groups could be established instead of 26 *i.e.* haploid chromosome number of cotton. This may be due to uneven distribution of polymorphic markers on the chromosome and the recombination frequency which is not equal along the chromosome (Semagn, *et al.*, 2006). In this study linkage map covered the 75.52 per cent of total cotton genome. The incomplete genome coverage was due to low nucleotide diversity among parents (Zhang, *et al.*, 2009; Ning *et al.*, 2014 and Tang, *et al.*, 2015).

The highest numbers of markers were harbored by LG 1 which spanned a distance of 461.74 cM with an average distance of 17.76 cM between the neighboring markers (Fig. 7). The linkage group 18 had only one marker (me8-em2b1000B), which indicated that marker me8-em2b1000B was not linked to any other markers utilized in the study (Zhang, *et al.*, 2009). The LG 3 and LG 7 markers were densely distributed with an average distance of 11.70 cM and 13.89 cM respectively between the adjacent pairs of markers (Table 18). In the present linkage map constructed the SRAP and

TRAP markers were evenly distributed with less clustering, within and among the linkage group (Lin *et al.*, 2005). The SRAP markers were distributed throughout the genome with wider genome coverage. It indicated that SRAP markers strengthened the linkage map and assisted in construction of high density map (Li and Quiros, 2001; Lin *et al.*, 2005; Guo *et al.*, 2014, Guindon *et al.*, 2016; Nadeem *et al.*, 2017). In some of the linkage groups TRAP marker was distributed between the SRAP markers which indicate that TRAP markers might have role in the filling of gaps in the linkage map generating high density linkage map (Menzo *et al.*, 2013).

Interestingly in the present study, SRAP and TRAP markers showed independent distribution in the linkage map synthesized. Several linkage groups viz., LG 13, LG 14, LG 15, LG 16 and LG 17 solely comprised of TRAP markers while, LG 8 and LG 9 and LG 18 comprised of SRAP markers alone. Lin *et al.* (2005) found a similar phenomenon in a study which involved construction of cotton linkage map when SRAP markers were employed along with other markers.

Wang *et al.* (2006), Wang *et al.* (2007) and Zhang *et al.* (2009) constructed the intraspecific cotton linkage map employing SRAP marker. He *et al.* (2007) used the SRAP marker in conjunction with other markers to establish the linkage map derived from interspecific hybridization. Only one study was reported where TRAP markers were utilized to build a linkage map in interspecific hybridization derived population of cotton (Ashok and Gerald, 2015). Michael *et al.* (2014), Tan *et al.* (2014), Tang *et al.* (2014), Xia *et al.* (2014), Hantao *et al.* (2015), Liu *et al.* (2015), Wang, *et al.* (2015), Shang *et al.* (2015), Zhang *et al.* (2015), Zhunget *et al.* (2015), Ashok and Gerald (2015), Jamshed *et al.* (2016), Lianguang *et al.* (2016), Jia *et al.* (2016), Kumar *et al.* (2016), Wang *et al.* (2016), Shu-Wen *et al.* (2016), Zhang *et al.* (2017), Tan *et al.* (2018), Ali *et al.* (2018a), Ayaz *et al.* (2018), Kumar *et al.* (2018), Li *et al.* (2019) and Kuang (2019) constructed linkage maps regardless of the marker and population in cotton.

5.2.4 Segregation distortion

Segregation distortion, in simple terms indicated deviation of observed genotypic frequency from the expected value or the ratios (Lu *et al.*, 2002).). The segregation distortion is a common phenomenon in plant (Xian-Liang *et al.*, 2006) and cotton (Shi *et al.*, 2015). The markers employed in genotyping were tested for expected

Mendelian 1:1 segregation ratio in RIL population through chi square test ($p < 0.05$) (Appendix I). Out of 146 markers, five markers exhibited segregation distortion up to 3.42 per cent (Table 19 and Fig. 9). The markers which showed segregation distortion on the linkage map were viz., me7-em4a400B, me7-em1a700B, me7-em16a350A, me9-em12a200B and me8-em5a250B located at 239.18 cM (LG 1), 74.49 cM (LG 2), 99.4 cM (LG 3), 80.51 cM (LG 6), 0 cM (LG 7) respectively. The SD loci were dispersed on various linkage groups. The single marker analysis suggested that three markers viz., me7-em1a700B, me7-em16a350A and me8-em5a250B significantly distorted out of five distorted markers (Table 20). The distorted loci such as me7-em4a400B and me9-em12a200B deviated towards the parent RHAP 12 while, me7-em1a700B, me7-em16a350A and me8-em5a250B loci deviated towards the parent RHAP 15. Lu *et al.* (2002) reported that distorted markers deviated towards either parent or both of the parents. The existence of the following forces viz., preferential gametal fertilization or gene incompatibility individually or in combination explained 3.42 per cent SD observed in the population (Shappley *et al.*, 1998a; Lacape *et al.*, 2003). The segregation distortion loci ranged from 13.29 to 63.77 per cent while constructing high density maps of cotton RIL populations (Wang *et al.*, 2015; Zhang *et al.*, 2015; Li *et al.*, 2016; Zhang *et al.*, 2017).

In the present study, the observed segregation distortion was very low which might be due to development of RIL population from intraspecific hybridization (*Gossypium hirsutum* × *Gossypium hirsutum*). Shappley *et al.* 1998 and Lacape *et al.* 2003 reported similar findings in the population resulting from intraspecific hybridization which showed less gene incompatibility, chromosome loss and genome dominance as compared to interspecific crosses. Also, Shen *et al.* (2005), Shen *et al.* (2007), Chen *et al.* (2008), Zhang *et al.* (2009), Sun *et al.* (2012), Ning *et al.* (2014) and Tang *et al.* (2015) reported segregation distortion in intraspecific crosses derived populations.

The marker system also influenced the extent of segregation distortion (Loreiux *et al.*, 1995). The SRAP and TRAP markers targeted open reading frame (Hu and Vick, 2003 and Li and Quiros, 2001). The markers which targeted open reading frame have low or negligible segregation distortion. In the present study, none of the TRAP markers generated segregation distortion as TRAP markers were specific to transcriptome region

or open reading frame (Lokeshkumar, 2018 and Vrinda, 2018). Also in the present study, five SRAP markers (me7-em4a400B, me7-em1a700B, me7-em16a350A, me9-em12a200B and me8-em5a250B) experienced very low segregation distortion compared to the previous studies, which utilized other molecular markers (Lin *et al.*, 2005). The studies of Xian-Liang *et al.*, 2007 and Zhang *et al.*, 2010 indicated that segregation distortion had negligible influence on identification of QTLs and hence, the distorted loci were included in the present investigation.

5.2.5 QTL mapping for yield and fibre quality traits

The QTL analysis was done by utilizing the linkage map information and phenotyping data in RIL population, using the *QTL Ici mapping* v. 3.2 software (<https://www.integratedbreeding.net>). The QTLs were identified at a threshold LOD value of 2.5 with the inclusive composite interval mapping method. Based on *t* statistics, kurtosis and skewness, 12 traits out of 15 traits were considered for QTL mapping in the population. The QTLs were identified following traits viz., plant height (*qPH-3-1*), number of bolls per plant (*qNBP-1-1*, *qNBP-3-1*), seed cotton yield per plant (*qSCYP-1-1*, *qSCYP-16-1*), boll weight (*qBWP-1-1*, *qBWP-3-1*, *qBWP-16-1*), fibre strength (*qFS-3-1*, *qFS-13-1*, *qFS-16-1*), upper half mean length (*qUHML-11-1*), micronaire value (*qMic-13-1*), fibre uniformity index (*qFUR-3-1* and *qFUR-3-2*) and maturity ratio (*qMR-13-1*) (Table 21 and Fig. 10).

The above mentioned QTL were distributed on LG 1, LG 3, LG 11, LG13 and LG 16 (Table 21 and Fig.10). A total of 6 QTLs were identified on linkage group 3 for various traits like plant height, number of bolls per plant (1), boll weight (1), fibre strength (1) and uniformity index (2). The linkage group 1 consists of 3 QTLs of number of bolls per plant (1), seed cotton yield per plant (1) and boll weight (1). In total 3 QTL were identified on linkage group 13 which harbored the QTL of fibre strength (1), micronaire value (1) and maturity ratio (1). The linkage group like LG 11 and LG 16 had one QTL each of upper half mean length and seed cotton yield per plant. This indicated that the linkage like LG 3, LG 1, LG 13, LG 11 and LG 16 seemed important and promising linkage group (Table 21).

The information regarding the flanking markers of QTL helps to know the adjacent sequence information of QTL and designated the QTL position with respect to

marker (Gutiérrez *et al.*, 2010; Kushanov *et al.*, 2016; Zhang *et al.*, 2015). The SRAP and TRAP marker targets the open reading frame so the occurrence of type I error in identification of QTL was less (Li *et al.*, 2006). The SRAP marker cover the larger part of the genome and hence helps to identify new and large number of QTLs (Guindon *et al.*, 2016; Nadeem *et al.*, 2017; Li *et al.*, 2006). Out of 16 QTL, 9 QTL were identified between pair of SRAP markers (Fig. 10). The QTLs related to fibre quality were found between the TRAP markers as one of the primer of TRAP marker was derived from the express sequence tag (Fig. 10). The Sequence information was derived from the differential gene expression studies which involved HBS 144 and HBS 187 genotypes, contrastingly different for fibre quality traits (Plate 3). These unigenes which exhibited the differential expression between the genotypes may have role in fibre development (Vrinda, 2018). These specific primers in combination with one of SRAP primers lead to development of TRAP marker (Fig. 3) which found complementary region of interest around the candidate gene of fibre quality traits (Miklas *et al.*, 2006; Lim *et al.*, 2014). These flanking makers which had strong linkage with QTL apart from high LOD values can be used in marker assisted selection and map based cloning.

The genomic regions contain the QTL which governs the variation in quantitative traits and amount of variation in the character that is explained by each QTL can be quantified as phenotypic variation (Burton *et al.*, 2014 and Wang *et al.*, 2016). The phenotypic variation (R^2) expressed from each QTL is given in Table 21. If the phenotypic variation (R^2) of a particular QTL is more than 10 per cent, it can be considered as major QTL and otherwise it can be considered as minor QTL (Burton *et al.*, 2014; Wang *et al.*, 2016; Ma *et al.*, 2019). In the present investigation, a QTL was identified for fibre strength (*qFS-16-1*), seed cotton yield per plant (*qSCYP-16-1*) and boll weight (*qBWP-3-1*) which had phenotypic variation of 18.44 per cent, 16.79 per cent and 12.44 per cent respectively. These three QTL were major QTLs which had major impact on trait expression. Some of the QTL like *qSCYP-1-1*, *qPH-3-1* and *qUHML-11-1* had phenotypic variation of 9.99 per cent, 9.70 per cent and 8.99 per cent respectively, even though these QTL were minor but need to be considered for further studies for validation.

Majority of the QTLs on the linkage group were found in clusters (Table 21 and Fig.10). This QTL clustering phenomenon is due to linkage of genes or QTL or as a result of pleiotropic effect of single QTLs in the same region (Yu *et al.*, 2013). This could be the reason for highly significant correlation among the various traits (Table 23 and 24). These significant correlations among the traits were due to linkage or pleiotropic. For eg., seed cotton yield per plant, number of bolls per plant and boll weight had significant correlation among each other (Table 23 and 24). In the present study, QTLs of these traits clustered on linkage group one (LG1) at 51 cM and another cluster on linkage group 16 (LG 16) at 27 and 29 cM. Also, QTLs of micronaire value and maturity ratio were found on the linkage group 13 at 58 cM and these traits were significantly correlated to each other. The QTL clusters offer the valuable information to establish genome region with different traits. The clustering of QTL in cotton has been reported by Reinisch *et al.*, 1994; Lacape *et al.*, 2003; Mei *et al.*, 2004; Frelichowski *et al.*, 2006; Flagel *et al.*, 2008; Su *et al.*, 2010; Ulloa *et al.*, 2011; Zhang *et al.*, 2012; Liang *et al.*, 2013; Page *et al.*, 2013; and Ning *et al.*, 2014.

Wang *et al.* (2006), Wang *et al.* (2007), Zhang *et al.* (2009), He *et al.* (2007), Ashok and Gerald (2015) employed SRAP and TRAP marker for QTL identification in cotton. Michael *et al.* (2014), Tan *et al.* (2014), Tang *et al.* (2015), Xia *et al.* (2014), Liu *et al.* (2015), Wang, *et al.* (2015), Shang *et al.* (2015), Zhang *et al.* (2015), Ashok and Gerald (2015), Jamshed *et al.* (2016), Li *et al.* (2016), Lianguang *et al.* (2016), Jia *et al.* (2016), Wang *et al.* (2016), Shu-Wen *et al.* (2016), Zhang *et al.* (2017), Tan *et al.* (2018), Ali *et al.* (2018a), Ayaz *et al.* (2018), Kumar *et al.* (2018), Li *et al.* (2019) and Kuang (2019) identified QTLs for various traits irrespective of population and marker type

The SRAP marker cover the genome of a species and assist in identification of new QTL while, TRAP markers assist in building high density map by gap filling and identification of QTL around the candidate genes along with low segregation distortion and hence suited for construction of linkage map. The QTLs identified for fibre strength (*qFS-16-1*), seed cotton yield per plant (*qSCYP-16-1*), boll weight (*qBWP-3-1*) were major QTLs found promising.

5.3 Genetic variability parameters for yield and yield attributing and fibre quality traits

Variability is the prime tool in crop improvement. The Selection within the population is effective if the population possesses the high variability. The assessment of magnitude of variation in the population is important for effective selection. The total variation is nothing but phenotypic variation, which is observable. The phenotypic variation is derived from interaction of genotypic variation and environmental variation. So it is necessary to measure the variation both at the phenotypic level and genotypic level. There are different ways to measure the variation in the population like simple measure of variability (range, mean, standard deviation and variance), estimating the various components of variance and genetic diversity.

Here we discussed variability in the population using the phenotypic and genetic variance for different quantitative traits. The different characters were measured with different units of measurement which is difficult to compare among traits. Hence, instead of phenotypic variance and genotypic variance the phenotypic coefficient of variance (PCV) and genotypic coefficient of variance (GCV) which is expressed in percentage for all traits is utilized. Along with PCV and GCV the estimate on heritability in broad sense (h^2) and genetic advance over the mean are also considered as estimation of heritability along with genetic advance assists to predict the gain under selection.

The population developed by crossing contrastingly different parents (Table 15) viz., RHAP 12 and RHAP 15 of *Gossypium hirsutum* L exhibited considerable amount of variation (Table 22 and Fig. 11).

Plant height

The trait recorded a PCV (12.76 %) and GCV (6.85 %) which were moderate and low respectively along with low heritability (28 %) and genetic advance over the mean (7.57 %). The present results indicated that the difference between PCV and GCV was more which indicated high environmental influence on the trait and hence, selection would be ineffective. These results were in agreement with observation of Tuteja *et al.*

(2006), Gitte *et al.* (2007), Fakhar *et al.* (2015) and Muhammad *et al.* (2015) and Nagaraju (2016).

Number of monopodia per plant

The number of monopodia revealed high PCV (21.65 %) and a moderate GCV (14.27 %). The heritability (43.50 %) and GAM (19.38 %) were moderate. These values indicated that character is highly influenced by environment and hence selection is not recommended. The results were similar to Tuteja *et al.* (2006) Vineela *et al.* (2013) and Ramesh *et al.* (2018)

Number of sympodia per plant

All the estimated parameters viz., GCV (7.48 %), heritability (17.30 %) and GAM (6.41 %) were low except PCV (17.97 %) which was found high. The obtained results were in accordance with studies of Tuteja *et al.* (2006), Choudki *et al.* (2012) and Deyi *et al.* (2016).

Number of bolls per plant

The high PCV (28.26 %) and GCV (21.34 %) was observed for number of bolls per plant which indicated that the population possessed sufficient variability for the trait. The heritability and GAM were moderate and high respectively which indicated that the character is governed by additive gene effect. The same results found by Hafiz *et al.* (2013), Muhammad *et al.* (2015) and Eswari *et al.* (2016).

Seed cotton yield per plant

The range of values (15.70 g to 135 g) of the trait indicated the amount of variability present in the population. The variability components viz., PCV (34.44 %), GCV (28.05 %), heritability (66.30) and GAM (47.04) were high in the population. It revealed that population had sufficient variability with respect to seed cotton yield and high heritability is due to additive gene effect and hence, the selection is effective for the trait. The results are in accordance with the findings of Dhivya *et al.* (2014), Ahsan *et al.* (2015), Fakhar *et al.* (2015) and Nagaraju (2016).

Seed index

The PCV (13.80 %) and GCV (6.82 %) were moderate and low respectively. The difference between PCV and GCV was more, which indicated environmental role in trait expression. The heritability (24.40 %) and genetic advance over the mean (6.95 %) were low which denoted that the selection would be unsuccessful. The results are in accordance with Choudki *et al.* (2012), Nagaraju (2016) and Deyi *et al.* (2016).

Boll weight

This trait exhibited PCV of 27.80 per cent and GCV of 19.97 per cent, which were high and moderate respectively along with a moderate heritability (51.30 %) and high genetic advance over the mean (29.47 %). It revealed that the character is governed by additive gene action and moderate heritability was exhibited due to high environmental influence. These results are in agreement with observation of Choudki *et al.* (2012), Muhammad *et al.* (2015), Eswari *et al.* (2016) and Ramesh *et al.* (2018).

Ginning outturn

The trait had low PCV (4.96 %) and GCV (3.13 %). The heritability (40 %) and GAM (4.08 %) were moderate and low respectively. The results indicated that the character is highly influenced by environment and selection is not recommended. The present findings are in conformity with the results of Choudki *et al.* (2012), Eswari *et al.* (2016) and Ramesh *et al.* (2018).

Lint index

Here PCV (16.06 %) and GCV (8.99 %) were moderate and low respectively along with a moderate heritability (31.40 %) and GAM (10.38 %). The results indicated that the character is highly influenced by environment and selection is not recommended. The results are in accordance with Choudki *et al.* (2012), Dhivya *et al.* (2014), Fakhar *et al.* (2015) and Deyi *et al.* (2016).

Fibre strength

The range of values (30.65 g/tex to 22.35 g/tex) in the RIL's for the trait revealed the amount of variability present in the population. The variability parameters

like PCV (8.04 %) and GCV (8.03 %) were low in the population. The difference between PCV and GCV was very less, which indicated less environmental influence in the trait expression. The heritability (99.80 %) and GAM (16.53) were high and moderate respectively which specified the high heritability is due to environment influence. The results were in accordance with Fakhar *et al.* (2015), Nagaraju (2016), Eswari *et al.* (2016) and Ramesh *et al.* (2018).

Upper half mean length

The low PCV (6.03 %) and GCV (6.00 %) was observed for upper half mean length. The heritability and GAM were high and moderate respectively which indicated that the character was influenced by environment and selection would be ineffective to improve the trait. Similar results were observed by Gitte *et al.* (2007), Malagouda *et al.* (2014), Fakharet *al.* (2015), Nagaraju (2016) and Ramesh *et al.* (2018).

Micronaire value

The micronaire value of fibre in population was found moderate PCV (12.28 %) and GCV (12.07 %). The heritability (96.70 %) and genetic advance over the mean (24.45 %) were high which denoted that the selection would be successful as the trait is under the influence of additive gene action. The results were in accordance with the findings of Richard *et al.* (2006), Choudkiet *al.* (2012) and Ramesh *et al.* (2018).

Uniformity index

A low PCV (5.57 %) and GCV (5.43 %) was observed for the trait which indicated that less variation existed for the trait. The heritability and GAM were high and moderate respectively which indicated that the character is governed by non additive gene effect. Similar results were observed by Choudki *et al.* (2012), Fakhar *et al.* (2015) and Nagaraju (2016).

Maturity ratio

A moderate PCV (16.08 %), GCV (11.68 %), h^2 (52.70 %) and GAM (17.46 %) was observed for the trait. The obtained present indicated that the selection would be ineffective to make significant gains. The result is in accordance with the findings of Ramesh *et al.* (2018).

Fibre elongation length

A low PCV of 8.66 per cent and GCV of 8.60 per cent were observed for the trait. A narrow difference was observed between the PCV and GCV which indicated less influence of environmental role and hence selection is fruitful to improve the trait. Also, heritability (98.60 %) and genetic advance over the mean (17.46 %) were high and moderate respectively which is an indication of possession of non additive gene action. Malagouda *et al.* (2014) and Deyi *et al.* (2016) observed similar results in their studies.

Considering the variability in all traits PCV was more than GCV which indicated that there is environmental influence in expression. The RIL population expressed high variability for seed cotton yield per plant, number of bolls per plant and boll weight, which indicated that selection in the RIL population was effective for the improvement of the traits. All the fibre quality traits had low PCV and GCV except micronaire value. It is not necessary that high heritability should have high genetic advance (Johnson, *et al.* 1955a).

5.4 Character association and path analysis

5.4.1 Association of seed cotton yield with agronomic and fibre quality traits

The seed cotton yield is a complex and multiplicative character which is the product of interaction of component characters. Grafius (1959) opined that “there may not be any gene for yield as such, but operates only through its components”. It is necessary to know the component characters involved in interaction and way they are in association with yield. Association study provides a better understanding of yield attributes which assists the plant breeder during the selection (Robinson *et al.*, 1951 and Johnson *et al.*, 1955b). Correlation coefficient is a statistical measure which is utilized to find out the strength and direction of relationship between the two or more variables. It is designated as ‘r’. Some of the characteristics of r value are: it is independent of the unit of measurement and its value is set between -1 to + 1. A positive value of r explains that the changes of two variables are in the same direction *i.e.* increase in one variable leads to increase in associated variable and vice-versa. When r is negative,

which denotes the movement are in negative direction *i.e.* increase in one variable leads to decrease in associated variable.

In crop improvement, association study measures the mutual relationship between the various plant traits and determines the component on which selection can be based for genetic improvement in economic trait *i.e.* plant yield. Simple correlation is of three types *i.e.* phenotypic, genotypic and environmental correlation. In case of phenotypic correlation the association between the two variables can be observed directly. It includes both genotypic and environmental effects. If the association between the variable was inherent or heritable in nature it is known as genotypic correlation. The pleiotropic and linkage are two phenomenon which influences the genotypic correlation (Falconer, 1989).

In pleiotropic action single gene governs two or more traits. If the association between two variables remains constant in parent and segregation population it might be due to pleiotropic action. If the association changes in segregation population, it is likely due to linkage between the genes governing the traits, where the linkage between two genes broken in segregating population. If the linkage or pleiotropic between the two desirable traits will accelerate the plant breeding.

In the present investigation in order to determine the extent and nature of relationship existing among the yield and its attributes along with the quality traits an attempt has been made to study the character association in the population both at phenotypic and genotypic levels (Table 23 and 24).

Plant height

It was observed that trait had a significant positive correlation with seed cotton yield at both phenotypic (0.216) and genotypic (0.249) level. Farooq *et al.*, 2014, Ramesh, 2015 and Gopi and Patil (2017) reported the similar findings in their study.

Number of monopodia per plant

In the RIL population number of monopodia per plant had a significant positive correlation with seed cotton yield at phenotypic (0.174) and genotypic (0.198) level. It indicated that number of monopodia per plant had correlated response with yield during

the course of selection. Similar results were observed by Kaushik *et al.* (2003), Farooq *et al.* (2014) and Ramesh (2015).

Number of sympodia per plant

At both phenotypic (0.294) and genotypic (0.648) level number of sympodia per plant had a positive significant association with seed cotton yield in the RIL population. The present findings were in accordance with findings of Kaushik *et al.* (2003), Kiran *et al.* (2004), Altaher and Singh (2003), Muthu *et al.* (2004), Farooq *et al.* (2014) and Ramesh (2015).

Number of bolls per plant

In the present study number of bolls per had a significant positive correlation with seed cotton yield (0.672, 0.759). Similar kind of association was observed by Kiran *et al.* (2004), Gururajan and Sundar (2004), Muthu *et al.* (2004), Sivaprasad (2004), Farooq *et al.* (2014) and Ramesh (2015) and Gopi and Patil (2017).

Seed index

The seed index had a non significant positive association with seed cotton yield at phenotypic level (0.085) but at genotypic level it had contrasting association *i.e.* significant positive (0.119). Murthy (1997), Yadav *et al.* (1998) and Reddy (2001) also reported non significant association between the traits however, Kumar and Katageri (2017) reported contrasting result of the significant association between the traits.

Boll weight

The boll weight had significant association with seed cotton yield at both genotypic (0.662) and phenotypic level (0.593). Similar findings were reported by Salahuddin *et al.* (2010), Alkuddsi *et al.* (2013a), Erande *et al.* (2014), Farooq *et al.* (2014), Baloch *et al.* (2015), Kumar and Katageri (2017), Raza *et al.* (2016) and Nikhil *et al.* (2018).

Ginning outturn

The trait recorded a significant, positive correlation with seed cotton yield per plant. The trait also registered significant positive correlation with lint index at phenotypic and genotypic level. Salahuddin *et al.* (2010), Tulasi *et al.* (2012), Alkuddsi *et al.* (2013a), Erande *et al.* (2014), Farooq *et al.* (2014) and Javed *et al.* (2016) reported significant association between the traits and on the contrary, Muthuswamy and Vivekanandan (2004) reported non significant association of ginning outturn with seed cotton yield.

Lint index

In the RIL population lint index exhibited a significant positive correlation with seed cotton yield at phenotypic (0.182) and genotypic (0.278) level. Similar results were observed by Farooq *et al.* (2014) and Javed *et al.* (2016).

Upper half mean length

Upper half mean length registered non significant negative correlation with seed cotton yield in RIL population at phenotypic (-0.065) and genotypic (-0.031) level. It indicated that if the breeder intends to increase both fibre length and yield of cotton, he would be vigilant in selecting the genotypes (Sangeetha, 1998 and Neelam and Potdukhe, 2002). Richard *et al.* (2006), Hafiz *et al.* (2013) and Malagouda *et al.* (2014) reported that upper half mean length had positive significant with seed cotton yield per plant.

Fibre strength

The fibre strength also registered a non significant negative correlation with seed cotton yield at phenotypic (-0.027) and genotypic (-0.080) level. Similar observations were made by Sangeetha (1998). Whereas, Altaher and Singh (2003) and Rao *et al.* (2013) reported that seed cotton yield and fibre strength had a significant positive correlation. Fibre strength and fibre length exhibited a significant positive association with each other at both phenotypic (0.640) and genotypic (0.639) level which indicated simultaneous improvement of the traits. Micronaire value and fibre strength exhibited a negative correlation at both genotypic (-0.164) and phenotypic (-0.200) level. The

present results obtained were in accordance with Malagouda *et al.* (2014), Ramesh (2015) and Kumar and Katageri (2017).

Micronaire value

The seed cotton yield had a significant positive correlation with micronaire value in RIL population only at genotypic (0.308) level. Whereas, a non significant negative correlation was observed between seed cotton yield and micronaire value at phenotypic level (-0.066). Reddy (2001), Neelima (2002) and Altaher and Singh (2003) reported that micronaire and seed cotton yield were positively associated each other.

Uniformity index

In the RIL population uniformity index had a non significant positive correlation with seed cotton yield at both genotypic and phenotypic level *i.e.* 0.060 and 0.080 respectively. Similar results of non significant positive correlation with seed cotton yield at both genotypic and phenotypic level were made by Neelima (2002).

Maturity ratio

The trait had a significant positive correlation with seed cotton yield at phenotypic and genotypic level in the population *i.e.* 0.154 and 0.278 respectively which suggested simultaneous improvement of maturity ratio and seed cotton yield. Reddy (2001) and Neelam and Potdukhe (2002) observed similar association between the traits.

Fibre elongation length

A non significant positive association was observed between fibre elongation length and seed cotton yield at both phenotypic (0.007) and genotypic level (0.009). The fibre elongation length and fibre strength had a positive significant association. Malagouda *et al.* (2014), Ramesh (2015) and Kumar and Katageri (2017) reported same findings.

In the present investigation, the estimates of genotypic correlation were higher than those of phenotypic correlation for most of the traits. These higher genotypic values indicated the relative stability of the genotypes (Davis *et al.*, 1961).

The seed cotton yield is a dependent and lowly heritable trait hence, selection of genotypes by considering the independent traits which had significant association with yield will assist the breeder. The traits viz., number of bolls, boll weight and number of sympodia had significant, positive correlation with seed cotton yield and hence relying on these traits for improvement would result in significant genetic gains. The quality traits, fibre strength and fibre length are positively and significantly associated with each other both at genotypic and phenotypic in the present investigation of RIL population which indicated simultaneous improvement of the traits. However, concomitant increase in the seed cotton yield could be made though the traits under the study show negative but non significant association with seed cotton yield.

5.4.2 Path analysis of seed cotton yield with agronomic and fibre quality traits.

Wright (1921a), first developed the idea of path analysis, but this method was applied in plant breeding by Dewey and Lu (1959). The path analysis estimates the cause of association between the two characters whereas; in case of correlation we measure the degree and direction of association of two characters. Path coefficient estimated through standardized partial regression coefficient which divides the correlation coefficient into two components *i.e.* direct and indirect effect. One component in path coefficient measures the direct effect of an independent variable upon dependent variable and the second component being the indirect effect (s) of an independent variable on the dependent variable through another independent variable.

In path analysis along with direct and indirect effect of various traits, we can estimate the residual effect. In plant breeding, it is very difficult to have complete knowledge of yield and yield attributes. The residual effect measures the role of other possible independent characters which were not included in the study.

If the correlation value and the direct effect is almost equal between the traits, the correlation explains the true relationship and along with that direct selection through a particular trait will be useful or not. If the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effect appears to be the cause of that positive correlation. In such a situation, the other factors are to be considered simultaneously for selection. Sometimes, correlation coefficient may be negative but the direct effect may be positive and high, under such circumstances, a restricted

simultaneous selection has to be followed *i.e.* restriction has to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect.

The simultaneous study of correlation and path analysis helps to formulate the basis for selection in cotton. The results of path analysis are discussed below (Table 25 and 26).

Plant height

The trait had a significant positive correlation with seed cotton yield (0.216, 0.249). The direct effect of plant height on seed cotton yield was low (0.02, 0.009) hence, indirect effects appeared to cause significant correlation. The boll weight (0.209, 0.342) exerted positive indirect effect on seed cotton yield via plant height. Similar findings were reported by Muthu *et al.* (2004) and Nikhil *et al.* (2018).

Number of monopodia per plant

The number of monopodia had a significant positive association with seed cotton yield (0.174, 0.198). In path analysis number of monopodia had 0.013 and -0.010 direct effects at phenotypic and genotypic level respectively. The significant positive correlation between the traits might be due to indirect effect of number of bolls (0.163, 146) and lint index (0.019, 0.042) via number of bolls. The results were in accordance with Kaushik *et al.* (2003), Altaher and Singh (2003), Muthu *et al.* (2004) and Alkuddsi *et al.* (2013).

Number of sympodia per plant

A positive significant relationship was observed between the number of sympodia and seed cotton yield but this relation might not be true because negligible direct effect. Number of sympodia had significant relationship which could be due to indirect effect through number of bolls (0.292, 0.770) via number of bolls. It indicated that simultaneously consideration of number of sympodia and number of bolls may enhance the seed cotton yield. Kaushik *et al.* (2003) and Kiran *et al.* (2004), Vinodhana *et al.* (2013), Alkuddsi *et al.* (2013), Rao and Gopinath (2013) reported similar findings in their study.

Number of bolls per plant

The trait had a significant positive correlation (0.672, 0.759) and high positive direct effect (0.782, 0.694) on seed cotton yield. The correlation explained the true relationship between the traits and direct selection of number of bolls to improve the cotton yield would be fruitful. Similar opinions were made by Kiran *et al.* (2004), Gururajan and Sundar (2004), Muthu *et al.* (2004), Saifullah, (2010), Vinodhana *et al.* (2013), Rao and Gopinath (2013), Reddy *et al.* (2017), Mahendra, (2017), Ali *et al.* (2018b) and Nikhil *et al.* (2018).

Seed index

Seed index had positive correlation with seed cotton yield but exhibited negative direct effect in path analysis (-0.189, -0.195). It revealed favorable correlation between the traits which was due to indirect effect of lint index (0.199, 0.200) and boll weight (0.111, 0.155) via seed index. Under this situation, multiple trait selection has been practiced. Altaher and Singh (2003), Muthu *et al.* (2004) and Alkuddsi *et al.* (2013), Vinodhana *et al.* (2013) obtained similar results in their study.

Boll weight

Boll weight had high positive direct effect (0.710, 0.618) on seed cotton yield. Whereas, in the correlation study both traits had a significant positive relationship. The association study explained the true relationship between traits. Therefore, direct selection for boll weight would assist enhancement of seed cotton yield. Similar relationship was noticed by Kiran *et al.* (2004), Muthu *et al.* (2004), Saifullah, (2010), Vinodhana *et al.* (2013), Alkuddsi *et al.* (2013), Rao and Gopinath (2013), Reddy *et al.* (2017) Mahendra, (2017), Ali *et al.* (2018b) and Nikhil *et al.* (2018)

Ginning outturn

A negligible negative direct effect (-0.064, -0.056) was observed between seed cotton yield and ginning outturn. However, ginning outturn exhibited a significant positive correlation with seed cotton yield. The desirable relationship was observed due to indirect effects of lint index (0.116, 0.153), boll weight (0.077, 0.103) and number of

boll (0.080, 0.161) *via* ginning outturn. It indicated that selection for these traits is likely to increase the ginning outturn and seed cotton yield. The results are in accordance with Sivaprasad *et al.* (2004), Kiran *et al.* (2004) and Muthu *et al.* (2004).

Lint index

To improve the seed cotton yield, direct selection of genotypes through lint index is recommended as lint index and seed cotton yield registered significant positive correlation (0.182, 0.278) and exerted the moderated direct effect (0.231, 0.243). Hence, boll weight (0.133, 0.177) could be considered for improvement because it had indirect effect on seed cotton yield *via* lint index. Neelima (2003), Kiran *et al.* (2004), Vinodhana *et al.* (2013), Rao and Gopinath (2013) and Nikhil *et al.* (2018) also obtained similar results.

Upper half mean length

Upper half mean length had a non significant negative (-0.027, -0.031) correlation with seed cotton yield. However, it had positive direct effect (0.040, 0.043) on seed cotton yield in the present investigation. The observed unfavorable relationship was due to indirect effect of upper half mean length through other independent traits. Under this situation multiple trait selection was suggested to improve the yield and fibre length simultaneously. Kiran *et al.* (2004), Muthu *et al.* (2004) and Nikhil *et al.* (2018) reported similar findings.

Fibre strength

The fibre strength had a non significant negative correlation (-0.066, -0.080) with seed cotton yield and similarly negligible negative direct effects (-0.016, -0.026) were observed. The lint index (0.023, 0.044) and upper half mean length (0.020, 0.028) exhibited the positive indirect effect on seed cotton yield *via* fibre strength. It indicated that lint index and upper half mean length will be considered for improvement. The similar results were observed by Kiran *et al.* (2004), Muthu *et al.* (2004) and Nikhil *et al.* (2018).

Micronaire value

Micronaire value had negligible direct effect (-0.005, 0.042) on seed cotton yield but exerted the positive significant correlation with seed cotton yield. The favorable relationship may be due to indirect effects of boll weight (0.183, 0.222), lint index (0.046, 0.086) and number of bolls (0.051, 0.064) on seed cotton yield via micronaire value. Sivaprasad *et al.* (2004), Kiran *et al.* (2004) and Muthu *et al.* (2004) reported similar findings in their study.

Uniformity index

Uniformity index had a non significant positive correlation with seed cotton yield and the trait exerted negative direct effect. The number of bolls (0.159, 0.195) and seed index (0.009, 0.022) exhibited positive indirect effect on seed cotton via uniformity index. The results were in accordance with Sivaprasad *et al.* (2004), Kiran *et al.* (2004).

Maturity ratio

Maturity ratio had significant positive correlation (0.154, 0.279) with seed cotton yield. Also, the trait exhibited a negative direct effect (-0.003, -0.060) on seed cotton yield. The bolls weight (0.117, 0.179) and number of bolls (0.033, 0.070) had positive indirect effect on seed cotton yield via maturity ratio. The results were in accordance with Reddy *et al.* (2001), Kiran *et al.* (2004) and Sivaprasad *et al.* (2004).

Fibre elongation length

A negative direct effect (-0.024, -0.046) was observed between the seed cotton yield and fibre elongation length. However, fibre elongation length exhibited positive non significant correlation (0.008, 0.010) with seed cotton yield. The desirable relationship was observed due to indirect effect of number of bolls (0.190, 0.226) and lint index (0.007, 0.011) via fibre elongation length on seed cotton yield. It indicated that simultaneous consideration of number of bolls and lint index is likely to improve fibre elongation length and seed cotton yield.

The residual effect at phenotypic and genotypic level was 0.175 and 0.079 respectively. This indicated that sufficient numbers of independent traits were considered in the present study.

The number of bolls, boll weight and lint index had positive direct effect on seed cotton yield. Hence, direct selection of these traits is suggested for enhancement of seed cotton yield. In the present study, the fibre quality traits had low or negligible direct effect on the seed cotton yield and hence, multiple traits selection is suggested to improve both seed cotton yield and fibre quality.

5.5 Intergeneration correlation and regression between the F_4 Vs F_5 and F_5 Vs F_6 generation

Improvement of genotypes requires a long period which is major constraint in plant breeding (Singh, 2009). The only solution this constraint is early generation selection. The only solution to this limitation is the early generation selection. Nevertheless, selection at early generation is not simple due to following factors like environment interaction, segregating population and quantitative nature of traits. Most of economic traits were quantitative in nature; the phenotypic value of these traits is the result of genotype and environment interaction. The presence of environment interaction can be reduces the efficiency of early generation selection (Whan *et al.*, 1981, Rahman and Bahl, 1986). The environment interaction can lead to deceiving the performance of parent and its progeny (Bartley and Weber, 1952 and Johnson, *et al.*, 1955b). Therefore, direct selection for yield improvement may not successful in segregating population. The parent progeny correlation and regression between two generations shows lesser susceptibility to environmental effect and is very useful for selection in segregating population for the production of improved genotypes.

Hence in the present study, the intergeneration correlation and regression was assessed for various quantitative traits across the generations viz., F_4 , F_5 and F_6 (Appendix IIIa and IIIb) and the results is presented in the Table 27 (Fig. 13).

5.5.1 Intergeneration correlation and regression between the F_4 Vs F_5 and F_5 Vs F_6 generation for yield and yield attributes

Intergeneration correlation between F_4 and F_5 exhibited positive, significant correlation for between each of the following traits viz., plant height (0.901), number of sympodia per plants (0.247), number of bolls per plant (0.314), seed cotton yield per

plant (0.270), seed index (0.144) and lint index (0.155). The characters viz., number of monopodia per plant (0.091), boll weight (0.0036) and ginning out turn (0.123) showed non significant association between F_4 and F_5 generation. The regression coefficient was estimated between the F_4 and F_5 generation for the yield and its components. Few traits, like plant height (0.918), number of sympodia per plants (0.201), number of number of bolls per plant (0.304), seed cotton yield per plant (0.110), seed index (0.108) and lint index (0.118) exhibited a significant parent and offspring regression coefficient. The traits, such as number of monopodia per plant (0.086), boll weight (0.0035) and ginning outturn (0.096) recorded a non-significant regression coefficient between the parent and their progeny. Ulloa *et al.* (2002) assessed the agronomic and fibre quality traits from F_2 generation to F_6 generation where lint percentage and boll weight exhibited significant intergeneration correlation across the generation. They concluded that selection for lint percentage and boll weight can be attempted at an early generation only for the trait enhancement. Similarly Jones and Smith (2005) reported that lint yield, fibre strength, fibre elongation, micronaire value, lint percentage, uniformity ratio traits had a significant positive correlation between F_3 and F_6 generation.

Intergeneration correlation (r) and regression (b) between F_5 and F_6 showed that significant relationship existed for the traits studied viz., plant height ($r=0.982$, $b=0.959$), number of sympodia per plants ($r=0.947$, $b=0.869$), monopodia per plant ($r=0.968$, $b=0.898$), number of number of bolls ($r=0.921$, $b=0.824$), boll weight ($r=0.936$, $b=0.948$), seed cotton yield per plant ($r=0.992$, $b=0.981$), seed index ($r=0.908$, $b=0.845$), ginning out turn ($r=0.870$, $b=0.887$) and lint index ($r=0.907$, $b=0.884$). The results were in accordance with Ulloa *et al.* (2002) and Jones and Smith (2006). Considering all the traits in the present investigation, magnitude of values of correlation and regression between F_4 and F_5 generations were lower than their corresponding advanced generation *eg.* F_5 and F_6 generation. The similar opinion emerged from the Whan *et al.* (1981) and Rahman and Bahl (1986) investigation. In the regression graph (Fig. 13) the dots indicated genotype distribution, In advanced generation (F_5 Vs F_6) dots which are the genotypes moved towards trend line (regression line), whereas these genotypes dispersed away from regression line between the F_4 and F_5 generation.

5.5.2 Intergeneration correlation and regression between the F₅ and F₆ generation for fibre quality traits,

The intergeneration correlation (r) between the F₅ and F₆ for fibre quality traits like upper half mean length (0.920), fibre strength (0.945), micronaire value (0.871), uniformity index (0.800), maturity ratio (0.884) and fibre elongation length (0.943) had significant positive association between them.

The intergeneration regression (r) between the F₅ and F₆ generation, registered a significant regression coefficient in between each of the fibre quality traits *viz.*, upper half mean length (0.830), fibre strength (0.880), micronaire value (0.830), uniformity index (0.750), maturity ratio (0.840) and fibre elongation length (0.860). Jones and Smith (2005) reported that fibre strength, fibre elongation, micronaire value, and uniformity ratio exhibited a significant positive correlation between F₃ and F₆ generation.

There was less difference between the correlation coefficient and regression coefficient in the present study which is in conformity with the study of Ntare, 1999. The estimation of intergeneration correlation assists in selection at early generation. If the correlation and regression values of a particular trait in a particular generation are significantly associated with previous generations correlation and regression values, it implied selection in the previous generation instead of in the advanced generations (Rahman and Bahl, 1986). Hence, in the present investigation, it is recommended that characters *viz.*, plant height, number of sympodia per plant, number of bolls per crop, seed cotton yield per plant, seed index and lint index at F₄ generation can be relied upon for such a selection. However, it is not recommended to rely upon F₄ generation for the selection of number of monopodia, boll weight and ginning outturn. The selection of the elite lines at F₅ generation for both agronomic and fibre quality performance traits is fruitful, whereas, it was worthless to wait for selection in F₆ generation to improve seed cotton yield and its components and fibre quality parameters as significant intergeneration correlation and regression existed between the F₅ and F₆ generations.

5.6 Identification of transgressive segregants in RIL population

In plant breeding, transgressive segregation defined as performance of progenies over the parents (Nolte and David, 2005). Hybridization has been practiced long before the onset of Mendelian genetics. In hybridization two genetically diverse genotypes are crossed to produce an array of variation in segregating population. Transgressive segregation appeared in both directions *i.e.* either positive or negative. The positive transgressives is as a result of combination of favorable alleles from both parents. Recombination is a natural phenomenon, where two or more loci recombine to form new combination and the combination/s of alleles, particularly recombination of additive allele from either of the parents gives rise to a transgressives (Basamma *et al.*, 2010).

The parents like RHAP 12 and RHAP 15 of *Gossypium hirsutum* L. were utilized as parents to develop the RILs population. The performance of parental lines are mentioned in Table 27. A “t test” was carried out between the parents employed for synthesis of RIL population to determine, if the parents differed significantly to each other for various characters (Table 15). The results indicated that a significant difference between the parents for all the characters except number of monopodia per plant, number of sympodia per plant and fibre elongation. Numerically, RHAP 12 was superior over the RHAP 15 in some of the traits like number of bolls per plant, seed cotton yield, seed index, boll weight, ginning outturn, lint index, upper half mean length, fibre strength, fibre elongation length. In contrast, RHAP 15 was superior over RHAP 12 in few traits like plant height, number of monopodia per plant and number of sympodia per plant. The contrasting nature in parents might be due to different sets of favorable alleles in the genotypes. The recombination between the alleles in the parents facilitated to produce the transgressive segregants in the population for various traits. In the present investigation, the RIL population underwent five recombinant events which ensured sufficient recombination between the alleles.

Here under the transgressives in the desirable direction *i.e.* positive transgressives for all the traits considered for the present study are described (Table 28).

5.6.1 Number of transgressive segregation

Out of 222 recombinant lines, maximum number of transgressive segregants were observed for ginning out turn (131), followed by micronaire value (110), seed cotton yield per plant (61), number of bolls per plant (39), lint index (38), boll weight (37), seed index (27), plant height (26), maturity ratio (18), upper half mean length (9), fibre strength (8), fibre elongation length (5), number of monopodia per plant (2), number of sympodia per plant (2), uniformity index (1). Girase *et al.* (2001), Pradeep and Sumalini (2003), Basamma *et al.* (2010) and Ramesh *et al.* (2018) reported that number of transgressive segregants observed depend on extent of diversity in each parent.

5.6.2 Improvement over the better parent for the traits

The transgressive segregants, which had 20 per cent superiority over the respective parent in desirable direction, are considered as promising transgressive lines. The highest number of transgressive segregants (>20 % superior over the parent) were observed for following traits viz., seed cotton yield per plant (21), number of bolls per plant (19), boll weight (14), micronaire value (13), maturity ratio (3), number of monopodia per plant (2) and lint index (2). In the present study, identification of transgressive segregants assisted to understand the potentiality of the parents, whereas undesirable transgressive segregants facilitated to know the genetic distance noticed among the RIL population. The success in producing the favorable transgressive segregants depends on genetic recombination between both linked and unlinked additive alleles (Briggs and Allard, 1953). The present study is indicative of the fact that transgressive segregants are the helpful for extending the limit of character expression in the parents.

Miller and Rawlings (1967), El-Adl and Miller (1971), Kamalanathan and Manivasakam (1987), Narayanan *et al.* (1987), Percy and Turcotte (1988), Girase *et al.* (2001), Pradeep and Sumalini (2003), Basamma *et al.* (2010) and Ramesh *et al.* (2018)

reported similar findings during identification of transgressive segregation in RIL population of cotton in their studies.

5.7 Identification superior lines over the check variety

In the present investigation MCU 5 and Sahana cotton varieties were utilized as commercial check varieties. Four important characters viz., seed cotton yield per plant, ginning outturn, upper half mean length and fibre strength with respect to production and processing view were considered in the present study. The list of Recombinant Inbred Lines superior over the check varieties, MCU 5 and Sahana are presented in the Tables 30, 31, 32 and 33.

In the RIL population, 31 lines were significantly superior over the check variety, Sahana (80 g/plant) for seed cotton yield. The RIL54 (135 g), RIL90 (122.5 g), RIL207 (110 g), RIL92 (107.2 g), RIL108 (101.6 g), RIL138 (100.2 g), RIL53 (96.7 g), RIL39 (94.75 g), RIL43 (93.4 g) and RIL109 (92.8 g) lines were significantly superior over check variety.

For ginning outturn the The RIL 31 (42.68%), RIL 54 (42.45 %), RIL 108 (42.40%), RIL 186 (42.38%), RIL 43 (42.30%) and RIL 207 (42.25%) were significantly superior over the check variety *i.e.* MCU 5 (40.2 %). These Recombinant Inbred Lines (RILs) were potential for ginning outturn.

The variety MCU 5 (29.10mm) was considered as commercial check line for upper half mean length. Only two Recombinant Inbred Lines (RILs) viz., RIL 3 (30.90 mm) and RIL 13 (29.60 mm) lines were significantly superior over the check variety.

Of the 222 lines, 33 lines were significantly superior over the check variety *i.e.* MCU 5 (28.10 g/tex) for fibre strength. The highest fibre strength was exhibited by the RIL 40 (30.63 g /tex). The recombinant inbred lines such as RIL40 (30.63 g/tex), RIL23 (30 g/tex), RIL3 (29.9 g/tex), RIL90 (29.9 g/tex), RIL101 (29.8 g/tex), RIL47 (29.43 g/tex), RIL13 (29.4 g/tex), RIL35 (29.4 g/tex), RIL52 (29.3 g/tex) and RIL63 (29.3 g/tex) were fruitful lines for both fibre strength.

5.8 Identification of superior recombinant inbred lines based on *per se* performance

The results presented in the Table 29 is an extract of Appendix II. The superior lines in the RILs assist in understanding the potential of lines for yield and fibre quality traits in the population. The ranking was given to each inbred line based on performance considering each character. Out of top 50 ranked lines, identified superior RILs for the seed cotton yield per plant (g), ginning outturn (%), upper half mean length (mm) and fibre strength (g/tex). The recombinant lines namely RIL 90 (122.5g, 42.2 %, 28.4 mm, 29.9g/tex), RIL54 (135g, 42.45 %, 26.4mm, 25.9g/tex) RIL 3 (77g, 40.2 %, 30.9mm, 29.9g/tex), RIL 63 (75.7g, 27.2mm, 29.3g/tex) and RIL 50 (75.9g, 38.33 %, 26.75mm, 28.93) were found promising by consideration of all the traits, particularly preferential for seed cotton yield per plant (g), ginning outturn (%), upper half mean length (mm) and fibre strength (g/tex).

The phenotypic evaluation of 222 inbred lines showed existence of low fibre quality in high yielding lines and vice versa. Liang *et al.* (2013) opined that it might be the reason for obtaining a few superior genotypes for both seed cotton yield and fibre quality.

The above mentioned lines could be utilized as parental lines in the hybridization programme and/or as donor parent in introgression breeding. The superior lines could be released as variety after assessment of stability through multi seasonal and multi location trail. The new Recombinant Inbred Lines (RIL) can assist in expanding the genetic resource in the *Gossypium hirsutum* L.

Future line of work

- 1 In the present investigation, a QTL was identified for fibre strength (*qFS-16-1*), seed cotton yield per plant (*qSCYP-16-1*) and boll weight (*qBWP-3-1*) which had a phenotypic variation of 18.44 per cent, 16.79 per cent and 12.44 per cent respectively. It appears that they are the good candidate for fine mapping by enhanced resolution. Also, the results indicated that QTL influencing yield and fibre quality may exist in clusters enabling map based cloning, marker introgression, pyramiding and marker aided selection.

- 2 The derived RIL population could be utilizing for fine mapping or marker validation. The new Recombinant Inbred Lines (RIL) can assist in expanding the genetic resource in the *Gossypium hirsutum* L.
- 3 The RIL 90, RIL54, RIL 3, RIL 63 and RIL 50 lines could be utilized as parental lines in the hybridization programme and/or as donor parent in introgression breeding.
- 4 The superior lines could be released as variety after assessment of stability through multi seasonal and multi location trails.

6. SUMMARY AND CONCLUSIONS

The present study on “RNA sequence based QTL mapping and genetic investigation for seed cotton yield and fibre strength in *Gossypium hirsutum* L.” is summarized below.

1. The present investigation was carried out to identify the QTLs governing the yield and fibre quality traits. The study material comprised the 222 F₆ Recombinant Inbred Lines (RIL), F₄ and F₅ segregating derived from hybridization between RHAP 12 and RHAP 15 of *G. hirsutum* L. The genotypic and phenotypic data of RIL population was utilized to construct the linkage map and QTL map.
2. The RNA seq based markers like Sequence Related Amplified Polymorphism (SRAP) and Target Region Amplified Polymorphism (TRAP) were employed for genotyping RIL population. Out of 153 SRAP and 230 TRAP markers a total of 69 and 76 polymorphic loci were observed between parental genotypes respectively. A genetic map was established by a set of 146 polymorphic markers to genotype 222 RIL populations generated in the present study by using *QTL IciMapping* v. 3.2 software (<https://www.integratedbreeding.net>) in which linkage groups were created at a threshold LOD (Logarithm of Odds) score of 3. The 146 polymorphic markers were localized on 18 linkage groups with genome span length of 2910.81 cM. The number of markers anchored on linkage groups varied from 1 (LG 18) to 26 (LG1). The results indicated that SRAP marker system suitability for linkage analysis because of wider genome coverage of species while TRAP marker had the role in development of high density linkage map by filling gaps.
3. The markers employed in genotyping were tested for expected Mendelian 1:1 segregation ratio in RIL population through chi square test ($p < 0.05$). Out of 146 markers, five markers exhibited segregation distortion viz., me7-em4a400B, me7-em1a700B, me7-em16a350A, me9-em12a200B and me8-em5a250B and located at 239.18 cM (LG 1), 74.49 cM (LG 2), 99.4 cM (LG 3), 80.51 cM (LG 6), 0 cM (LG 7) respectively. The low segregation distortion was due to

development of RIL population from intraspecific hybridization and utilization of markers targeting Open Reading Frames (ORFs).

4. The QTL analysis was done by utilizing the linkage map information and phenotyping data in RIL population, using the *QTL Ici mapping* v. 3.2 software (<https://www.integratedbreeding.net>). The QTLs were identified at a threshold LOD value of 2.5 with the inclusive composite interval mapping method. Based on *t* statistics, kurtosis and skewness, 12 traits out of 15 traits were considered for QTL mapping in the population. The QTLs were identified following traits viz., plant height (*qPH-3-1*), number of bolls per plant (*qNBP-1-1*, *qNBP-3-1*), seed cotton yield per plant (*qSCYP-1-1*, *qSCYP-16-1*), boll weight (*qBWP-1-1*, *qBWP-3-1*, *qBWP-16-1*), fibre strength (*qFS-3-1*, *qFS-13-1*, *qFS-16-1*), upper half mean length (*qUHML-11-1*), micronaire value (*qMic-13-1*), fibre uniformity index (*qFUR-3-1* and *qFUR-3-2*) and maturity ratio (*qMR-13-1*). The above mentioned QTL were distributed on LG 1, LG 3, LG 11, LG13 and LG 16. The QTLs related to fibre quality were found between the TRAP markers as one of the primer of TRAP marker was derived from the Express Sequence Tag. In the present investigation, a QTL was identified for fibre strength (*qFS-16-1*), seed cotton yield per plant (*qSCYP-16-1*) and boll weight (*qBWP-3-1*) which had a phenotypic variation of 18.44 per cent, 16.79 per cent and 12.44 per cent respectively. These three QTLs were major QTLs which had major impact on trait expression. Majority of the QTLs on the linkage group were found in clusters. This QTL clustering phenomenon is due to linkage of genes or QTL or as a result of pleiotropic effect of single QTLs in the same region. It could also be the reason for highly significant correlation found among various traits.
5. Variability is the prime tool for crop improvement. Selection within the population is effective if the population possessed high variability. The population derived by crossing RHAP 12 and RHAP 15 of *Gossypium hirsutum* L lines which were highly contrasting for the traits, obviously population exhibited a higher variation due to recombination and also independent assortment. The RIL population had high variability for seed cotton yield per plant, number of bolls per plant and boll weight which indicated that selection in the RIL population was effective by consideration of above mentioned three

traits. All the fibre quality traits had low PCV and GCV except micronaire value. The RIL population had less variability considering the fibre quality traits because the population was derived from intraspecific hybridization.

6. In crop improvement, association study measures the mutual relationship between the various plant traits and determines the component on which selection can be based for genetic improvement of a trait. In the present investigation, traits like number of bolls per plant, boll weight and number of sympodia per plant had significant positive correlation with seed cotton yield per plant. The quality traits like fibre strength and fibre length could be improved simultaneously. However, seed cotton yield and fibre quality traits exhibited the negative correlation with each other. Therefore it may become necessary to compromise with yield while considering fibre quality traits. The Path analysis estimates the cause of association between the two characters. The number of bolls per plant, boll weight and lint index had direct positive effect on seed cotton yield per plant hence direct selection through this trait will be useful. All the observed fibre quality traits had low or negligible direct effect on yield and hence in such a situation simultaneously considered multiple traits which exerted the positive indirect effect on seed cotton yield.
7. The intergeneration correlation and regression help in estimating the amount of genetic potentiality transferred from one generation to next generation. The intergeneration correlation and regression were lesser sensitivity to environmental influence and efficient for selection in segregating population. Based on inter generation correlation and regression calculation between F_4 Vs F_5 and F_5 Vs F_6 , it is recommended to rely upon F_4 generation for selection following characters viz., plant height, number of sympodia per plant, number of bolls per crop, yield of seed cotton per plant, index of seeds and index. However, for selecting the number of monopodia, boll weight and ginning outturn it is not proposed to rely on F_4 generations. The selection of the elite lines at F_5 generation for both agronomic and fibre quality performance traits is fruitful, whereas, it was worthless to wait for selection in F_6 generation to improve seed cotton yield and its components and fibre quality parameters as

significant intergeneration correlation and regression existed between the F_5 and F_6 generations.

8. Out of 222 recombinant lines highest number of transgressive segregants were observed for ginning outturn (131), followed by micronaire value (110), seed cotton yield per plant (61), number of bolls per plant (39), lint index (38), boll weight (37), seed index (27), plant height (26), maturity ratio (18), upper half mean length (9), fibre strength (8), fibre elongation length (5), number of monopodia per plant (2), number of sympodia per plant (2), uniformity index (1). The highest number of transgressive segregants (>20 % superior over the parent) was observed for seed cotton yield per plant (21), number of bolls per plant (19), boll weight (14), micronaire value (13), maturity ratio (3), number of monopodia per plant (2) and lint index (2).
9. In the RIL population 31 lines were significantly superior over the check variety Sahana (80gm/plant) for seed cotton yield per plant. RIL54 (135 g), RIL90 (122.5 g), RIL207 (110 g), RIL92 (107.2 g), RIL108 (101.6 g), RIL138 (100.2 g), RIL53 (96.7 g), RIL39 (94.75 g), RIL43 (93.4 g) and RIL109 (92.8 g) lines were found promising lines for seed cotton yield. The some of recombinant inbred lines like RIL31 (42.67 %), RIL54 (42.45 %), RIL108 (42.4 %), RIL186 (42.38 %), RIL43 (42.3 %), RIL207 (42.25 %), RIL208 (42.25 %), RIL15 (42.22 %), RIL90 (42.20 %) and RIL35 (42.18 %) were significantly superior over commercial check variety *i.e.* MCU 5 (40.2 %) for ginning outturn. The variety MCU 5 (29.10mm) was considered as check for upper half mean length. For UHML only two lines such as RIL 3 and RIL 13 lines which had fibre length of 30.9 mm and 29.60 mm respectively were superior over the check variety *i.e.* MCU 5. Out of 222 RILs, 33 lines surpassed the MCU 5 variety (28.10 g/tex) for fibre strength while, RIL 40 (30.63g / tex) had the highest fibre strength. The RIL population had some of promising line *wrt* fibre strength such as RIL40 (30.63 g/tex), RIL23 (30 g/tex), RIL3 (29.9 g/tex), RIL90 (29.9 g/tex), RIL101 (29.8 g/tex), RIL47 (29.43 g/tex), RIL13 (29.4 g/tex), RIL35 (29.4 g/tex), RIL52 (29.3 g/tex) and RIL63 (29.3 g/tex). The recombinant inbred lines such as RIL 90 (122.5g, 42.2 %, 28.4 mm, 29.9g/tex), RIL54 (135g, 42.45 %, 26.4mm, 25.9g/tex) RIL 3 (77g, 40.2 %, 30.9mm, 29.9g/tex), RIL 63 (75.7g,

27.2 mm, 29.3g/tex) and RIL 50 (75.9g, 38.33 %, 26.75mm, 28.93) were found promising by consideration of all the traits, preferential for seed cotton yield per plant (g), ginning outturn (%), upper half mean length (mm) and fibre strength (g/tex).

REFERENCES

- 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. *J. Agric. Sci.*, 7 (2): 147-151.
- Ali, I., Teng, Z., Bai, Y., Yang, Q., Hao, Y., Hou, J. and Zhang, Z., 2018a, A high density SLAF-SNP genetic map and QTL detection for fibre quality traits in *Gossypium hirsutum*. *BMC Genomics*, 19 (1): 1-18.
- Ali, R. I., Sun, Y., Jinying, Y. D., 2018b, Genetic variability, association analysis and path analysis in advance breeding material of *Gossypium hirsutum* L. *Int. J. Biosci.* 12(1):294-299.
- Alkuddsi, A. Y., Gururaja Rao, M.R. and Patil, S.S., 2013, Correlation and Path Coefficient Analysis of Yield Components In Cotton (*Gossypium hirsutum* L.). *Int. J. Agri. Bio.*, 6(4): 686–688.
- Alkuddsi, Y., Patil, S. S., Manjula, S. M. and Patil, B. C., 2013a, Correlation studies on yield and its components in Inter specific cotton hybrids (*G. hirsutum* × *G. barbadense*) for developing heterotic box. *Mol. Plant Breed.*, 4 (28): 228-237.
- Alkuddsi, Y., Patil, S. S., Manjula, S. M., Patil, B. C., Nadaf, H. L. and Nandihali, B. S., 2013b, Genetic variability studies in segregating generation of *Gossypium barbadense* lines in cotton. *Mol. Plant Breed.*, 4 (25): 209-213.
- Altaher, A. F. and Singh, R. P., 2003, Genetic diversity studies in upland cotton (*Gossypium hirsutum* L.). *J. Indian Soc. cotton improv.* 28 (3): 158-163.
- Alwala S, Suman A, Arro, J. A., Veremis, J. C., Kimbeng, C. A., 2006, Target region amplification polymorphism (TRAP) for assessing genetic diversity in sugarcane germplasm collections. *Crop Sci.*, 46: 448–455.
- Anonymous, 2019, ICAC Forecasts that world production will grow by 2 per cent in 2018/19. *Cotton. Stat. New.*, 46: 6-7.

- Anthony, W. S., 1999, Postharvest management of fibre quality. Research gate, 1-8.
- Ashok, B. and Gerald, O. M., 2015, Construction of genetic linkage map and QTL analysis for fiber traits in diploid cotton (*Gossypium arboreum* x *Gossypium herbaceum*). *J. Cotton Sci.*, 19: 15–26.
- Ayaz, A. K., Chao, S., Yichun, N., Muhammad, M. A., Xianlong, Z. and Zhongxu, Lin., 2018, QTL mapping for fiber quality and yield traits based on introgression lines derived from *Gossypium hirsutum* × *G. tomentosum*. *Int. J. Mol. Sci.*, 19 (1): 1-19.
- Baloch, M., Baloch, A. W., Baloch, M. K., Mallano, I. A., Baloch, A. M., Baloch, N. J. and Abro, S., 2015, Association and heritability analysis for yield and fibre traits in promising genotypes of cotton (*G. hirsutum* L.). *Res. J.*, 47 (2): 303-306.
- Barma, N., Islam, M., Hakim, M., and Sarker, D., 2011, Genetic variability and selection response to heat tolerance through membrane thermostability in spring wheat (*Triticum Aestivum* L). *Bangladesh J. Plant Breed. Genet*, 23 (2), 15-22.
- Barman, D. and Barah, S. P., 2012, Effect of selection response on F₃ and F₄ generation for yield and yield component characters in mutant rice strain (*Oryza sativa* L.). *Elsevier J. Sci.* 4: 183-187.
- Bartley, B. G and Weber, C. R. 1952. Heritable and non heritable relationship and variability of agronomic characters in successive generations of soybean crosses. *Agron. J.*, 44 (9): 487-493.
- Basamma K., Kajjidoni¹, S. T., Salimath, P. M. and Malagouda, P., 2010, Productivity and fiber quality improvement through transgressive breeding in desi cotton. *IJAS*, 6 (2): 609-614.
- Briggs, F. N. and Allard, R. W. 1953. The current status of the backcross method of plant breeding. *Agron. J.*, 45: 131-138.

- Burr, B., Burr, F. A., Thompson, K. H., Albertson, M. C. and Stuber, C. W., 1988, Gene mapping with recombinant inbreds in maize. *Genetics*, 118 (3): 519-528
- Burton, G. N. and Devane, E. M., 1953, Estimating heritability in fall fescue (*Festuca arundinacea* L.) from replicated clonal material. *Agron. J.*, 45: 478-481.
- Burton, N. A., Schurmann, N., Casse, O., Steeb, A. K., Claudi, B., Zankl, J., Schmidt, A. and Bumann, D., 2014, Disparate impact of oxidative host defenses determines the fate of Salmonella during systemic infection in mice. *Cell Host Microb.*, 15: 72-83
- Calhoun, D. S. and Bowman, D. T., 1999, Techniques for Development of New Cultivars. In: Cotton, Smith, W. C. and J. T. Cothren (Eds.). John Wiley and Sons Inc., New York: 361-414.
- Chen, L., Zhang, Z. S., Hu, M. C., Wang, W. W., Zhang, J., Liu, D. J., 2008, Genetic linkage map construction and QTL mapping for yield and fiber quality in upland cotton (*Gossypium hirsutum* L.). *Acta Agronomica Sinica*, 7: 1-15.
- Choudki, V. M., Katageri, I. S., Patil, R. S. and Vamadevaiah, H. M., 2012, Evaluation of F₁₁ recombinant lines of *G. herbaceum* × *G. anomalum* and *G. herbaceum* × *G. barbadense* crosses for fibre traits in cotton. *Karnataka J. Agric. Sci.*, 25 (4): 414-417.
- Chu, C. G., Xu, S. S., Friesen, T. L. and Faris, J. D., 2008, Whole genome mapping in a wheat doubled haploid population using SSRs and TRAPs and the identification of QTL for agronomic traits. *Mol. Breed.*, 22 (2): 251–266.
- Cochran, W. G. and Cox, G. M., 1957, Experimental Designs, John Wiley and Sons, New York, pp: 611.
- Collard, B. C. Y, Jahufer, M. Z. Z., Brouwer, J. B., Pang, E. C. K., 2005, An introduction to markers, quantitative trait loci (QTL) mapping and marker-assisted selection for crop improvement: the basic concepts. *Euphytica*. 142: 169–196.

- Comlekcioglu, N., Simsek, O., Boncuk, M. and Aka-Kacar, Y., 2010, Genetic characterization of heat tolerant tomato (*Solanum lycopersicon*) genotypes by SRAP and RAPD markers. *Genet. Mol. Res.* 9 (4): 2263-2274.
- Darvasi, A. and Soller, M., 1995, Advanced intercross lines, an experimental population for fine genetic mapping. *Genetics*, 141: 1199-1207.
- Davis, W. H., Middleton, G. K. and Hebert, T. T., 1961, Inheritance of protein, texture and yield in wheat. *Crop Sci.*, 1: 235-238.
- Dewey, D. R. and Lu, K. H., 1959, Correlation and path analysis of component of created wheat grass seed production. *Agron. J.*, 51: 513-518.
- Deyi, S., Tao, W., Haiping, Z., Jianmei, Z. and Feiyu, T., 2016, Variation, heritability and association of yield, fiber and morphological traits in a near long staple upland cotton population. *Pakistan. J. Bot.*, 48 (5): 1945-1949.
- Dhamayanthi, K. P. M., Manickam, S. and Rathinavel, K., 2010, Genetic variability studies in *Gossypium barbadense* L. genotypes for seed cotton yield and its yield components. *Electron. J. Pl. Breed.*, 1 (4): 961-965.
- Dhivya, R. P., Amalabalu, R. P. and Kavithamani, D., 2014, Variability, heritability and genetic advance in upland cotton (*Gossypium hirsutum* L.). *African J. Plant Sci.*, 8 (1): 1-5.
- El-Adl, A. M. and Miller, P. A., 1971, Transgressive Segregation and the Nature of Gene Action for Yield in an Intervarietal Cross of Upland Cotton. *Crop Sci.*, 11 (3): 381-384.
- Erande, C. S., Kalpande, H. V., Doesarkar, D. B., Chavan, S. K., Patil, V. S., Deshmukh, J. D., Chinchane, V. N., Kumar, A., Dey, U. and Puttawar, M. R., 2014, Genetic variability, correlation and path analysis among different traits in desi cotton (*Gossypium arboreum* L.). *African J. Biotech.*, 29: 2278-2286.
- Eswari, K. B., Sudheer, K., S., Gopinath, and Rao, M. V. B., 2016, Genetic variability heritability and genetic advance studies in cotton. *Int. J. Dev. Res.*, 3: 1-3.

- Fakhar, Z. K., Shoaib, U. R., Muhammad, A. A., Waqas, M., Chaudhry, M. H., Muhammad, B., Ghulam, Q., Asif, L., Javaria, A. and Umar, F., 2015, Exploitation of germplasm for plant yield improvement in cotton (*Gossypium hirsutum* L.). *J. Green Physiol. Genet. Genomics.*, 11: 1-10.
- Falconer, D. S., 1989. Introduction to Quantitative Genetics. John Wiley, New York.
- Fang, D. D., Jenkins, J. N., Deng, D. D., McCarty, J. C., Li, P. and Wu, J., 2014, Quantitative trait loci analysis of fiber quality traits using a random-mated recombinant inbred population in upland cotton (*Gossypium hirsutum* L.). *Genomics*, 15: 397.
- Farooq, J., Anwar, M., Riaz, M., Farooq, A., Mahmood, A., Shahid, M. T. H., Rafiq, M. and Ilahi, F., 2014. Correlation and path coefficient analysis of earliness, fibre quality and yield contributing traits in cotton (*Gossypium hirsutum* L.). *J. Anim. Plant Sci.*, 24 (3): 781-790.
- Fisher, R. A., 1918, The correlation between relatives on the supposition of mendelian inheritance. *Trans. Rew. Soc. Edinb.*, 52: 399-433.
- Flagel, L., Udall, J., Nettleton, D., Wendel, J., 2008, Duplicate gene expression in allopolyploid *Gossypium* reveals two temporally distinct phases of expression evolution. *BMC Biol.* 6: 16.
- Frelichowski, J. E., Palmer, M. B., Main, D., Tomkins, J. P., Cantrell, R. G., Stelly, D. M., Yu, J., Kohel, R. J. and Ulloa, M. 2006, Cotton genome mapping with new microsatellites from Acala 'Maxxa' BAC-ends. *Mol. Genet. Genomics.* 275 (5): 479-491.
- Fryxell, P. A., 1979, natural history of cotton tribe, college station. Texas A and M University Press.
- Fryxell, P. A., 1992, A revised taxonomic interpretation of *Gossypium* L. (Malvaceae). *Rheda*, 2 (2): 108-165.
- Girase, V. S., Patil, V. R. and Mehetre, S. S., 2001, Transgressive Segregation for Yield and its Components in Cotton (*Gossypium hirsutum* L.). *Sci. Cult.*, 67 (1): 63-64.

- Gitte, V. K., Misal, M. B., Kalpande, H. V. and Deshmukh, J. D., 2007, Genetic variability studies in F₂ population of upland cotton (*G. hirsutum* L.). *J. Cotton Res. Dev.*, 21 (1): 27-28.
- Gopi, T. J. S. and Patil, B. R., 2017, Genetic variability, correlation and path analysis in F₂ generation of interspecific cross of *Gossypium arboreum* and *Gossypium herbaceum* for yield and its component traits. *Int. J. Pure Appl. Biosci.*, 5 (6): 300-306.
- Govintharaj, P., Shalini, T., Manonmani, S. and Robin, S., 2017, Effectiveness of selection, parent-offspring correlation and regression in bacterial blight resistance genes introgressed rice segregating population. *Crop Prot.*, 47 (9): 1-5.
- Grafius, J. E., 1959, Heterosis in barley. *Agron. J.*, 51: 551-554.
- Groeneveld, R. A. and Meeden, G., 1984, Measuring skewness and kurtosis. *The Statistician*, 33: 391-399.
- Guindon, M. F., Martin, E., Zayas, A., Cointy, E. and Cravero, V., 2016, Evaluation of SRAP markers for mapping of *Pisum sativum* L. *Crop Breed. Appl. Biotechnol.*, 16 (3): 182–188.
- Guo, H., Ding, W., Chen, J., Chen, X., Zheng, Y., Wang, Z. and Liu, J., 2014, Genetic linkage map construction and QTL mapping of salt tolerance traits in zoysia grass (*Zoysia japonica*). *PLoS ONE*, 9 (9): 1-6.
- Guo, Y., Lin, H., Liu, Z., Zhao, Y., Guo, X. and Li, K., 2014, SSR and SRAP marker-based linkage map of *Vitis vinifera* L. *Biotechnol. Biotechnological Equipment*, 28 (2): 221–229.
- Gururajan, K. N. and Sundar, S., 2004, Yield component analysis in American cotton. Paper presented In: “*International Symposium on “Strategies for sustainable cotton production - A Global Vision”* held at University of Agricultural Sciences, Dharwad. 23rd – 25th November, 2004.

- Gutiérrez, O. A., Robinson, A. F., Jenkins, J. N., McCarty, J. C., Wubben, M. J., Callahan, F. E. and Nichols, R. L., 2010, Identification of QTL regions and SSR markers associated with resistance to reniform nematode in *Gossypium barbadense* L. accession GB713. *Theo. Appl. Gen.*, 122 (2): 271–280.
- Hafiz, G. A., Abid, M. and Qurban, A., 2013, Genetic variability, heritability, genetic advance and correlation studies in cotton (*Gossypium hirsutum* L.). *Int. Res. J. Microbiol.*, 4 (6): 156-161.
- Hantao, W., Cong, H., Huanle, G., Ximei, L., Wenxia, Z., Baosheng, D., Zhenhua, Y. and Zhongxu, L., 2015, QTL mapping for fiber and yield traits in upland cotton under multiple environments. *PLoS ONE.*, 10 (6): 1-14.
- He, D. H., Lin, Z. X., Zhang, X. L., Nie, Y. C., Guo, X. P., Zhang, Y. X. and Li, W., 2007, QTL mapping for economic traits based on a dense genetic map of cotton with PCR-based markers using the interspecific cross of *Gossypium hirsutum* × *Gossypium barbadense*. *Euphytica*, 153 (1-2): 181–197.
- Hongde, Q., Wangzhen, G., Yuan-Ming, Z. and Tianzhen, Z., 2008, QTL mapping of yield and fiber traits based on a four-way cross population in *Gossypium hirsutum* L. *Theor. Appl. Genet.*, 117: 883–894.
- Hu, J. and Vick, B. A., 2003, Target region amplification polymorphism: a novel marker technique for plant genotyping. *Plant Mol. Biol. Rep.*, 21: 289-294.
- Hu, J., Ochoa, O. E., Truco, M. J., Vick, B. A., 2005, Application of the TRAP technique to lettuce (*Lactuca sativa* L.) genotyping. *Euphytica*, 244: 225–235.
- Huang, J. K., Pray, C. and Rozelle, S., 2002, Enhancing the crops to feed the poor. *Nature.*, 418: 678–684.
- Jamshed, M., Fei, J., Juwu, G., Koffi, K. P., Yuzhen, S., Junwen, L., Haihong, S., Aiyang, L., Tingting, C., Zhen, Z., Juan, C., Qun, G., Zhi, L., Quanwei, L., Xiaoying, D., Yunna, T., Harun, Zareen, S., Murtaza, H., Wankui, G. and Youlu, Y., 2016, Identification of stable quantitative trait loci (QTLs) for fiber quality traits across multiple environments in *Gossypium hirsutum* recombinant inbred line population. *BMC Genomics*, 17 (197): 1-13.

- Jansen, R. C., 1993, Interval mapping of multiple quantitative trait loci. *Genet.*, 135: 205- 211.
- Jarwar, A. H., Wang, X., Wang, L., Ma, Q. and Fan, S., 2018, Genetic advancement, variability and heritability in upland cotton (*Gossypium hirsutum* L.). *J. Agric. Environ. Sci.*, 16: 24-31.
- Javed, H. S., Shibin, G., Zhi, N., Saifullah, A., Siraj, A. C. and Niaz, A. W., 2016, Correlation analysis of yield and fiber traits in upland cotton (*Gossypium hirsutum* L.). *Am-Euras. J. Agric. Environ. Sci.*, 16 (7): 1358-1361.
- Jia, X., Pang, C., Wei, H., Wang, H., Ma, Q., Yang, J. and Yu, S., 2016, High-density linkage map construction and QTL analysis for earliness-related traits in *Gossypium hirsutum* L. *BMC Genomics*, 17 (1): 1-14.
- Jiang, C. J. and Zeng, Z. B., 1995, Multiple trait analysis of genetic mapping for quantitative trait loci. *Genet.*, 140 (3): 1111-1127.
- Jin, M., Li, J., Fu, F., Zhang, Z., Zhang, X., and Liu, L., 2007, QTL analysis of the oil content and the hull content in *Brassica napus* L. *Agril. Sci. China*, 6 (4): 414-421.
- Johnson, H. W., Robinson, H. F. and Comstock, R. E., 1955a, Estimates of genetic and environmental variability in soybean. *Agron. J.*, 47: 314-318.
- Johnson, H. W., Robinson, H. F. and Comstock, R. E., 1955b, Genotypic and phenotypic correlations in soybean and their implications in selection. *Agron. J.*, 47: 477-483.
- Jones, D. G. and Smith, C. W., 2005, Early generation testing in cotton. *Crop Sci.*, 46 (1): 1-6.
- Kamalanathan, S. and Manivasakam. P., 1987, Variability in yield and other quantitative characters in *Gossypium barbadense* (L.), *Madras. Agric. J.* 74 (8-9): 360-364.

- Kaushik, S. K., Kapoor, C. J. and Koli, N. R., 2003, Association and path analysis in American cotton (*Gossypium hirsutum* L.). *J. Cotton Res. Dev.*, 17 (1): 24-26.
- Khan, F. Z., Rehman, S. U., Abid, M. A., Malik, M., Hanif, C. M., Bilal, M., Qanmber, C., Latif, A., Ashraf, J. and Farhan, U., 2015, Exploitation of germplasm for plant yield improvement in cotton (*Gossypium hirsutum* L.). *J. Green Physiol. Genet. Genomics*, 1 (1): 1-10.
- Khan, M. Q., Awan, S. I. and Mughal, M. M., 2005, Estimation of genetic parameters in spring wheat genotypes under rainfed conditions. *Indian J. Biol. Sci.*, 2: 367-370.
- Kiran, L. S., Narisi, R. A. and Neelima, S., 2004, Studies on genetic divergence in American cotton (*Gossypium hirsutum* L.). paper presented In *National Symposium on changing world order – Cotton Research, Development and Policy in context*, 10th – 12th August 2004, Acharya N G Ranga Agricultural University, Rajendranagar, Hyderabad, India.
- Koli, N. R. and Patidar, B. K., 2018, Effectiveness of selection response on F₃ and F₄ generations for grain yield and yield attributing traits in aromatic rice (*Oryza sativa* L.). *Electron. J. Pl. Breed.*, 9 (1): 368-371.
- Kosambi, D. D., 1943, The estimation of map distances from recombination values. *Ann. Eugenics*; 12: 172–5.
- Kuang, Z., 2019, Linkage map construction and QTL analyses for fiber quality, yield and agronomic traits using 63k array-based SNPs in upland cotton (*Gossypium hirsutum* L.). *M. Sc. Thesis*, Graduate Faculty of North Carolina State Univ.
- Kumar, M. N. V. and Katageri, I. S., 2017, Genetic variability and heritability study in F₂ population of *Gossypium barbadense* L. cotton for yield and its components. *Int. J. Curr. Microbiol. Appl. Sci.*, 6 (6): 975-983.

- Kumar, N. V. M., Katageri, I. S., Gowda, S. A., Adiger, S., Yadava, S. K., and Lachagari, V. B. R. 2018, 63K SNP chip based linkage mapping and QTL analysis for fibre quality and yield component traits in *Gossypium barbadense* L. cotton. *Euphytica*, 215 (1): 1-16.
- Kumar, P., He, Y., Singh, R., Davis, R. F., Guo, H., Paterson, A. H. and Chee, P. W., 2016. Fine mapping and identification of candidate genes for a QTL affecting *Meloidogyne incognita* reproduction in Upland cotton. *BMC Genomics*, 17 (1): 1-12.
- Kumar, P., Singh, R., Lubbers, E. L., Shen, X., Paterson, A. H., Campbell, B. T. and Chee, P. W., 2012, Mapping and Validation of Fiber Strength Quantitative Trait Loci on Chromosome 24 in Upland Cotton. *Crop Sci.*, 52 (3): 1115-1122.
- Kushanov, F. N., Pepper, A. E., Yu, J. Z., Buriev, Z. T., Shermatov, S. E., Saha, S. and Abdurakhmonov, I. Y., 2016, Development, genetic mapping and QTL association of cotton PHYA, PHYB, and HY5-specific CAPS and dCAPS markers. *BMC Genetics*, 17 (1): 1-15.
- Lacape, J. M., Nguyen, T. B., Thibivilliers, S., Bojinov, B., Courtois, B. and Cantrell, R. G., 2003, A combined RFLPSSR-AFLP map of tetraploid cotton based on a *Gossypium hirsutum* x *Gossypium barbadense* backcross population. *Genome.*, 46 (4): 612–626.
- Lacape, J., Jacobs, J., Arioli, T., Derijcker, R., Forestier-Chiron, N., Llewellyn, D., Jean, J., Thomas, E. and Viot, C., 2009, A new interspecific, *Gossypium hirsutum* x *G. barbadense*, RIL population: towards a unified consensus linkage map of tetraploid cotton. *Theor. Appl. Genet.*, 119 (2): 281-292.
- Lander, E. S. and Botstein, D., 1989, Mapping mendelian factors underlying quantitative traits using RFLP linkage maps. *Genetics*, 121: 185-199.
- Lander, E. S., Green, P., Abrahamson, J., Barlow, A., Daly, M. J., Lincoln, S. E. and Newburg, L., 1987, MAPMAKER: An interactive computer package for constructing primary genetic linkage maps of experimental and natural populations. *Genomics* 1: 174-181.

- Lee, M. 1995, Markers and plant breeding programs. *Adv. Agron.*, 55: 265-344.
- Li, C., Dong, Y., Zhao, T., Li, L., Li, C., Yu, E., Mei, L., Daud, M. K., He, Q., Chen, J and Zhu, S., 2016. Genome-Wide SNP linkage mapping and qtl analysis for fiber quality and yield traits in the upland cotton recombinant inbred lines population. *Front. Plant Sci.*, 7: 1356.
- Li, G. and Quiros, C. F., 2001, Sequence-related amplified polymorphism (SRAP), a new marker system based on a simple PCR reaction: Its application to mapping and gene tagging in *Brassica*. *Theor. App. Genet.*, 103: 455–461.
- Li, H., Ye, G. and Wang, J., 2007, A modified algorithm for the improvement of composite interval mapping. *Genetics*, 175 (1): 361- 374.
- Li, J., Klindworth, D. L., Shireen, F., Cai, X., Hu, J., Xu, S. S., 2006, Molecular characterization and chromosome-specific TRAP-marker development for Langdon durum D-genome disomic substitution lines. *Genome*, 49: 1545–1554.
- Li, S., Liu, A., Kong, L., Gong, J., Li, J., Gong, W., Lu, Q., Li, P., Ge, Q., Shang, H., Xiao, X., Liu, R., Zhang, Q., Shi, Y. and Yuan, Y., 2019, QTL mapping and genetic effect of chromosome segment substitution lines with excellent fiber quality from *Gossypium hirsutum* × *Gossypium barbadense*. *Mol. Genet. Genomics*, 1-14.
- Li, Y., Shen, J., Wang, T., Chen, Q., Zhang, X., Fu, T. and Ma, C., 2007, QTL analysis of yield-related traits and their association with functional markers in *Brassica napus* L. *Australian J. Agril. Res.*, 58 (8): 759-766.
- Liang, Q. Z., Hu, C., Hua, H., Li, Z. H., Hua, J. P., 2013, Construction of a linkage map and QTL mapping for fiber quality traits in upland cotton (*Gossypium hirsutum* L.). *Chin. Sci. Bull.*, 58 (26): 3233-3243.
- Liang, S., Yumei, W., Xiaocui, W., Fang, L., Abdugheni, A., Shihu, C., Yuhua, Li., Lingling, M., Kunbo, W. and Jinping, H., 2016, Genetic analysis and QTL detection on fiber traits using two recombinant inbred lines and their backcross populations in upland cotton. *Genetics*, 6: 2717-2724.

- Lim, G. T. T., Wang, G. P., Hemming, M. N., McGrath, D. J. and Jones, D. A., 2008, High resolution genetic and physical mapping of the I-3 region of tomato chromosome 7 reveals almost continuous microsynteny with grape chromosome 12 but interspersed microsynteny with duplications on Arabidopsis chromosomes 1, 2 and 3. *Theor. Appl. Genet.*, 118 (1): 57–75.
- Lim, J. H., Yang, H. J., Jung, K. H., Yoo, S. C. and Paek, N. C., 2014, Quantitative Trait Locus Mapping and Candidate Gene Analysis for Plant Architecture Traits Using Whole Genome Re-Sequencing in Rice. *Mol. Cells*, 37 (2): 149–160.
- Lin, Z. X., He, D. H., Zhang, X. L., Nie, Y. C., Guo, X. P. and Feng, C. H., 2005, Linkage map construction and mapping QTL for cotton fibre quality using SRAP, SSR and RAPD. *Plant Breed.*, 124 (2): 180–187.
- Lin, Z., Zhang, X., Nie, Y., He, D. and Maoqing, W. U., 2003, Construction of a genetic linkage map for cotton based on SRAP. *Chin. Sci. Bull.*, 48 (19): 2064–2068.
- Liu, B., 1998, Statistical Genomics: Linkage, mapping and QTL analysis. CRC press, Boca Raton. p. 7.
- Liu, D., Liu, F., Shan, X., Zhang, J., Tang, S., Fang, X. and Liu, D., 2015, Construction of a high-density genetic map and lint percentage and cottonseed nutrient trait QTL identification in upland cotton (*Gossypium hirsutum* L.). *Mol. Genet. Genomics*, 290 (5): 1683–1700.
- Liu, Z. H., Anderson, J. A., Hu, J., Friesen, T. L., Rasmussen, J. B., Faris, J. D., 2005, A wheat intervarietal genetic linkage map based on microsatellite and target region amplified polymorphism markers and its utility for detecting quantitative trait loci. *Theor. Appl. Genet.*, 111: 782–794.
- Lokeshkumar, B. M., 2018, Identification of qtls and combining ability studies for fiber quality and yield traits in cotton (*Gossypium hirsutum* L.). *Ph. D Thesis*, Univeristy of Agricultural science Dharwad, Karnataka, India.

- Lorieux, M., Perrier, X., Goffinet, B., Lanaud, C. and León, D. G., 1995, Maximum-likelihood models for mapping genetic markers showing segregation distortion. *Theo. Appl. Gen.*, 1995, 90 (1): 81-89.
- Lu, H., Romero-Severson, J. and Bernardo, R., 2002, Chromosomal regions associated with segregation distortion in maize. *Theor. Appl. Genet.* 105 622–628.
- Lungu, D. M., Kaltsikes, P. J. and Larter, E. N., 1990, Intra- and intergeneration relationships among yield, its components and other related characteristics in spring wheat. *Euphytica*, 45: 139-153.
- Luo, Z. W. and Kearsey, M. J., 1989, Maximum likelihood estimation linkage between a marker gene and a quantitative trait locus. *J. Hered.*, 63: 401-408.
- Lush, J. L., 1949, Heritability, genetic advance and character association on *rabi* sorghum. *Hereditas.*, 2: 356-375.
- Ma, J., Pei, W., Ma, Q., Geng, Y., Liu, G., Liu, J. and Yu, J., 2019, QTL analysis and candidate gene identification for plant height in cotton based on an interspecific backcross inbred line population of *Gossypium hirsutum* × *Gossypium barbadense*. *Theor. Appl. Genetics.* (7): 1-14.
- Mahendra, C., 2017, Genetic variability, Correlation and Path coefficient analysis in cotton (*Gossypium hirsutum* L.). *Adv. Biores.*, 8 (6): 226-233.
- Malagouda, P., Khadi, B. M., Basamma, K. and Katageri, I. S., 2014, Genetic variability and correlation analysis for fibre quality traits in diploid cotton (*Gossypium* spp.). *American Eurasian J. Agric. Environ. Sci.*, 14 (5): 392-395.
- Mangelsdorf, P. C. and Jones, D. F., 1926, The expression of mendelian factors in the gametophyte of Maize. *Genetics*, 11 (606): 1-6.
- Manohara, K. K. and Shashidhar, H. E., 2018, Selection efficiency for grain yield and its attributing traits in early segregating generations of rice (*Oryza sativa* L.) under aerobic condition. *Int. J. Pure App. Biosci.*, 6 (6): 393-397.

- Mariappan, R., Rana, D., Koona, S. and Mahalingam, G., 2019, Genetic linkage map construction for fibre quality traits in intraspecific upland cotton (*Gossypium hirsutum* L.). *European. Asia. J. Biosci* 13, 127-134.
- McDonald, J. H., Handbook of Biological Statistics Sparky House Publishing, Baltimore, 2008.
- Mei, M., Syed, N. H., Gao, W., Thaxton, P. M., Smith, C. W., Stelly, D. M. and Chen, Z. J., 2004, Genetic mapping and QTL analysis of fiber-related traits in cotton (*Gossypium*). *Theor. Appl. Genet.*, 108 (2): 280–291.
- Meng, L., Li, H., Zhang, L., and Wang, J., 2015, QTL IciMapping: Integrated software for genetic linkage map construction and quantitative trait locus mapping in biparental populations. *Crop J.*, 3 (3): 269–283.
- Menzo, V., Giancaspro, A., Giove, S., Nigro, D., Zacheo, S., Colasuonno, P. and Gadaleta, A., 2013, TRAP molecular markers as a system for saturation of the genetic map of durum wheat. *Euphytica*, 194 (2): 151–160.
- Meredith, W. R. Jr., and Bridge, R. R., 1973, The relationship between F_2 and selected F_3 progenies in cotton (*Gossypium hirsutum* L.). *Crop Sci.*, 13: 354–356.
- Michael, A. G., David, D. F., Jesse, A. P., Jinfa, Z., Richard, G. P., Roy, G. C., Gregory, T. and Alexander, E. L., 2014, Linkage map construction and quantitative trait locus analysis of agronomic and fiber quality traits in cotton. *Plant Genome*, 7 (1): 1-10.
- Miklas, P. N., Hu, J., Grünwald, N. J. and Larsen, K. M. 2006. Potential Application of TRAP (Targeted Region Amplified Polymorphism) Markers for Mapping and Tagging Disease Resistance Traits in Common Bean. *Crop Sci.*, 46 (2): 910-916
- Miles, C. and Wayne, M., 2008, Quantitative trait locus (QTL) analysis. *Nature Education.*, 1 (1): 1-4.
- Miller, P. A. and Rawlings, J. O., 1967, Selection for increased lint yield and correlated responses in upland cotton. *Crop Sci.*, 7: 637-646.

- Muhammad, A. K., Tanwir, A. M., Nida, F., Aamir, S., Ihsan, K., Muhammad, A., Sabah, M. and Plosha, K., 2018, Correlation for economic traits in upland cotton. *Acta Scientif Agric.*, 2 (10): 59-62.
- Muhammad, Z. A., Muhammad, S. M., Hidayatullah, B., Abdul, W. S., Hussain, F. P., Abdul, R. C. and Karim, B. S., 2015, Genetic variability, coefficient of variance, heritability and genetic advance of some *Gossypium hirsutum* L. accessions. *J. Agril. Sci.*, 7 (2): 38-42.
- Muralidhara, Y. S., Lokeshkumar, B. M., Uday, G. and Savithramma, D. L., 2015, Intergeneration correlation and narrow-sense heritability between F₂ and F₃ generations for yield components in green gram [*Vigna radiata* L. wilczek]. *Int. J. Agric. Sci. Res.*, 5 (4): 357-362.
- Murthy, J. S., 1997, Analysis of characters association and component analysis in American cotton. *Ann. Agric. Res.*, 18 (4): 573-576.
- Muthu, R., Kandasamy, G. and Jayaramachandran, M., 2004, Correlation and path coefficient analysis for yield and fibre quality traits in cotton (*Gossypium hirsutum* L.). *J. Indian Soc. cotton improv.* 29 (1): 17-20.
- Muthuswamy, A. and Vivekanandan, P., 2004, Correlation studies on seed yield and its components in hirsutum cotton (*Gossypium hirsutum* L.). *J. Indian Soc. cotton improve.*, 29 (1): 7-9.
- Nadeem, M. A., Nawaz, M. A., Shahid, M. Q., Doğan, Y., Comertpay, G., Yıldız, M. and Baloch, F. S., 2017, DNA molecular markers in plant breeding: current status and recent advancements in genomic selection and genome editing. *Biotechnol. Biotechnol. Equip*, 32 (2): 261–285.
- Nagaraju, C. H., 2016, Studies on genetics of QTLs for yield, yield component and fibre quality traits in cotton. *Ph. D. Thesis*, Univ. Agric. Sci., Dharwad, Karnataka (India).
- Narayanan, S. S., P., Singh, V. V., Singh & S. K., Chauhan, 1987, Disruptive selection for genetic improvement of upland cotton. *Indian. J. Agri. Sci.* 57: 449–452.

- Neelam, G. D. and Potdukhe, N. R., 2002, Studies on variability and correlations in upland cotton for yield and its components. *J. Indian Soc. cotton Improv.*, 27 (3): 148-152.
- Neelima, S., 2002, Heterosis and combining ability analysis for yield and yield components in cotton (*Gossypium hirsutum* L.). *M. Sc (Ag). Thesis*, Acharya N. G. Ranga Agricultural University, Rajendranagar, Hyderabad, India.
- Nikhil, P. G, Nidagundi, J. M and Anusha, H. 2018, A Correlation and path analysis studies of yield and fibre quality traits in cotton (*Gossypium hirsutum* L.). *J. Pharma. Phytochemi.*, 7(5): 2596-2599.
- Ning, Z. Y., Chen, H., Mei, H. X. and Zhang, T. Z., 2014, Molecular tagging of QTLs for fiber quality and yield in the upland cotton cultivar Acala-Prema. *Euphytica*, 195 (1): 143–156.
- Nolte, A. W. and David, H. S., 2005, Shape based assignment tests suggest transgressive phenotypes in natural sculpin hybrids (Teleostei, Scorpaeniformes, Cottidae). *Front. Zool.* 2 (1): 1-12.
- Ntare, B. R., 1999, Early generation testing for yield and physiological components in groundnut (*Arachis hypogaea* L.). *Euphytica*, 107 (2): 141-147.
- Ortiz, R., 1998, Critical role of plant biotechnology for the genetic improvement of food crops: perspectives for the next millennium. *Electron. J. Biotechnol.*, 1 (3): 151-159.
- Page, J. T., Huynh, M. D., Liechty, Z. S., Grupp, K., Stelly, D., Hulse, A. M. and Udall, J. A., 2013, Insights into the Evolution of Cotton Diploids and Polyploids from Whole-Genome Re-sequencing. *Gen. Genome Genet.*, 3 (10), 1809–1818.
- Panse, V. G., 1940, Application of genetics to plant breeding II. The inheritance of quantitative characters and plant breeding. *J. Genet.*, 40: 283-302.
- Paterson, A. H., 1996, Plant genome mapping: strategies and applications. *Biotechnol.*, 7: 1-9.

- Paterson, A. H., Lan, T. H., Reischmann, K. P., Chang, C., Lin, Y. R., Liu, S. C. and Wendel, J. F., 1996, Toward a unified genetic map of higher plants, transcending the monocot–dicot divergence. *Nature Genet.*, 14 (4): 380–382.
- Patil, B. R., 2017, Presentation on, RNA sequence mediated transcriptome analysis of *Gossypium hirsutum* genotypes for fibre strength. Cotton research and development network meeting, ICAC India. p. 6.
- Pearson, K., 1900, On the criterion that a given system of deviations from the probable in the case of a correlated system of variables is such that it can be reasonably supposed to have arisen from random sampling. *Philos. Mag.*, 50 (302): 157–175.
- Percival, A. E., Wendel, J. F. and Stewart, J. M., 1999, Taxonomy and germplasm resources in Swith, C. W. and Cothren, J. T. Cotton: origin, history, technology and production, New York, John Wiley and Sons Inc., 33-63.
- Percy R. G. and Turcotte, E. L., 1988, Development of Short and Coarse-Fibered American Pima Cotton for Use as Parents of Interspecific Hybrids. *Crop Sci.*, 28 (6): 913-916.
- Pradeep, T. and Sumalini, K. 2003. Transgressive segregation for yield and yield components in some inter and intra specific crosses of desi cotton. *Madras. Agric. J.* 90 (1-3): 152-154.
- Rafalski, J. A., Vogel, J. M., Morgante, M., Powell, W., Andre, C. and Tingey, S. V., 1996, Generating and Using Dna Markers in Plants. In: Nonmammalian Genome Analysis. *Acad. Press, San Diego*: 75-134.
- Rahman, M. A. and Bahl, P. N., 1986, Evaluation of early generation testing in chickpea. *Plant Breeding*, 97 (1): 82-85.
- Ramesh, 2015, Genome mapping and identification of molecular markers for various agronomic and fibre quality traits in tetraploid cotton. *Ph. D. Thesis*, Univ. Agric. Sci., Dharwad, Karnataka (India).

- Ramesh, U. M., Katageri, I. S. and Mohan Kumar, N. V., 2018, Genetic variability and transgressive segregation studies in inter specific cotton (*Gossypium hirsutum* × *G. barbadense*) recombinant inbred lines population. *J. Farm Sci.*, 31 (4): 373-377.
- Rao, P. J. M. and Gopinath, M., 2013, Association analysis of Yield and Fibre quality Characters in upland cotton (*Gossypium hirsutum* L.). *Australian J. Basic App. Sci.*, 7(8): 787-790.
- Raza, H., Khan, N. U., Khan, S. A., Gul, S., Latif, A., Hussain, I., Khan, J., Raza, S. and Baloch, M., 2016, Genetic variability and correlation studies in F₄ populations of upland cotton. *J. Anim. Plant Sci.*, 26 (4): 1048-1055.
- 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, Rajendra Nagar, Hyderabad.
- Reddy, K. B., Reddy, V. C., Ahamed, M. L., Naidu, T. C. M. and Rao, V. S., 2017, Character association and path coefficient analysis for yield and component traits in upland cotton (*Gossypium hirsutum* L.). *J. Cotton Res. Develop.*, 31 (1): 29-33.
- Reddy, Y. and Sarma, A. S. R., 2014. Genetic variability for yield components and fibre characters in cotton (*Gossypium arboreum* L.). *Plant Arch.*, 14 (1): 417-419.
- Reinisch, A. J., Dong, J. M., Brubaker, C. L., Stelly, D. M., Wendel, J. F. and Paterson, A. H., 1994, A detailed RFLP map of cotton, *Gossypium hirsutum* × *Gossypium barbadense*: chromosome organization and evolution in a disomic polyploid genome. *Genetics*, 138 (3): 829–847.
- Richard, G. P., Roy, G. C. and Jinfa, Z., 2006, Genetic Variation for Agronomic and Fiber Properties in an Introgressed Recombinant Inbred Population of Cotton. *Crop Sci.*, 46: 1311-1317.
- Robinson, H. F., Comstock, R. E. and Harvey, P. H., 1951, Genotypic and phenotypic correlations in corn and their implications in selection. *Agron. J.*, 43: 262-267.

- Ronin, Y. I., Kirzhner, V. M. and Korol, A. B., 1995, Linkage between loci of quantitative traits and marker loci: multi-trait analysis with a single marker. *Theor. Appl. Genet.*, 90 (6): 776-786.
- Russell, J. K., John, Y., Yong-Ha, P. and Gerard, R. L., 2004, Molecular mapping and characterization of traits controlling fiber quality in cotton. *Euphytica*, 121: 163-172.
- Ruttan, V. W., 1999, The transition to agricultural sustainability. *Proc. Natl Acad. Sci. USA.*, 96: 5960–5967.
- Saeed, F., Farooq, J., Mahmood, A., Hussain, T., Riaz, M. and Ahmad, S., 2014, Genetic diversity in upland cotton for cotton leaf curl virus disease, earliness and fibre quality. *Pakistan J. Agric. Res.*, 27 (3): 226-236.
- Saifullah, A., 2010, Correlation and path coefficient analysis of yield components of upland cotton (*Gossypium hirsutum* L.). *World Appl. Sci.* J.8:71-75
- Salahuddin, S., Abro, S., Kandgro, M. M., Salahuddin, L. and Laghari, S., 2010, Correlation and path coefficient analysis of yield components of upland cotton (*Gossypium hirsutum* L.). *World Appl. Sci. J.*, 8: 71-75.
- Sangeetha, K., 1998, Character association of quality traits on yield and yield components in cotton (*Gossypium hirsutum* L.). *M. Sc. (Agri.) Thesis*, Acharya N. G. Ranga Agricultural University, Rajendranagar, Hyderabad, India.
- Schneider, K. A., Grafton, K. F. and Kelly, J. D., 2001, QTL analysis of resistance to fusarium root rot in bean. *Crop Sci.*, 41: 535–542
- Schneider, K., 2005, Mapping Populations and Principles of Genetic Mapping. *The Handbook of Plant Genome Mapping*, 1–21.
- Semagn, K., Bjornstad, A. and Ndjiondjop, M. N., 2006, Principles, requirements and prospects of genetic mapping in plants. *African J. Biotechn.*, 5 (25): 2569-2587.

- Sewall Wright, 1921, Coefficients of inbreeding and relationship, *West. N. Am. Nat.*, 56: 330-338.
- Shang, L., Liang, Q., Wang, Y., Wang, X., Wang, K., Abduweli, A., Hua, J. 2015, Identification of stable QTLs controlling fiber traits properties in multi-environment using recombinant inbred lines in Upland cotton (*Gossypium hirsutum* L.). *Euphytica*, 205 (3): 877–888.
- Shappley, Z. W., Jenkins, J. N., Zhu, J. and McCarty, J. C., 1998, Quantitative trait loci associated with agronomic and fiber traits of Upland Cotton. *J. Cotton Sci.*, 4: 153–163.
- Shen, X. L., Guo, W. Z., Lu, Q. X., Zhu, X. F., Yuan, Y. L. and Zhang, T. Z., 2007, Genetic mapping of quantitative trait loci for fiber quality and yield trait by RIL approach in upland cotton. *Euphytica.*, 155 (3): 371–380.
- Shen, X. L., Guo, W. Z., Zhu, X. F., Yuan, Y. L., Yu, J. Z. and Kohel, R. J., 2005, Molecular mapping of QTLs for fiber qualities in three diverse lines in upland cotton using SSR markers. *Mol. Breed*, 15 (2): 169–181.
- Sheskin, D. J., 2011, Handbook of Parametric and Non-Parametric Statistical Procedures. Publication Chapman and Hall/CRC, London, 5th Edition.
- Shi, Y., Li, W., Li, A., Ge, R., Zhang, B., Li, J., Liu, G., Liu, A., Shang, H. and Gong, J., 2015, Constructing a high-density linkage map for *Gossypium hirsutum* x *Gossypium barbadense* and identifying QTLs for lint percentage. *J. Integr. Plant Biol.*, 57 (5): 450–67.
- Shridhar, A., Collins, A., Kimbeng, W. P., Williams and Manjit, S. K., 2008, Molecular Markers Associated with Resistance to *Aspergillus flavus* in Maize Grain: QTL and Discriminant Analyses, *Journal of New Seeds*, 9 (1): 1-18,
- Shu-Wen, Z., Xie-Fei, Z., Liu-Chun, F., Xiang, G., Biao, Y., Tian-Zhen, Z. and Bao-Liang, Z., 2016, Mapping of fiber quality QTLs reveals useful variation and footprints of cotton domestication using introgression lines. *Nature*, 6: 1-12.

- Singh, B. D., 2009, Plant Breeding: Principles and Methods, Kalyani Publishers, New Delhi, India.
- Singh, K., Punia M. S., Singh, V. and Jagdale, V., 2017, Inter-generation correlation and regression analysis in F_2 and F_3 generations of wheat. *Int. J. Pure App. Biosci.* 5 (6): 809-816.
- Singh, R. K. and Chaudhary, B. D., 1977, Biometrical methods in quantitative genetic analysis. *Kalyani Publ., New Delhi.*
- Singh, R. K. and Choudhary, B. D., 1977, *Biometrical Methods in Quantitative Genetic Analysis*, Kalyani Publishers, New Delhi. pp. 177-188.
- Sivaprasad, U., Chenga, R. V. and Narisi, R. A., 2004, Studies on genetic variability in American Cotton (*Gossypium hirsutum* L.). paper presented In: *International symposium on "Strategies for sustainable cotton production - A Global Vision*, 23rd – 25th November 2004, University of Agricultural Sciences, Dharwad.
- Sturtevant, A. H., 1913, The Linear Arrangement of Six Sex-linked Factors in *Drosophila*, as Shown by their Mode of Association. *J. Exp. Zool.*, 14: 43-59.
- Su, C. F., Lu, W. G., Zhao, T. J. and Gai, J. Y., 2010, Verification and fine-mapping of QTLs conferring days to flowering in soybean using residual heterozygous lines. *Chin. Sci. Bull.*, 55 (6): 499–508.
- Sun, F. D., Zhang, J. H., Wang, S. F., Gong, W. K., Shi, Y. Z., Liu, A. Y. and Yuan, Y. L., 2012, QTL mapping for fiber quality traits across multiple generations and environments in upland cotton. *Molecular Breeding*, 30 (1): 569–582.
- Suwarto, Untung, S. and Nurchasanah, S., 2015, Performance of selected plants in F_2 and F_3 generation for yield and yield component characters of new plant type rice genotypes at aerobic rice. *Res. J. Pharmacol. Biol. Chem. Sci.*, 6 (1): 1165-1170.
- Swarup, V. and Chagule, D. S., 1962, Studies on genetic variability in sorghum II. correlation of some important quantitative characters for varietal selection. *Indian. J. Genet.*, 22: 37-44.

- Tan, Z., Fang, X., Tang, S., Zhang, J., Liu, D., Teng, Z. and Zhang, Z., 2014, Genetic map and QTL controlling fiber quality traits in upland cotton (*Gossypium hirsutum* L.). *Euphytica*, 203 (3): 615–628.
- Tan, Z., Zhang, Z., Sun, X., Li, Q., Sun, Y., Yang, P. and Zhang, Z., 2018, Genetic map construction and fiber quality QTL mapping using the CottonSNP80K array in upland cotton. *Front. Plant Sci.*, 9 (225): 1-11.
- Tang, S. Y., Teng, Z. H., Zhai, T. F., Fang, X. F., Liu, F. and Liu, D. J., 2015, Construction of genetic map and QTL analysis of fiber quality traits for Upland cotton (*Gossypium hirsutum* L.). *Euphytica*, 201 (2): 195–213.
- Taylor, D. R. and Ingvarsson, P. K., 2003, Common features of segregation distortion in plants and animals. *Genetica*, 117: 27–35.
- Tulasi, J., Lal, M. A., Murthy, J. S. V., Samba, R. Y. and Ashoka, 2012, Correlation and path analysis in American cotton. *Electron. J. Plant Breed.*, 3 (4): 1005-1008.
- Tuteja, O. P., Sunil, K. and Mahender, S., 2006, Selection parameters and yield enhancement of upland cotton (*G. hirsutum*) under irrigated ecosystems of north India. *Indian J. Agric. Sci.*, 76 (2): 77-80.
- Ulloa, M., Wang, C., Hutmacher, R. B., Wright, S. D., Davis, R. M., Saski, C. A., Roberts, P. A., 2011, Mapping fusarium wilt race 1 resistance genes in cotton by inheritance, QTL and sequencing composition. *Mol. Genet. Genomics*, 286 (1): 21–36.
- Ulloa, M., William, R. and Meredith, Jr., 2002, Assessment of agronomic and fiber traits in an upland cotton population from F_{2.3} to F_{2.6} generations. Paper Presented In: *Beltwide Cotton Conferences*, Alanta, GA- January 8-12.
- Viana, J. M. S., Silva, F. F., Mundim, G. B., Azevedo, C. F. and Jan, H. U., 2016, Efficiency of low heritability QTL mapping under high SNP density. *Euphytica*, 213 (1):1-12
- Vineela, N., Samba, J. S. V., Ramakumar, P. V. and Ratna, K., 2013, Variability studies for physio-morphological and yield components traits in American cotton (*Gossypium hirsutum* L.). *J. Agric. Veter. Sci.*, 1: 7-10.

- Vinodhana, Gunasekaran, M., Vindhiyavarman, P. and Kumari, N., 2013, Genetic Studies of Variability, Correlation and Path Coefficient analysis in Cotton genotypes *Int. J. Pure App. Biosci.*, 1 (5): 6-10.
- Vos, P., Hogers, R., Bleeker, M., Reijans, M., van de Lee, T., Hornes, M., Freijters, A., Pot, J., Peleman, J., Kuiper, M. and Zabeau, M., 1995, AFLP: a new concept for DNA fingerprinting. *Nucleic Acids Res.*, 21: 4407-4414.
- Vrinda, J., 2018, RNA sequence mediated transcriptome, pathway analysis and qtl mapping in cotton (*Gossypium hirsutum* L.), *Ph. D Thesis*, Univeristy of Agricultural Sciences, Dharwad, Karnataka, India.
- Wadeyar, B. S. and Kajjdoni, S. T., 2014, Genetic variability and diversity studies in the progenies derived from irradiation and recombination in desi cotton. *Plant Arch.*, 14 (2): 711-716.
- Wakelyn, P. J. and Chaudhry, R. M., 2010, Cotton: technology for the 21st Centunry. publisher Internation Cotton Advisory Committee, United states.
- Wang, B., Guo, W., Zhu, X., Wu, Y., Huang, N. and Zhang, T., 2007, QTL Mapping of Yield and Yield Components for Elite Hybrid Derived-RILs in Upland Cotton. *J. Genet. Genomics*, 34 (1): 35–45.
- Wang, B., Liu, L., Zhang, D., Zhuang, Z., Guo, H., Qiao, X. and Chee, P. W., 2016, A Genetic map between *Gossypium hirsutum* and the brazilian endemic *G. mustelinum* and its application to QTL mapping. *Gene. Genomes Genet.*, 6 (6): 1673–1685.
- Wang, B., Wangzhen, G., Xiefei, Z., Yaoting, W., Naitai, H. and Tianzhen, Z., 2006, QTL mapping of fiber quality in an elite hybrid derived-RIL population of upland cotton. *Euphytica*, 152: 367–378.
- Wang, F., Zhang, C., Liu, G., Chen, Y., Zhang, J., Qiao, Q. and Zhang, J., 2016, Phenotypic variation analysis and QTL mapping for cotton (*Gossypium hirsutum* L.) fiber quality grown in different cotton-producing regions. *Euphytica*, 211 (2): 169–183.

- Wang, J., 2009, Inclusive composite interval mapping of quantitative trait genes. *Acta Agron. Sin.*, 35: 3239–245.
- Wang, R. L., Stec, A., Hey, J., Lukens, L. and Doebley, J. F., 1999, The limits of selection during maize domestication. *Nature*, 398: 236-239.
- Wang, Y., Ning, Z., Hu, Y., Chen, J., Zhao, R., Chen, H., and Zhang, T., 2015, Molecular mapping of restriction-site associated DNA markers in allotetraploid upland cotton. *PLOS ONE*, 10 (4): 1-13.
- Wendel, J. F. and Cronn, R. C., 2003, Polyploidy and evolution history of cotton. *Adv. Agron.*, 78: 139-186.
- Wendel, J. F. and Udall, J. A., 2013, Insights into the evolution of cotton diploids and polyploids from whole-genome re-sequencing. *Gen. Genom. Genet.*, 3: 1809–18.
- Westfall, P. H., 2014, Kurtosis as Peakedness. *The American Statistician*, 68: 191-195.
- Whan, B. R., Rathjen A. J. and Night R., 1981 The relation between wheat lines derived from F₁, F₃, F₄ and F₅ generations for grain yield and harvest index. *Euphytica*, 30: 419-430.
- William, R. Meredith, W. R. and Bridge, R. R. 1972, The relationship between F₂ and selected F₃ progenies in cotton (*Gossypium hirsutum* L.). *Crop Sci.*, 13 (3): 354-356.
- Worley, S., Culp, T. W., Harrell, D. C., 1974, The relative contributions of yield components to lint yield of upland cotton, *Gossypium hirsutum* L. *Euphytica*, 23: 399-403.
- Wright, S., 1921a, Coefficients of inbreeding and relationship. *American Naturalist*, 56: 330-338.
- Wright, S., 1921b, Correlation and causation. *J. Agric. Res.*, 20: 202-209.
- Wynne, J. C., 1976, Evaluation of early generation testing in peanuts. *Peanut Sci.*, 3 (2): 62-63.

- Xia, Z., Zhang, X., Liu, Y., Jia, Z., Zhao, H., Li, C. and Wang, Q., 2014, Major gene identification and quantitative trait locus mapping for yield-related traits in upland cotton (*Gossypium hirsutum* L.). *J. Integrative Agric.*, 13 (2): 299-309.
- Xian-Liang, S., Xue-Zhen, S., Tian-Zhen, Z., 2006, Segregation distortion and its effect on genetic mapping in plants. *Chin. J. Agric. Biotechnol.*, 3 (3): 163–169.
- Yadav, I. S., Singh, G. S. and Yadav, B., 1998, Correlation studies on seeds per boll with other traits in cotton. *J. Cotton Res. Development*. 12 (1): 104-110.
- Yang, J., Bai, G. and Shaner, G. E., 2005, Novel quantitative trait loci (QTL) for Fusarium head blight resistance in wheat cultivar Chokwang. *Theor. Appl. Genet.*, 111 (8): 1571–1579.
- Yu, J. W., Yu, S. X., Lu, C. R., Wang, W., Fan, S. L. and Song, M. Z., 2007, High-density linkage map of cultivated allotetraploid cotton based on SSR, TRAP, SRAP and AFLP markers. *J. Integr. Plant Biol.*, 49 (5): 716-724.
- Yu, J. W., Zhang, K., Li, S. Y., Yu, S., Zhai, H. H. and Wu, M., 2013, Mapping quantitative trait loci for lint yield and fiber quality across environments in a *Gossypium hirsutum* $\times$ *Gossypium barbadense* backcross inbred line population. *Theor. Appl. Genet.*, 126 (1): 275–287.
- Yu, Y., Yuan, D. J., Liang, S. G., Li, X. M., Wang, X. Q., Lin, Z. X., 2011, Genome structure of cotton revealed by a genome-wide SSR genetic map constructed from a BC₁ population between *Gossypium hirsutum* and *G. barbadense*. *Genomics*, 11 (12): 1-15.
- Yue, B., Radi, S. A., Vick, B. A., Cai, X., Tang, S., Knapp, S. J. and Hu, J., 2008, Identifying quantitative trait loci for resistance to sclerotinia head rot in two USDA sunflower germplasms. *Phytopathology*, 98 (8): 926–931.
- Zeng, Z. B., 1993, Theoretical basis of precision mapping of quantitative trait loci. *Proc. Natl. Acad. Sci., USA*, 90: 10972-10976.

- Zeng, Z. B., 1994, Precision mapping of quantitative trait loci. *Genetics*, 136: 1457-1468.
- Zhang, J. and Stewart, J. M., 2000, Economical and rapid method for extracting cotton genomic DNA. *J. Cotton Sci.* 4: 193-201.
- Zhang, J., James, M. and Stewart., 2000, Economical and rapid method for extracting cotton genomic DNA. *J. Cotton Sci.*, 4 (3): 193-201
- Zhang, K., Zhang, J., Ma, J., Tang, S. Y., Liu, D. J., Teng, Z. H., Liu, D. X., Zhang, Z. S., 2012, Genetic mapping and quantitative trait locus analysis of fiber quality traits using a three-parent composite population in upland cotton (*Gossypium hirsutum* L.). *Mol. Breeding.*, 29 (2): 335–348.
- Zhang, L., Li, H., Li, Z., and Wang, J., 2008, Interactions between markers can be caused by the dominance effect of quantitative trait loci. *Genetics*, 180 (2): 1177–1190.
- Zhang, Y. X., Lin, Z. X., Xia, Q. Z., Zhang, M. J. and Zhang, X. L., 2008, Characteristics and analysis of simple sequence repeats in the cotton genome based on a linkage map constructed from a BC₁ population between *Gossypium hirsutum* and *G. barbadense*. *Genome*, 51 (7): 534–546.
- Zhang, Z. S., Yue, H. X., Ming, L., Xian, B. L., Xiao, Y. L., Lei, H., Li, D. M. and Yan, P., 2005, Construction of a genetic linkage map and QTL analysis of fiber-related traits in upland cotton (*Gossypium hirsutum* L.). *Euphytica*, 144: 91–99.
- Zhang, Z., Ge, Q., Liu, A., Li, J., Gong, J., Shang, H., and Yuan, Y. 2017, Construction of a high-density genetic map and its application to QTL identification for fiber strength in upland cotton. *Crop Sci.*, 57 (2): 774-788.
- Zhang, Z., Hu, M., Zhang, J., Liu, D., Zheng, J., Zhang, K., Wang, W. and Wan, Q., 2009, Construction of a comprehensive PCR-based marker linkage map and QTL mapping for fiber quality traits in upland cotton (*Gossypium hirsutum* L.). *Mol. Breed.*, 24: 49–61.

- Zhang, Z., Li, J., Muhammad, J., Cai, J., Jia, F. and Shi, Y., 2015, High resolution consensus mapping of quantitative trait loci for fiber strength, length and micronaire on chromosome 25 of the upland cotton (*Gossypium hirsutum* L.). *PLoS ONE* 10 (8): 1-17.
- Zhang, L. Y., Wang, S. Q., Li, H. H., Deng, Q. M., Zheng, A. P., Li, S. C., Li, P., Li, Z. L. and Wang, J. K., 2010, Effects of missing marker and segregation distortion on QTL mapping in F₂ populations. *Theor. Appl. Genet.*, 121: 1071–1082.
- Zhao, L., Lv, Y. D., Cai, C. P., Tong, X. C., Chen X. D., Zhang, W., 2012, Toward allotetraploid cotton genome assembly: integration of a high-density molecular genetic linkage map with DNA sequence information. *BMC Genomics.*, 13 (1): 539.
- Zhou, X., Xia, Y., Ren, X., Chen, Y., Huang, L., Huang, S. and Jiang, H., 2014, Construction of a SNP-based genetic linkage map in cultivated peanut based on large scale marker development using next-generation double-digest restriction-site-associated DNA sequencing (ddRADseq). *BMC Genomics*, 15 (1): 1-15.

Appendix I: Chi-square value of polymorphic SRAP and TRAP markers employing in genotype of RIL population

Marker ID	Marker name	Chi-square	Pr > ChiSq	Marker ID	Marker name	Chi-square	Pr > ChiSq
1	me4-em1b800A	0.075	0.785	37	me4-em4a800B	0.173	0.677
3	me3-em5a900A	0.005	0.944	38	me4-em7a200B	0.961	0.327
4	me4-em7b400A	0.076	0.784	39	me5-em6d800B	2.692	0.101
5	me3-em7a900A	0.078	0.779	40	13F-me6-350B	0.230	0.632
6	me4-em13d1000B	0.177	0.674	41	12F-me9-200B	0.288	0.591
7	me4-em17b800B	0.080	0.777	42	12F-me8-250B	0.246	0.620
8	me7-em17a340B	0.164	0.686	43	me4-em2a100B	0.121	0.728
9	me8-em7a600B	0.123	0.726	44	me7-em1b400B	0.314	0.575
10	me5-em3b800B	0.291	0.590	45	me8-em2c400A	0.121	0.728
11	me4-em13b400A	0.251	0.616	46	me7-em16a350A	14.385	0.000
12	me7-em8b500B	0.005	0.942	47	me7-em5b600B	0.044	0.834
13	me5-em16a900A	0.538	0.463	48	me4-em2b500A	0.000	1.000
14	me7-em4a400B	3.843	0.050	49	me7-em9b500A	0.044	0.833
15	me4-em2c900B	0.020	0.889	50	me7-em8d1000B	0.005	0.946
16	me4-em13c900B	0.078	0.781	51	4R-me8-500B	0.228	0.633
17	5R-me9-800A	0.074	0.786	52	me7-em17c950B	0.415	0.519
18	me5-em6b600A	0.020	0.888	53	me8-em6a600A	0.005	0.946
19	me7-em10a300B	0.005	0.946	54	me8-em2a750B	0.005	0.946
20	me4-em13a200A	0.080	0.777	55	me8-em1a550A	0.045	0.832
21	me4-em7c600A	0.182	0.670	56	me4-em17a700A	0.167	0.683
22	me5-em17a700B	0.045	0.832	57	me6-em8a500A	0.391	0.532
23	me5-em6c700B	0.020	0.888	58	me7-em8c900A	0.018	0.893
24	me4-em8a300A	0.170	0.680	59	me7-em1b600B	0.043	0.836
25	me7-em3b400A	0.330	0.566	60	me7-em5c800A	0.164	0.686
26	me5-em3a700A	0.005	0.944	61	me5-em6a200B	0.294	0.588
27	12F-me5-100B	0.000	1.000	62	me7-em2a150A	0.020	0.888
28	15F-me8-400B	0.055	0.814	63	me4-em4b600B	0.020	0.889
29	me7-em1a700B	4.269	0.039	64	me7-em3a250B	0.415	0.519
30	me7-em9c1000A	0.020	0.887	65	me7-em9a400A	1.980	0.159
31	me7-em14a200B	0.080	0.777	66	me8-em2b300A	0.020	0.888
32	me7-em5a500A	0.384	0.536	67	me8-em1b600A	0.045	0.832
33	me4-em1a700B	0.164	0.686	68	me8-em9a320A	0.019	0.891
34	me3-em10a900A	0.019	0.889	69	me7-em17b520A	0.407	0.524
35	me7-em8a300A	0.000	1.000	70	14R-me9-650A	0.073	0.787
36	me3-em15a800A	0.311	0.577	71	6R-me3-350B	0.005	0.946

Contd.....

Marker ID	Marker name	Chi-square	Pr > ChiSq	Marker ID	Marker name	Chi-square	Pr > ChiSq
72	5R-me6-700B	0.230	0.632	110	10R-me5-250A	0.046	0.830
73	5R-me1-200A	0.113	0.737	111	13R-me8-300B	0.000	1.000
74	1R-me5-350A	0.019	0.892	112	15R-me5-700A	0.005	0.946
75	20F-me1-800A	0.113	0.737	113	4F-me2-750A	0.042	0.839
76	me8-em15c950A	0.041	0.840	114	2R-me8-250B	0.121	0.728
77	me8-em1c1000A	0.075	0.785	115	1R-me3-300A	0.019	0.890
78	4F-me4-350B	0.005	0.946	116	1R-me1-200B	0.041	0.840
79	me9-em12a200B	14.070	0.000	117	1R-me4-350A	0.162	0.687
80	me8-em5a250B	13.796	0.000	118	18F-me8-700A	0.020	0.888
81	15R-me7-350B	0.130	0.719	119	15F-me6-650A	0.044	0.834
82	16R-me8-500A	0.005	0.945	120	15F-me2-450A	0.077	0.782
83	17R-me2-450B	0.117	0.732	121	12F-me4-800B	0.074	0.786
84	18R-me6-550B	0.165	0.685	122	9F-me1-500B	0.042	0.839
85	18R-me7-250B	0.023	0.880	123	6F-me7-550A	0.018	0.893
86	18R-me8-500B	0.000	1.000	124	6F-me3-300A	0.171	0.679
87	me8-em7b840B	0.114	0.736	125	6F-me1-350B	0.113	0.737
88	me8-em10b800A	0.005	0.946	126	5F-me9-250A	0.000	1.000
89	me8-em13a450A	0.072	0.788	127	6F-me5-400B	1.320	0.251
90	me8-em7c950A	0.005	0.946	128	3R-me6-650B	0.019	0.892
91	me8-em8a300A	0.019	0.891	129	12F-me3-900A	0.117	0.732
92	me8-em10a500B	0.019	0.890	130	6R-me1-300A	0.041	0.839
93	me8-em15a450B	0.073	0.787	131	5R-me8-1000B	0.224	0.636
94	me8-em12a550A	0.164	0.686	132	5R-me5-750A	0.114	0.736
95	me8-em10c950B	0.018	0.893	133	5R-me7-600A	0.173	0.677
96	me8-em12b900B	0.075	0.785	134	5R-me4-650B	0.000	1.000
97	me8-em15b600B	0.073	0.787	135	5R-me3-250B	0.254	0.615
98	me8-em16a250B	0.019	0.891	136	4R-me7-4500A	0.020	0.889
99	2F-me8-200B	0.018	0.892	137	4R-me9-500A	0.019	0.891
100	3F-me3-400A	0.117	0.732	138	4R-me5-550A	0.005	0.946
101	4F-me3-350B	0.005	0.946	139	3R-me9-350B	0.005	0.945
102	4F-me5-400B	0.232	0.630	140	3R-me6-800A	0.000	1.000
103	15R-me6-800A	0.120	0.730	141	2R-me9-300B	0.113	0.737
104	4F-me9-600B	0.000	1.000	142	3R-me8-550B	0.046	0.831
105	4F-me7-500A	0.000	1.000	143	4R-me1-500B	0.072	0.788
106	4F-me1-700A	0.078	0.781	144	3R-me2-700A	0.019	0.891
107	15F-me7-600B	0.076	0.784	145	4R-me3-450B	0.167	0.683
108	6R-me4-350B	0.005	0.945	146	me8-em2b1000B	0.000	1.000
109	15R-me4-550B	0.041	0.839				

Appendix II: Phenotypic observation on yield and its attributes and fibre quality traits in RIL population delivered from intraspecific hybridization between RHAP 12 × RHAP 15 of *G. hirsutum*

RILs	PH	MNP	SNP	NBP	SCYP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL
1	115.75	2.58	12.50	25.58	68.50	6.86	2.69	37.35	4.09	26.45	22.33	3.07	87.60	0.43	6.50
2	125.88	2.25	11.10	28.65	75.68	6.21	2.62	39.75	4.13	22.35	22.63	3.64	79.80	0.52	5.70
3	122.30	2.30	11.80	29.60	77.00	5.72	2.66	40.20	3.85	30.90	29.90	3.19	94.40	0.54	6.20
4	119.90	2.20	12.40	29.50	72.50	6.82	2.48	35.96	3.84	22.50	25.10	3.69	80.70	0.61	5.70
5	98.00	2.63	10.30	22.23	46.53	6.61	2.21	40.27	4.45	23.70	25.40	3.49	87.10	0.58	5.80
6	103.80	1.70	12.20	22.90	58.70	7.21	2.71	40.26	4.82	24.30	25.60	3.75	80.80	0.62	5.60
7	99.63	1.80	11.30	23.80	61.15	6.06	2.55	36.78	3.53	25.40	25.00	3.72	76.20	0.62	5.40
8	130.90	2.60	11.60	28.00	83.90	7.62	2.98	40.21	5.19	22.90	25.00	3.55	81.50	0.59	5.70
9	108.60	2.10	12.10	25.70	44.40	6.65	1.73	40.67	4.53	21.10	22.90	3.41	78.30	0.57	5.90
10	110.60	2.60	12.30	33.10	92.70	5.82	2.81	41.40	4.11	23.85	25.13	3.29	58.40	0.47	5.70
11	114.10	2.90	12.60	35.70	91.70	6.72	2.57	41.16	4.70	22.80	22.90	3.47	83.10	0.58	5.70
12	103.90	2.50	10.80	32.90	86.80	6.67	2.62	40.12	4.53	22.30	22.80	3.17	81.40	0.53	6.00
13	102.63	2.37	9.25	24.67	61.93	7.01	2.51	38.46	4.38	29.60	29.40	2.41	81.60	0.40	6.20
14	96.00	2.85	12.25	30.60	82.05	6.83	2.66	38.75	4.33	24.40	25.20	3.05	81.50	0.51	5.50
15	85.75	2.75	10.50	34.25	81.20	5.32	2.38	42.23	3.89	26.20	29.10	2.57	85.30	0.43	6.00
16	126.50	2.30	13.05	34.70	82.70	7.22	2.37	38.24	4.39	22.70	25.40	3.68	80.80	0.61	5.50
17	108.10	2.80	10.00	30.20	57.70	7.06	1.90	38.82	4.47	27.75	25.53	2.87	83.00	0.40	5.80
18	93.00	2.40	9.30	15.90	19.90	6.37	1.26	40.11	4.26	24.60	25.80	2.85	79.90	0.47	5.60
19	94.00	2.30	10.60	19.60	42.00	6.19	2.13	38.74	3.97	24.90	25.40	3.04	80.80	0.50	5.80

Contd.....

RILs	PH	MNP	SNP	NBP	SCYP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL
20	109.88	2.85	10.30	27.23	49.85	5.33	1.84	37.63	3.22	21.80	22.90	2.83	87.30	0.47	5.40
21	116.50	2.30	10.70	21.80	58.60	6.60	2.79	41.10	4.61	25.20	25.60	4.05	82.90	0.67	5.80
22	91.20	1.90	5.90	17.50	22.00	5.17	1.26	40.78	3.56	26.10	25.70	2.86	80.40	0.48	6.00
23	107.00	2.10	8.80	24.80	52.30	5.00	2.12	39.26	3.23	26.90	30.00	3.66	78.00	0.61	5.00
24	107.90	1.80	10.20	23.33	48.50	7.57	2.09	38.03	4.65	20.40	25.00	3.25	83.60	0.54	5.40
25	69.88	1.50	9.50	24.75	55.75	6.27	2.28	40.25	4.25	24.20	22.80	2.99	78.30	0.50	6.00
26	108.17	2.63	12.75	30.53	65.65	6.30	2.14	38.07	3.87	26.70	22.60	3.39	69.30	0.56	6.60
27	103.00	2.60	11.20	28.80	60.40	5.62	2.14	38.55	3.52	24.40	29.20	3.04	82.60	0.50	5.00
28	113.50	2.10	11.40	22.50	46.40	6.89	2.06	36.67	3.99	26.10	29.20	3.13	80.30	0.52	6.60
29	110.25	2.60	9.60	31.00	83.05	6.65	2.69	36.48	3.84	25.60	25.30	2.82	80.30	0.47	5.10
30	109.50	2.70	10.50	25.20	52.70	5.65	2.13	40.31	3.82	22.80	22.80	3.20	78.20	0.53	5.10
31	109.17	1.83	8.83	21.58	46.58	5.93	2.16	42.68	4.41	23.40	25.10	3.24	77.20	0.54	4.90
32	107.70	2.70	11.20	29.40	58.80	6.22	1.99	37.01	3.66	23.35	25.23	3.74	77.90	0.54	4.70
33	112.50	2.50	9.50	22.50	53.30	7.18	2.37	36.97	4.21	25.60	25.30	3.47	75.60	0.58	4.70
34	119.60	2.80	11.20	18.80	50.10	7.11	2.66	36.00	4.02	24.00	25.10	3.42	72.10	0.57	4.80
35	113.20	2.30	11.00	19.40	40.40	7.22	2.04	42.19	5.28	27.30	29.40	3.52	73.30	0.58	4.90
36	93.80	3.10	8.10	24.30	52.40	5.56	2.12	41.75	3.98	24.80	22.70	4.29	75.80	0.71	4.80
37	108.90	2.80	10.10	21.10	61.50	7.48	3.09	39.91	4.98	25.70	25.70	4.09	76.50	0.68	4.50
38	117.70	2.50	10.50	19.50	42.10	6.73	2.13	41.50	4.77	24.60	25.50	3.78	75.80	0.63	4.90
39	99.38	3.25	9.63	31.25	94.75	6.79	3.03	41.85	4.88	23.80	22.80	4.26	77.70	0.71	4.90
40	94.40	3.80	9.40	14.40	39.60	6.81	2.75	40.65	4.67	26.55	30.63	3.52	82.10	0.50	5.40

Contd.....

RILs	PH	MNP	SNP	NBP	SCYP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL
41	133.00	3.20	12.90	32.30	70.75	6.80	2.18	36.60	3.93	25.30	25.30	3.98	73.10	0.66	5.10
42	116.20	1.80	10.90	19.70	37.10	6.73	1.85	38.22	4.16	26.90	29.10	3.81	73.10	0.63	5.00
43	108.30	2.10	9.85	33.30	93.40	6.65	2.82	42.30	4.87	24.30	25.40	4.19	78.70	0.70	5.00
44	105.30	2.70	9.20	30.70	79.10	6.94	2.64	39.73	4.60	26.80	25.90	3.42	78.00	0.57	5.30
45	91.50	1.40	9.70	19.40	31.30	5.55	1.63	38.26	3.44	25.15	25.03	3.84	73.50	0.56	4.70
46	99.30	2.20	8.60	18.20	29.30	7.29	1.61	38.14	4.50	24.00	25.60	3.13	69.80	0.52	5.50
47	129.10	2.70	9.70	31.70	70.40	6.55	2.23	35.98	3.69	24.35	29.43	3.35	78.20	0.48	5.00
48	137.00	2.60	7.40	14.80	23.50	7.53	1.64	37.34	4.48	26.00	25.60	3.66	76.00	0.61	4.80
49	121.83	2.57	8.93	19.93	38.90	5.88	2.03	39.85	3.89	27.20	29.10	3.85	75.50	0.64	5.50
50	124.60	3.00	8.90	17.75	75.90	7.33	4.29	38.34	4.56	26.75	28.93	3.50	75.40	0.50	4.90
51	127.30	3.20	9.30	20.40	60.70	7.24	2.98	35.54	4.03	24.50	22.80	3.59	75.10	0.60	4.70
52	123.50	2.60	9.30	20.20	51.30	7.95	2.53	40.90	5.50	26.00	29.30	3.40	74.00	0.56	5.20
53	148.40	2.30	10.80	32.30	96.70	7.82	2.98	40.45	5.34	26.10	25.70	4.39	78.60	0.73	5.50
54	137.70	2.60	12.85	41.50	135.00	5.61	3.27	42.45	4.13	26.40	25.90	3.12	78.80	0.52	4.60
55	108.20	2.20	8.80	19.40	52.90	6.25	2.73	36.83	3.71	25.05	25.13	3.31	75.80	0.47	4.90
56	102.00	2.80	7.70	17.80	55.10	6.66	3.08	38.45	4.15	26.90	25.10	3.74	70.60	0.62	4.40
57	107.50	2.80	8.20	20.20	70.70	6.23	3.50	39.23	4.02	24.65	28.83	3.89	79.70	0.57	5.20
58	108.00	2.10	8.20	20.30	77.90	6.45	3.91	40.26	4.34	23.80	25.10	3.77	74.50	0.63	5.10
59	103.30	2.20	8.00	20.50	60.20	7.36	2.98	38.79	4.65	25.40	25.90	3.46	76.40	0.57	5.20
60	124.25	2.23	8.08	21.70	79.93	7.24	3.87	38.56	4.54	24.35	25.43	3.45	75.90	0.49	4.90
61	127.50	3.20	10.40	13.70	40.70	6.58	2.98	38.41	4.10	24.80	25.70	3.26	75.00	0.54	5.20

Contd.....

RILs	PH	MNP	SNP	NBP	SCYP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL
62	111.55	3.38	7.98	19.23	47.43	5.48	2.47	38.20	3.39	22.90	22.70	3.15	78.10	0.52	4.40
63	109.20	2.60	8.80	24.00	75.70	6.62	3.17	38.62	4.16	27.20	29.30	3.16	78.80	0.52	5.20
64	116.00	2.20	9.30	22.20	82.50	6.60	3.89	39.45	4.31	26.40	25.90	2.78	69.60	0.46	4.70
65	105.20	2.30	8.50	17.30	45.00	5.89	2.64	39.77	3.90	26.55	28.93	4.14	75.50	0.61	5.10
66	116.10	2.50	8.50	21.90	48.40	5.18	2.23	37.76	3.13	24.90	25.20	4.09	74.70	0.68	5.00
67	125.00	3.00	8.80	18.70	51.70	6.75	2.79	38.13	4.15	28.50	29.30	3.58	75.40	0.59	5.30
68	124.70	2.30	9.10	21.70	65.80	6.27	3.00	40.52	4.26	22.40	22.80	3.86	77.30	0.64	4.70
69	107.20	2.30	10.10	21.50	62.00	6.87	2.89	39.23	4.44	25.20	22.90	3.31	73.30	0.55	4.70
70	120.10	3.10	9.20	24.00	67.00	6.16	2.81	37.18	3.65	22.50	22.80	3.15	76.10	0.52	4.50
71	106.70	2.10	7.80	12.80	34.40	6.55	2.66	40.32	4.44	24.90	25.40	3.05	77.80	0.51	5.00
72	112.20	2.10	8.60	16.20	38.30	7.19	2.47	41.34	5.07	24.90	25.00	3.36	75.00	0.56	4.80
73	107.00	2.70	9.20	19.80	43.50	5.59	2.19	37.30	3.33	24.40	22.90	2.73	72.80	0.45	4.70
74	110.00	1.60	8.30	14.30	41.00	5.87	2.82	38.95	3.76	23.40	25.20	2.89	72.80	0.48	4.90
75	104.00	2.00	9.00	18.70	49.20	6.58	2.64	36.51	3.78	23.40	22.90	3.03	72.50	0.50	4.80
76	106.90	3.00	7.80	13.70	35.50	7.80	2.61	40.55	5.32	25.60	25.40	3.58	76.10	0.59	4.80
77	99.38	3.33	8.98	19.70	57.63	6.87	2.98	36.19	3.85	23.50	22.70	3.76	72.30	0.62	4.60
78	114.50	2.30	9.50	22.60	63.20	6.79	2.81	36.19	3.85	26.45	25.53	2.72	73.10	0.37	4.80
79	114.40	2.70	9.80	17.10	81.10	6.57	4.74	39.60	4.32	23.80	22.80	3.62	71.70	0.60	4.80
80	138.40	2.50	9.20	13.40	32.40	7.43	2.43	40.25	5.01	23.80	25.40	3.63	77.50	0.60	4.50
81	122.30	1.80	9.80	15.40	49.20	6.82	3.18	38.25	4.24	24.10	22.90	3.52	75.00	0.58	4.90
82	128.30	2.40	10.30	21.40	62.20	6.66	2.90	37.91	4.07	24.05	24.83	3.67	73.20	0.53	5.00

Contd.....

RILs	PH	MNP	SNP	NBP	SCYP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL
83	125.30	2.50	7.80	20.33	39.10	6.57	1.94	41.35	4.63	22.90	22.80	3.74	72.00	0.62	4.80
84	109.50	2.30	8.40	21.50	50.60	5.47	2.30	38.77	3.47	23.30	22.70	3.81	69.50	0.63	4.70
85	111.00	2.30	9.80	21.90	61.70	6.72	2.82	37.81	4.08	22.35	22.53	3.66	69.00	0.53	4.60
86	96.30	2.20	9.10	19.40	62.40	6.20	3.31	39.39	4.01	27.40	25.40	3.38	76.50	0.56	4.60
87	101.00	2.70	9.30	22.00	54.80	7.67	2.49	40.29	5.17	25.15	25.13	3.89	70.70	0.57	4.40
88	111.50	2.20	8.90	15.40	50.70	6.48	3.29	41.18	4.54	25.90	25.90	3.78	76.30	0.63	5.20
89	106.90	2.20	9.50	21.50	37.80	5.76	1.76	40.98	4.00	25.20	25.50	3.74	75.20	0.62	5.10
90	104.00	3.00	14.50	38.00	122.50	7.02	3.22	42.20	5.13	28.40	29.90	4.26	77.00	0.71	4.80
91	106.80	2.20	10.20	26.13	83.70	6.60	3.21	39.91	4.38	26.10	25.20	3.61	75.00	0.60	5.00
92	126.90	2.10	12.10	30.20	107.20	6.90	3.54	42.15	5.03	24.90	25.10	3.54	72.50	0.59	5.10
93	108.10	2.70	11.40	29.10	84.90	6.38	2.94	40.45	4.34	26.05	28.83	3.96	75.90	0.58	5.90
94	121.10	2.80	11.00	23.80	58.20	6.85	2.44	40.32	4.63	25.10	25.10	3.83	79.30	0.64	5.00
95	117.90	1.80	10.50	14.10	37.70	7.46	2.61	37.98	4.56	25.60	25.90	3.53	73.70	0.59	5.50
96	125.10	1.60	10.30	16.00	34.20	6.22	2.06	40.52	4.23	25.90	25.40	3.35	68.00	0.56	4.70
97	130.50	3.15	11.10	18.00	43.60	7.16	2.41	38.40	4.46	27.50	25.70	3.50	75.10	0.58	5.00
98	114.60	2.60	12.70	32.70	87.80	7.14	2.70	40.13	4.80	24.75	25.33	3.55	72.80	0.51	5.10
99	117.10	2.70	9.90	14.90	32.40	7.46	2.18	39.97	4.97	26.40	25.50	3.68	71.60	0.61	5.00
100	106.90	1.90	12.40	21.00	52.30	6.49	2.47	37.44	3.88	25.90	29.00	3.24	78.40	0.54	5.80
101	119.60	2.60	11.80	18.30	39.00	6.65	2.13	35.72	3.70	28.30	29.80	3.22	74.00	0.53	5.50
102	132.00	3.20	12.00	25.00	55.80	5.26	2.25	35.39	2.88	24.10	25.20	3.81	78.30	0.63	5.00
103	107.88	2.48	12.28	21.90	60.48	6.33	2.80	39.87	4.21	25.60	25.50	3.69	72.00	0.61	4.50

Contd.....

RILs	PH	MNP	SNP	NBP	SCYP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL
104	145.90	1.90	12.50	27.40	92.40	6.92	3.37	40.74	4.77	25.25	25.73	3.64	73.80	0.52	5.00
105	119.00	2.60	11.60	20.40	69.70	5.93	3.41	41.43	4.19	22.60	22.70	3.52	75.50	0.58	5.10
106	124.70	2.50	11.60	23.70	68.50	6.28	2.88	39.76	4.14	25.60	25.30	3.64	77.20	0.60	5.20
107	118.10	2.80	11.30	30.10	89.40	6.09	2.98	41.95	4.40	23.50	22.70	4.68	75.80	0.78	5.20
108	110.30	2.60	11.00	30.80	101.60	6.29	3.34	42.40	4.63	23.55	24.93	4.21	75.00	0.62	5.20
109	110.00	3.20	10.00	24.90	92.80	7.36	3.73	42.10	5.35	24.55	25.23	4.22	72.60	0.62	5.00
110	117.50	3.70	9.60	23.70	62.60	7.01	2.64	39.34	4.54	25.80	25.30	3.84	76.40	0.64	5.20
111	118.17	1.97	10.77	15.47	40.53	7.45	2.63	39.58	4.94	25.40	29.20	3.51	78.80	0.58	5.60
112	119.20	2.00	10.50	17.10	66.80	7.07	4.14	38.36	4.39	24.30	25.00	3.39	71.00	0.56	4.60
113	121.10	2.55	9.80	20.50	55.60	6.13	2.70	40.11	4.11	24.60	22.90	4.02	72.50	0.67	4.90
114	132.60	3.30	10.40	22.90	74.10	5.87	3.23	39.37	3.80	24.60	22.80	3.61	71.90	0.60	4.50
115	131.70	3.20	11.30	24.30	69.20	6.20	2.89	38.63	3.90	23.90	22.80	4.07	73.20	0.68	4.70
116	131.60	2.80	11.80	21.40	75.20	6.63	3.57	41.15	4.66	24.90	25.20	3.90	74.80	0.65	4.70
117	124.70	2.30	8.90	16.30	41.20	6.75	2.52	39.83	4.50	24.35	22.73	3.33	71.30	0.47	4.70
118	126.50	2.50	8.80	18.50	72.00	6.82	3.87	38.97	4.36	24.00	22.80	3.88	75.60	0.64	4.80
119	124.30	2.20	9.20	15.70	46.40	6.30	2.95	38.95	4.02	25.10	25.60	3.69	74.00	0.61	5.10
120	132.80	2.30	10.70	21.80	69.20	5.92	3.23	37.91	3.63	23.60	22.70	3.51	71.10	0.58	4.50
121	135.60	1.50	10.40	19.70	63.60	5.74	3.22	39.08	3.69	23.30	22.80	3.63	72.10	0.60	4.50
122	138.80	2.20	10.60	21.70	65.70	5.01	3.10	38.58	3.16	23.20	22.60	3.59	74.00	0.60	4.80
123	125.60	2.30	9.00	22.40	58.80	7.03	2.71	39.75	4.61	24.40	22.80	3.97	74.00	0.66	4.90
124	128.40	2.70	10.30	23.95	67.40	6.25	2.84	40.51	4.26	23.55	22.73	3.57	73.90	0.51	5.20

Contd.....

RILs	PH	MNP	SNP	NBP	SCYP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL
125	116.80	2.50	9.50	18.50	61.70	5.35	3.49	35.64	2.98	24.00	22.80	2.84	73.40	0.47	4.50
126	116.60	2.50	8.90	19.60	51.70	7.26	2.73	39.62	4.76	23.30	22.80	4.17	72.30	0.69	4.70
127	115.03	1.73	9.33	28.00	74.73	6.15	2.67	35.66	3.34	24.20	22.90	3.31	76.80	0.55	4.60
128	106.60	2.30	9.50	24.80	58.40	7.47	2.55	38.52	4.69	25.60	25.40	3.60	74.80	0.60	4.90
129	110.50	2.50	7.50	16.00	32.40	6.05	2.02	39.77	3.98	23.90	22.80	4.00	75.60	0.66	5.40
130	105.30	2.50	8.40	18.30	72.50	5.89	3.97	40.17	3.98	24.30	22.60	3.67	73.30	0.61	4.20
131	120.30	2.50	8.10	23.10	62.80	6.34	2.74	39.36	4.12	22.60	22.60	4.02	72.00	0.67	4.30
132	131.10	2.40	9.60	20.00	64.10	5.83	3.18	39.92	3.88	23.20	22.70	3.94	74.50	0.65	4.80
133	119.60	2.00	9.80	25.40	59.20	5.45	2.34	38.50	3.42	24.90	25.40	3.17	75.90	0.53	5.00
134	115.30	2.30	9.60	20.00	54.10	5.78	2.73	38.64	3.64	24.50	25.40	3.70	75.30	0.61	5.00
135	112.40	2.00	9.60	18.40	53.70	5.52	2.94	38.48	3.46	23.30	22.90	3.15	75.10	0.52	5.00
136	119.00	1.60	11.00	27.60	77.00	5.91	2.93	37.44	3.54	26.50	25.20	3.76	74.20	0.62	5.30
137	109.80	2.00	9.50	22.80	68.10	6.63	2.95	40.40	4.50	24.70	25.20	3.54	77.10	0.59	5.10
138	128.60	2.10	9.40	24.30	100.20	6.59	4.16	42.15	4.80	24.80	25.10	3.69	81.30	0.61	4.50
139	133.10	2.50	11.00	21.70	90.40	6.46	4.24	41.16	4.51	23.55	25.33	3.70	80.70	0.53	5.50
140	142.00	2.35	9.90	19.90	56.30	6.59	2.84	40.61	4.50	25.90	29.10	3.07	76.00	0.51	5.50
141	98.70	2.10	9.70	17.80	37.60	6.77	2.01	38.03	4.15	26.00	25.60	2.27	70.80	0.38	5.20
142	93.10	1.90	10.00	24.10	57.70	6.75	2.44	38.38	4.19	26.20	25.30	2.77	72.20	0.46	5.60
143	117.50	1.80	10.00	17.30	36.10	6.11	2.10	37.12	3.61	25.10	25.20	3.26	74.50	0.54	5.10
144	111.30	1.80	10.10	11.60	15.70	5.95	1.36	38.15	3.67	25.60	25.90	2.16	77.30	0.36	5.00
145	108.40	1.90	9.90	21.20	52.30	7.00	2.48	37.43	4.20	27.90	29.20	3.16	73.50	0.52	5.00

Contd.....

RILs	PH	MNP	SNP	NBP	SCYP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL
146	144.70	2.60	8.90	16.80	71.10	5.79	4.29	40.89	3.99	23.55	22.63	3.36	75.90	0.48	5.00
147	122.80	2.90	7.70	14.80	35.30	5.37	2.38	39.82	3.54	23.40	22.80	3.49	74.90	0.58	4.60
148	121.30	2.50	8.10	14.20	31.10	5.65	2.20	39.81	3.74	24.20	25.00	4.22	77.90	0.70	4.80
149	116.50	2.70	8.70	22.90	65.00	5.84	2.85	38.78	3.70	25.90	25.30	3.09	76.50	0.51	4.80
150	122.70	2.30	8.10	14.90	45.30	7.39	3.01	37.86	4.50	24.60	25.20	3.72	77.80	0.62	5.00
151	106.13	1.73	9.83	17.43	47.50	6.45	2.72	38.25	3.96	26.10	25.30	3.15	76.00	0.52	5.60
152	121.65	2.50	10.43	16.93	33.28	6.33	2.04	36.36	3.70	23.40	22.80	3.28	81.70	0.54	4.80
153	109.20	1.90	8.80	19.40	69.00	7.54	3.56	39.25	4.86	23.80	25.00	3.77	71.30	0.63	4.20
154	111.40	2.20	8.80	28.10	47.00	6.54	1.68	40.05	4.37	23.10	25.30	3.48	75.10	0.58	4.80
155	108.60	1.90	8.20	17.80	67.80	6.38	3.84	39.58	4.18	22.00	22.60	4.63	76.00	0.77	4.80
156	126.10	1.80	9.10	19.00	72.10	6.98	3.79	37.91	4.27	25.90	25.40	4.34	76.10	0.72	4.80
157	128.60	2.20	10.80	15.30	43.10	6.53	2.83	41.08	4.54	25.10	25.40	3.83	73.90	0.64	4.90
158	112.80	2.50	10.20	25.30	71.20	6.39	2.83	37.49	3.84	25.00	25.10	3.74	74.60	0.62	4.40
159	113.70	2.50	10.10	24.20	68.30	5.51	2.80	41.37	3.89	23.90	22.80	3.92	74.50	0.65	4.60
160	126.30	2.40	10.30	22.90	65.20	5.44	2.83	40.28	3.65	25.30	25.50	4.18	77.00	0.69	4.80
161	135.40	2.60	10.90	21.30	77.70	7.61	3.66	41.49	5.35	24.05	22.73	4.25	71.00	0.63	5.00
162	126.40	2.10	9.80	19.80	67.70	6.43	3.43	37.99	3.94	26.00	25.60	3.42	81.00	0.57	4.80
163	115.40	3.00	8.50	16.80	63.60	8.56	3.82	37.03	5.03	25.40	25.30	3.40	76.50	0.56	4.90
164	122.70	2.00	8.80	16.50	68.60	5.77	4.19	38.10	3.56	24.15	25.23	3.65	75.50	0.53	4.80
165	116.50	1.80	11.40	17.10	58.50	6.46	3.47	37.87	3.94	24.80	25.10	4.05	76.60	0.67	4.80
166	116.90	2.30	9.70	18.70	70.70	7.39	3.87	38.22	4.57	24.85	25.43	3.51	72.50	0.50	4.50

Contd.....

RILs	PH	MNP	SNP	NBP	SCYP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL
167	111.70	2.90	9.90	18.20	59.00	7.54	3.54	37.43	4.54	23.30	22.90	4.30	73.40	0.71	4.70
168	114.30	2.10	7.30	15.70	42.70	7.27	2.73	40.05	4.86	26.10	25.70	3.78	75.80	0.63	5.00
169	130.40	2.30	9.80	16.30	64.90	7.66	4.11	41.11	5.36	25.90	25.60	3.72	72.10	0.62	4.50
170	123.80	1.90	9.00	19.50	65.70	6.55	3.35	40.70	4.50	26.00	25.50	3.45	76.50	0.57	5.00
171	137.40	1.90	9.30	18.00	57.70	7.65	3.18	40.64	5.23	26.20	25.60	3.93	74.80	0.65	5.00
172	127.80	1.80	9.80	17.90	45.60	6.11	2.55	38.56	3.83	24.85	25.23	3.16	73.20	0.44	4.50
173	122.40	1.68	10.20	18.60	54.80	5.44	3.05	39.01	3.48	26.30	29.20	3.32	74.90	0.55	5.10
174	124.10	2.80	9.50	18.70	59.70	5.55	3.20	38.48	3.47	24.40	25.10	3.06	71.80	0.51	4.70
175	134.20	2.60	9.20	16.20	55.00	6.85	3.45	39.93	4.56	25.05	25.13	3.53	77.50	0.51	5.20
176	131.60	2.10	9.40	15.40	69.70	7.42	4.51	36.85	4.32	27.00	25.60	4.02	75.40	0.67	4.50
177	114.10	1.90	9.80	19.20	63.70	6.43	3.46	37.69	3.89	23.75	22.63	3.68	74.60	0.53	5.40
178	118.38	2.78	11.33	20.23	74.90	6.58	3.87	38.64	4.14	24.50	25.60	4.39	74.10	0.73	4.70
179	130.20	2.60	10.30	21.60	85.70	8.06	3.96	39.33	5.25	25.90	25.90	3.71	77.90	0.62	4.90
180	126.10	2.00	10.70	18.30	77.90	6.99	4.26	38.58	4.39	25.55	25.43	3.44	75.60	0.49	4.90
181	117.30	3.10	8.80	20.30	63.40	6.59	3.14	38.85	4.20	24.20	25.10	3.62	76.90	0.60	4.60
182	132.50	2.60	10.60	26.30	82.10	6.07	3.10	37.75	3.68	26.10	25.60	3.74	78.00	0.62	5.00
183	118.70	2.10	10.10	22.05	42.40	7.32	1.91	39.85	4.84	26.10	29.10	3.36	75.30	0.56	5.20
184	96.00	2.15	11.46	19.83	49.90	6.53	2.51	38.61	4.11	23.50	22.90	4.36	72.50	0.72	5.40
185	104.10	2.50	9.60	21.60	68.70	7.10	3.31	39.22	4.59	24.45	25.13	3.21	72.20	0.45	4.80
186	107.50	2.30	9.00	12.10	27.10	6.97	2.22	42.38	5.12	25.50	25.50	3.30	74.90	0.55	5.10
187	120.10	2.30	10.20	18.30	32.00	5.83	1.80	39.83	3.86	24.30	22.90	2.80	70.80	0.47	5.00

Contd.....

RILs	PH	MNP	SNP	NBP	SCYP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL
188	104.00	2.90	8.30	27.10	66.30	5.53	2.42	39.71	3.64	24.10	22.80	3.37	72.40	0.56	4.80
189	113.60	2.20	8.50	25.25	55.70	6.52	2.22	39.02	4.17	25.80	25.50	3.09	75.40	0.51	5.00
190	105.70	1.80	8.60	17.40	45.70	6.57	2.58	41.69	4.67	24.05	22.63	2.92	68.80	0.40	4.00
191	103.00	2.40	9.00	18.33	31.90	6.84	1.70	38.20	4.25	25.50	25.40	3.50	76.80	0.58	4.60
192	112.10	3.10	9.70	14.05	26.60	6.42	2.05	39.37	4.16	25.10	25.30	3.98	72.60	0.66	4.60
193	117.40	2.30	10.50	21.50	45.40	6.50	2.21	38.23	4.02	24.85	25.13	3.23	73.30	0.46	4.80
194	125.90	2.70	9.70	22.40	91.50	7.92	4.07	40.30	5.35	26.00	25.80	3.91	76.20	0.65	4.60
195	126.10	2.80	9.30	10.90	24.30	5.81	2.27	39.78	3.85	26.95	28.93	2.21	72.30	0.29	4.70
196	120.40	2.70	9.30	17.20	53.20	7.24	3.11	39.02	4.63	25.10	25.90	4.16	80.60	0.69	5.20
197	118.20	2.40	8.30	23.20	78.70	5.95	3.40	40.43	4.06	27.00	25.90	3.64	75.30	0.60	4.80
198	121.20	2.90	8.00	18.80	57.30	6.47	3.07	40.97	4.49	26.30	25.80	3.34	76.40	0.55	4.90
199	117.00	2.40	7.80	14.40	70.90	5.65	4.92	40.63	3.87	24.80	29.10	3.54	76.00	0.59	5.00
200	111.60	2.20	7.90	16.20	33.30	6.22	1.98	39.23	4.02	25.70	29.10	3.21	76.50	0.53	5.00
201	118.20	1.60	8.40	16.90	43.00	6.90	2.69	40.07	4.61	25.55	25.63	3.71	79.50	0.54	4.60
202	122.30	2.10	9.10	17.85	67.70	6.72	3.84	37.65	4.06	26.20	22.90	3.65	76.30	0.61	5.80
203	112.30	2.40	9.10	19.20	64.80	8.55	3.37	39.76	5.64	22.70	29.10	3.64	58.20	0.60	5.20
204	120.80	2.30	9.10	20.30	46.20	5.69	2.27	37.94	3.47	25.20	25.20	3.27	71.50	0.54	5.10
205	123.30	2.30	8.80	21.20	70.70	7.51	3.31	38.96	4.78	23.35	22.63	3.16	71.20	0.44	5.10
206	116.30	2.00	8.30	18.90	37.20	6.84	2.00	36.32	3.90	27.95	28.93	2.74	74.40	0.38	4.80
207	122.50	3.00	8.50	37.00	110.00	5.67	2.99	42.25	4.15	26.40	25.80	3.44	76.80	0.57	4.90
208	137.10	3.30	9.30	27.30	76.30	8.90	2.78	42.25	6.51	25.05	25.63	3.37	77.60	0.48	5.30

Contd.....

RILs	PH	MNP	SNP	NBP	SCYP	SI	BWP	GOT	LI	UHML	FS	Mic	UI	MR	EL
209	127.10	2.35	9.50	22.00	61.70	6.71	2.89	39.65	4.44	24.90	25.20	4.07	76.00	0.68	4.60
210	112.20	2.50	9.50	24.50	83.40	7.48	3.47	40.15	5.03	23.30	22.90	4.11	76.00	0.68	4.80
211	109.10	1.30	10.20	18.80	55.05	6.45	3.01	39.54	4.22	25.05	24.83	3.03	72.30	0.42	4.80
212	132.15	1.70	7.70	20.75	76.30	6.25	3.78	40.55	4.26	23.80	25.00	4.07	58.40	0.68	4.90
213	137.00	2.40	8.20	18.40	84.20	7.41	4.58	41.71	5.28	24.90	25.60	3.39	78.30	0.56	4.80
214	138.60	2.40	9.30	18.70	53.00	7.05	2.85	36.80	4.11	24.40	25.80	3.80	80.60	0.63	5.30
215	105.20	2.90	7.20	17.80	63.20	5.81	3.51	39.19	3.75	26.30	25.30	3.26	76.50	0.54	4.80
216	134.00	2.00	8.90	16.60	71.00	6.64	4.35	39.93	4.36	26.75	28.83	3.47	73.50	0.50	5.30
217	127.40	2.10	8.80	16.10	60.30	4.88	3.74	38.66	3.08	24.80	25.40	3.87	78.30	0.64	4.90
218	120.50	1.80	8.60	15.70	58.10	6.30	3.69	39.33	4.08	28.10	25.40	3.13	73.90	0.52	4.80
219	114.50	2.30	7.70	17.00	47.20	4.95	2.78	40.75	3.41	23.50	25.50	3.09	78.30	0.51	5.20
220	111.70	2.00	7.70	18.30	58.70	6.01	3.22	40.24	4.04	23.35	25.03	3.45	76.70	0.49	5.00
221	125.20	2.30	9.50	19.60	66.90	6.39	3.44	37.89	3.89	26.80	25.90	3.56	75.30	0.59	5.00
222	117.10	2.90	8.45	17.90	63.10	6.74	3.54	39.17	4.34	24.40	29.00	3.50	79.40	0.58	5.60

PH= plant height (cm), MNP= number of monopodia per plant, SNP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value ($\mu\text{g/inch}$), UI = Uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).

Appendix IIIa: Phenotypic observation on yield and its attributes in F₄, F₅ and F₆ segregating population delivered from intraspecific hybridization between RHAP 12 × RHAP 15 of *G. hirsutum*

RIL	PH (F4)	PH (F5)	PH (F6)	SN (F4)	SNP (F5)	SNP (F6)	MN (F4)	MNP (F5)	MNP (F6)	BN (F4)	NBP (F5)	NBP (F6)	BW (F4)	BW (F5)	BW (F6)	SCYP (F4)	SCYP (F5)	SCYP (F6)	SI (F4)	SI (F5)	SI (F6)	GOT (F4)	GOT (F5)	GOT (F6)	LI (F4)	LI (F5)	LI (F6)
1	140.50	120.75	115.75	13.60	13.46	12.50	2.74	2.77	2.58	37.63	30.58	25.58	4.27	2.40	2.69	160.77	73.50	68.50	8.61	7.37	6.86	34.46	37.35	37.35	4.70	4.40	4.09
2	150.63	129.88	125.88	14.40	11.71	11.10	3.16	2.37	2.25	40.40	32.65	28.65	4.54	2.42	2.62	183.50	79.68	75.68	6.86	6.54	6.21	38.32	39.40	39.75	4.26	4.41	4.13
3	147.05	126.30	122.30	12.80	12.46	11.80	2.59	2.42	2.30	34.20	33.60	29.60	3.84	2.44	2.66	132.10	81.00	77.00	6.56	6.02	5.72	37.36	40.20	40.20	3.91	4.05	3.85
4	144.65	122.90	119.90	14.40	12.95	12.40	3.03	2.29	2.20	39.10	32.50	29.50	4.31	2.33	2.48	170.60	75.50	72.50	7.60	7.11	6.82	40.87	35.96	35.96	5.25	4.02	3.84
5	122.75	102.50	98.00	12.40	11.34	10.30	2.30	2.89	2.63	32.90	26.73	22.23	3.55	1.97	2.21	119.68	51.03	46.53	8.11	7.26	6.61	39.81	40.27	40.27	5.37	4.89	4.45
6	128.55	108.80	103.80	14.30	13.28	12.20	3.00	1.84	1.70	39.13	27.90	22.90	4.19	2.38	2.71	166.40	63.70	58.70	6.84	7.83	7.21	38.69	40.26	40.26	4.33	5.25	4.82
7	124.38	100.63	99.63	20.30	11.45	11.30	3.69	1.84	1.80	46.40	24.80	23.80	4.88	2.52	2.55	225.20	62.15	61.15	6.57	6.19	6.06	38.85	36.78	36.78	4.17	3.61	3.53
8	155.65	129.90	130.90	15.10	11.47	11.60	3.38	2.57	2.60	43.60	27.00	28.00	4.80	3.17	2.98	209.00	82.90	83.90	8.41	7.56	7.62	41.38	39.73	40.21	5.94	5.02	5.19
9	133.35	108.10	108.60	13.10	11.85	12.10	2.51	2.07	2.10	35.40	25.20	25.70	3.85	1.77	1.73	138.38	43.90	44.40	5.67	6.51	6.65	38.04	39.82	40.67	3.48	4.31	4.53
10	135.35	111.10	110.60	13.00	12.16	12.30	2.75	2.60	2.60	36.90	33.60	33.10	4.13	2.86	2.81	157.50	93.20	92.70	7.48	5.84	5.82	38.96	40.00	41.40	4.77	3.92	4.11
11	138.85	114.60	114.10	15.30	12.64	12.60	3.16	2.92	2.90	43.10	36.20	35.70	4.19	2.58	2.57	184.33	92.20	91.70	7.29	6.77	6.72	38.41	41.16	41.16	4.57	4.74	4.70
12	128.65	104.90	103.90	14.10	10.81	10.80	2.91	2.52	2.50	38.70	33.90	32.90	4.25	2.59	2.62	165.40	87.80	86.80	7.40	6.75	6.67	37.63	39.97	40.12	4.48	4.56	4.53
13	126.08	104.63	102.63	11.40	9.54	9.25	2.22	2.44	2.37	30.20	26.67	24.67	2.89	2.41	2.51	87.38	63.93	61.93	8.24	7.23	7.01	39.73	38.46	38.46	5.46	4.52	4.38
14	120.75	97.00	96.00	12.90	12.36	12.25	2.51	2.88	2.85	35.30	31.60	30.60	3.98	2.64	2.66	140.88	83.05	82.05	8.12	6.97	6.83	35.53	38.52	38.75	4.48	4.35	4.33
15	110.50	86.25	85.75	10.50	10.51	10.50	2.06	2.73	2.75	28.90	34.75	34.25	2.66	2.41	2.38	77.30	81.70	81.20	6.05	5.32	5.32	40.03	42.04	42.23	4.04	3.86	3.89
16	151.25	129.00	126.50	12.60	13.38	13.05	2.51	2.36	2.30	33.80	37.20	34.70	3.68	2.29	2.37	124.58	85.20	82.70	4.38	7.49	7.22	38.26	38.65	38.24	2.73	4.60	4.39
17	132.85	111.60	108.10	11.60	10.72	10.00	2.20	3.00	2.80	31.00	33.70	30.20	3.10	1.81	1.90	96.00	61.20	57.70	6.50	7.47	7.06	39.72	38.82	38.82	4.28	4.72	4.47
18	117.75	96.50	93.00	10.80	11.07	9.30	2.16	2.84	2.40	29.50	19.40	15.90	2.69	1.22	1.26	79.70	23.40	19.90	8.05	7.52	6.37	40.82	37.61	40.11	5.55	4.54	4.26
19	118.75	98.00	94.00	10.10	11.60	10.60	1.81	2.52	2.30	26.63	23.60	19.60	2.46	1.94	2.13	65.75	46.00	42.00	7.10	6.77	6.19	41.08	37.24	38.74	4.95	4.04	3.97
20	134.63	114.38	109.88	13.10	11.25	10.30	2.66	3.12	2.85	35.90	31.73	27.23	4.09	1.72	1.84	147.40	54.35	49.85	5.77	5.82	5.33	38.42	37.63	37.63	3.60	3.51	3.22

Contd.....

RIL	PH (F4)	PH (F5)	PH (F6)	SN (F4)	SNP (F5)	SNP (F6)	MN (F4)	MNP (F5)	MNP (F6)	BN (F4)	NBP (F5)	NBP (F6)	BW (F4)	BW (F5)	BW (F6)	SCYP (F4)	SCYP (F5)	SCYP (F6)	SI (F4)	SI (F5)	SI (F6)	GOT (F4)	GOT (F5)	GOT (F6)	LI (F4)	LI (F5)	LI (F6)
21	141.25	119.50	116.50	12.80	11.34	10.70	2.67	2.43	2.30	35.40	24.80	21.80	3.83	2.60	2.79	136.68	61.60	58.60	6.98	6.95	6.60	40.76	40.89	41.10	4.81	4.81	4.61
22	115.15	94.20	91.20	12.00	6.71	5.90	2.36	2.16	1.90	32.10	20.50	17.50	3.32	1.22	1.26	106.50	25.00	22.00	6.76	5.88	5.17	35.29	38.78	40.78	3.69	3.72	3.56
23	131.75	110.50	107.00	14.80	9.40	8.80	3.24	2.23	2.10	40.40	28.30	24.80	4.62	1.97	2.12	189.00	55.80	52.30	5.32	5.32	5.00	39.77	39.26	39.26	3.52	3.44	3.23
24	132.65	111.90	107.90	12.70	11.04	10.20	2.43	1.95	1.80	34.00	27.33	23.33	3.73	1.93	2.09	127.10	52.50	48.50	7.40	8.19	7.57	39.07	38.03	38.03	4.79	5.04	4.65
25	94.63	74.88	69.88	12.00	10.35	9.50	2.32	1.63	1.50	31.20	29.75	24.75	3.39	2.06	2.28	109.23	60.75	55.75	6.13	6.83	6.27	39.87	41.10	40.25	4.07	4.81	4.25
26	132.92	111.17	108.17	14.60	13.34	12.75	3.01	2.77	2.63	40.70	33.53	30.53	4.45	2.05	2.14	182.00	68.65	65.65	7.11	6.60	6.30	38.28	38.07	38.07	4.41	4.06	3.87
27	127.75	107.00	103.00	13.00	11.92	11.20	2.59	2.77	2.60	35.23	32.80	28.80	3.93	2.01	2.14	138.60	64.40	60.40	7.60	5.96	5.62	40.26	38.55	38.55	5.13	3.75	3.52
28	138.25	115.50	113.50	10.40	12.04	11.40	1.97	2.20	2.10	27.70	24.50	22.50	2.46	2.00	2.06	68.15	48.40	46.40	8.11	7.30	6.89	38.75	36.67	36.67	5.13	4.23	3.99
29	135.00	111.25	110.25	13.40	9.72	9.60	2.72	2.63	2.60	36.90	32.00	31.00	4.06	2.68	2.69	150.80	84.05	83.05	8.40	6.74	6.65	37.31	36.48	36.48	5.06	3.90	3.84
30	134.25	110.00	109.50	12.80	11.00	10.50	2.41	2.81	2.70	34.90	25.70	25.20	3.90	2.28	2.13	136.30	53.20	52.70	6.40	5.89	5.65	39.42	40.31	40.31	4.20	3.99	3.82
31	133.92	108.17	109.17	13.20	8.97	8.83	2.72	1.84	1.83	36.90	20.58	21.58	4.32	2.35	2.16	161.00	45.58	46.58	8.88	5.85	5.93	40.35	40.96	42.68	6.01	4.06	4.41
32	132.45	108.70	107.70	15.75	11.86	11.20	3.43	2.79	2.70	45.90	30.40	29.40	4.78	2.03	1.99	219.00	59.80	58.80	7.77	6.48	6.22	37.85	37.01	37.01	4.80	3.83	3.66
33	137.25	113.00	112.50	15.60	9.72	9.50	3.55	2.56	2.50	46.10	23.00	22.50	4.83	2.41	2.37	222.50	53.80	53.30	7.69	7.28	7.18	37.28	36.97	36.97	4.57	4.29	4.21
34	144.35	118.10	119.60	13.50	11.00	11.20	2.71	2.75	2.80	37.40	17.30	18.80	4.29	2.90	2.66	160.57	48.60	50.10	8.51	6.97	7.11	41.64	36.00	36.00	6.07	3.95	4.02
35	137.95	113.20	113.20	14.00	11.57	11.00	2.87	2.43	2.30	38.45	19.40	19.40	3.81	2.19	2.04	154.25	40.40	40.40	8.32	7.60	7.22	39.85	39.74	42.19	5.52	4.94	5.28
36	118.55	94.30	93.80	11.40	8.42	8.10	2.39	3.20	3.10	32.50	24.80	24.30	3.27	2.11	2.12	112.75	52.90	52.40	8.32	5.73	5.56	39.54	41.75	41.75	5.46	4.12	3.98
37	133.65	108.40	108.90	13.30	10.08	10.10	2.61	2.82	2.80	36.10	20.60	21.10	3.66	3.49	3.09	138.50	61.00	61.50	6.94	7.43	7.48	39.83	39.91	39.91	4.59	4.93	4.98
38	142.45	119.20	117.70	13.10	11.14	10.50	2.76	2.66	2.50	35.40	21.00	19.50	3.73	2.09	2.13	136.20	43.60	42.10	7.78	7.13	6.73	41.33	42.40	41.50	5.48	5.25	4.77
39	124.13	98.38	99.38	11.50	9.59	9.63	2.15	3.25	3.25	31.00	30.25	31.25	3.09	3.10	3.03	96.00	93.75	94.75	6.15	6.75	6.79	41.02	41.64	41.85	4.27	4.81	4.88
40	119.20	92.40	94.40	11.40	8.93	9.40	2.10	3.61	3.80	30.10	12.40	14.40	2.95	3.16	2.75	88.67	37.60	39.60	6.34	6.47	6.81	42.24	39.65	40.65	4.64	4.27	4.67
41	157.75	133.50	133.00	23.60	13.36	12.90	3.09	3.28	3.20	46.40	32.80	32.30	3.86	2.19	2.18	184.00	71.25	70.75	5.16	6.92	6.80	42.30	36.60	36.60	3.79	4.00	3.93
42	140.95	120.70	116.20	15.40	12.31	10.90	3.54	2.02	1.80	45.30	24.20	19.70	4.89	1.69	1.85	221.25	41.60	37.10	6.21	7.59	6.73	40.76	37.72	38.22	4.27	4.60	4.16
43	133.05	112.80	108.30	17.60	10.33	9.85	3.70	2.20	2.10	47.60	37.80	33.30	4.76	2.60	2.82	225.00	97.90	93.40	7.91	6.97	6.65	37.61	41.24	42.30	4.77	4.89	4.87

Contd.....

RIL	PH (F4)	PH (F5)	PH (F6)	SN (F4)	SNP (F5)	SNP (F6)	MN (F4)	MNP (F5)	MNP (F6)	BN (F4)	NBP (F5)	NBP (F6)	BW (F4)	BW (F5)	BW (F6)	SCYP (F4)	SCYP (F5)	SCYP (F6)	SI (F4)	SI (F5)	SI (F6)	GOT (F4)	GOT (F5)	GOT (F6)	LI (F4)	LI (F5)	LI (F6)
44	130.05	108.80	105.30	13.00	9.63	9.20	2.47	2.82	2.70	35.00	34.20	30.70	3.95	2.47	2.64	138.20	82.60	79.10	8.30	7.25	6.94	41.65	39.92	39.73	5.92	4.84	4.60
45	116.25	95.00	91.50	12.20	10.90	9.70	2.31	1.56	1.40	32.30	22.90	19.40	3.47	1.54	1.63	113.15	34.80	31.30	5.15	6.12	5.55	38.67	37.76	38.26	3.26	3.71	3.44
46	124.05	103.80	99.30	12.50	9.91	8.60	2.36	2.54	2.20	33.30	22.70	18.20	3.60	1.49	1.61	121.00	33.80	29.30	6.90	8.42	7.29	42.54	37.64	38.14	5.10	5.08	4.50
47	153.85	130.60	129.10	11.60	9.87	9.70	2.49	2.78	2.70	34.10	33.20	31.70	3.62	2.16	2.23	131.43	71.90	70.40	7.21	6.74	6.55	38.66	35.98	35.98	4.55	3.80	3.69
48	161.75	136.50	137.00	12.40	7.12	7.40	2.59	2.47	2.60	35.00	14.30	14.80	3.79	1.60	1.64	135.50	23.00	23.50	8.14	7.53	7.53	38.81	36.34	37.34	5.19	4.22	4.48
49	146.58	121.83	121.83	12.40	8.74	8.93	2.55	2.50	2.57	35.40	19.93	19.93	3.84	1.93	2.03	141.90	38.90	38.90	6.63	5.79	5.88	39.97	41.88	39.85	4.42	4.19	3.89
50	149.35	123.60	124.60	10.80	8.65	8.90	1.98	2.93	3.00	28.10	16.75	17.75	2.71	4.45	4.29	78.00	74.90	75.90	7.06	7.19	7.33	36.38	38.34	38.34	4.03	4.47	4.56
51	152.05	128.30	127.30	14.80	9.31	9.30	2.99	3.25	3.20	50.30	21.40	20.40	3.47	3.00	2.98	185.00	61.70	60.70	7.60	7.37	7.24	38.15	35.54	35.54	4.68	4.13	4.03
52	148.25	124.50	123.50	14.70	9.50	9.30	2.99	2.69	2.60	41.33	21.20	20.20	4.37	2.55	2.53	182.40	52.30	51.30	5.99	8.23	7.95	42.52	41.40	40.90	4.43	5.81	5.50
53	173.15	149.90	148.40	16.00	10.95	10.80	3.73	2.35	2.30	49.63	33.80	32.30	4.91	2.90	2.98	244.55	98.20	96.70	7.28	7.96	7.82	37.92	40.20	40.45	4.45	5.37	5.34
54	165.00	139.20	137.70	15.33	12.97	12.85	3.46	2.64	2.60	44.30	43.00	41.50	4.86	3.23	3.27	215.00	136.50	135.00	6.08	5.64	5.61	42.82	41.49	42.45	4.55	3.99	4.13
55	162.45	108.20	108.20	17.37	8.64	8.80	3.92	2.19	2.20	52.20	19.40	19.40	4.94	2.86	2.73	256.00	52.90	52.90	5.83	6.15	6.25	39.42	36.83	36.83	3.79	3.64	3.71
56	132.95	105.00	102.00	12.30	8.08	7.70	2.39	2.93	2.80	32.40	20.80	17.80	3.48	2.80	3.08	113.38	58.10	55.10	5.83	7.00	6.66	39.49	38.45	38.45	3.81	4.36	4.15
57	126.75	112.00	107.50	12.70	8.75	8.20	2.75	2.98	2.80	35.70	24.70	20.20	3.92	3.04	3.50	141.70	75.20	70.70	6.66	6.63	6.23	37.77	39.23	39.23	4.07	4.28	4.02
58	132.25	111.00	108.00	12.30	8.56	8.20	2.42	2.19	2.10	32.80	23.30	20.30	3.52	3.57	3.91	118.80	80.90	77.90	7.36	6.70	6.45	39.13	40.26	40.26	4.77	4.52	4.34
59	132.75	106.30	103.30	11.10	8.39	8.00	1.94	2.31	2.20	29.40	23.50	20.50	2.88	2.72	2.98	84.80	63.20	60.20	7.16	7.73	7.36	40.84	38.79	38.79	4.94	4.89	4.65
60	128.05	129.25	124.25	13.40	8.59	8.08	2.63	2.36	2.23	36.80	26.70	21.70	4.21	3.29	3.87	154.97	84.93	79.93	6.34	7.69	7.24	38.86	38.56	38.56	4.04	4.82	4.54
61	149.00	131.50	127.50	13.00	11.42	10.40	2.81	3.51	3.20	37.03	17.70	13.70	4.18	2.53	2.98	159.25	44.70	40.70	7.05	7.23	6.58	38.91	38.41	38.41	4.49	4.51	4.10
62	152.25	114.05	111.55	13.50	8.40	7.98	2.85	3.55	3.38	38.35	21.73	19.23	4.48	2.30	2.47	173.40	49.93	47.43	5.95	5.77	5.48	40.46	38.20	38.20	4.04	3.57	3.39
63	136.30	113.20	109.20	14.20	9.31	8.80	3.19	2.74	2.60	41.00	28.00	24.00	4.71	2.85	3.17	193.00	79.70	75.70	6.77	6.97	6.62	36.97	38.62	38.62	4.00	4.39	4.16
64	133.95	119.00	116.00	12.80	9.68	9.30	2.56	2.29	2.20	35.10	25.20	22.20	3.85	3.47	3.89	135.80	85.50	82.50	6.02	6.85	6.60	40.04	39.29	39.45	4.03	4.43	4.31
65	140.75	109.70	105.20	16.97	9.38	8.50	3.81	2.53	2.30	51.70	21.80	17.30	4.95	2.30	2.64	254.00	49.50	45.00	6.93	6.47	5.89	36.25	39.77	39.77	3.94	4.27	3.90
66	129.95	119.60	116.10	14.10	9.05	8.50	2.97	2.67	2.50	40.20	25.40	21.90	4.67	2.07	2.23	188.75	51.90	48.40	6.17	5.55	5.18	37.83	37.76	37.76	3.83	3.35	3.13

Contd.....

RIL	PH (F4)	PH (F5)	PH (F6)	SN (F4)	SNP (F5)	SNP (F6)	MN (F4)	MNP (F5)	MNP (F6)	BN (F4)	NBP (F5)	NBP (F6)	BW (F4)	BW (F5)	BW (F6)	SCYP (F4)	SCYP (F5)	SCYP (F6)	SI (F4)	SI (F5)	SI (F6)	GOT (F4)	GOT (F5)	GOT (F6)	LI (F4)	LI (F5)	LI (F6)
67	140.85	128.50	125.00	12.10	9.39	8.80	2.42	3.20	3.00	32.04	22.20	18.70	3.40	2.49	2.79	111.17	55.20	51.70	6.50	7.21	6.75	37.16	38.13	38.13	3.85	4.43	4.15
68	149.75	129.70	124.70	12.30	9.87	9.10	2.30	2.49	2.30	33.20	26.70	21.70	3.55	2.62	3.00	118.40	70.80	65.80	7.48	6.79	6.27	37.33	40.77	40.52	4.47	4.68	4.26
69	149.45	108.70	107.20	12.80	10.57	10.10	2.39	2.38	2.30	34.20	23.00	21.50	3.79	2.85	2.89	130.80	63.50	62.00	7.36	7.14	6.87	38.84	39.23	39.23	4.68	4.62	4.44
70	131.95	121.60	120.10	13.30	9.47	9.20	2.63	3.16	3.10	36.00	25.50	24.00	4.11	2.68	2.81	148.30	68.50	67.00	8.54	6.31	6.16	37.58	37.18	37.18	5.18	3.75	3.65
71	144.85	106.20	106.70	14.50	8.01	7.80	3.19	2.14	2.10	41.70	12.30	12.80	4.75	2.79	2.66	197.95	33.90	34.40	7.12	6.68	6.55	41.90	38.82	40.32	5.13	4.23	4.44
72	131.45	112.20	112.20	12.90	8.99	8.60	2.73	2.14	2.10	35.90	16.20	16.20	4.00	2.36	2.47	145.00	38.30	38.30	8.03	7.41	7.19	40.30	40.33	41.34	5.42	4.96	5.07
73	136.95	107.50	107.00	12.20	9.44	9.20	2.25	2.74	2.70	32.80	20.30	19.80	3.38	2.20	2.19	111.00	44.00	43.50	7.30	5.67	5.59	40.18	37.30	37.30	4.91	3.38	3.33
74	131.75	109.00	110.00	10.20	8.09	8.30	1.87	1.56	1.60	26.70	13.30	14.30	2.31	3.01	2.82	62.50	40.00	41.00	5.87	5.69	5.87	39.29	38.45	38.95	3.81	3.61	3.76
75	134.75	107.50	104.00	13.20	9.66	9.00	2.53	2.13	2.00	35.70	22.20	18.70	4.00	2.36	2.64	143.30	52.70	49.20	5.94	7.05	6.58	40.16	36.51	36.51	3.99	4.07	3.78
76	128.75	110.40	106.90	14.48	8.67	7.80	3.33	3.34	3.00	42.90	17.20	13.70	4.77	2.25	2.61	207.50	39.00	35.50	8.29	8.41	7.80	41.37	40.40	40.55	5.85	5.70	5.32
77	131.65	101.88	99.38	13.10	9.41	8.98	2.47	3.48	3.33	35.40	22.20	19.70	4.06	2.72	2.98	144.00	60.13	57.63	8.37	7.22	6.87	41.91	36.19	36.19	6.04	4.06	3.85
78	124.13	119.00	114.50	12.20	10.19	9.50	2.43	2.47	2.30	32.90	27.10	22.60	3.47	2.50	2.81	114.30	67.70	63.20	6.47	7.28	6.79	41.12	36.19	36.19	4.52	4.13	3.85
79	139.25	117.90	114.40	11.65	10.19	9.80	2.24	2.81	2.70	30.90	20.60	17.10	3.11	4.13	4.74	96.20	84.60	81.10	6.78	6.84	6.57	41.76	41.60	39.60	4.86	4.87	4.32
80	139.15	140.90	138.40	12.20	9.92	9.20	2.33	2.71	2.50	33.30	15.90	13.40	3.48	2.25	2.43	118.00	34.90	32.40	6.62	8.05	7.43	42.00	39.25	40.25	4.79	5.19	5.01
81	163.15	123.30	122.30	13.10	9.73	9.80	2.51	1.80	1.80	35.53	16.40	15.40	3.91	3.12	3.18	140.13	50.20	49.20	9.02	6.86	6.82	42.09	38.25	38.25	6.55	4.24	4.24
82	147.05	125.80	128.30	12.00	9.88	10.30	2.36	2.31	2.40	32.50	18.90	21.40	3.34	3.14	2.90	109.20	59.70	62.20	8.74	6.41	6.66	36.62	37.91	37.91	5.04	3.92	4.07
83	153.05	122.80	125.30	11.00	7.30	7.80	2.18	2.34	2.50	29.70	17.83	20.33	2.71	2.07	1.94	80.70	36.60	39.10	8.39	6.15	6.57	37.68	41.62	41.35	5.11	4.39	4.63
84	150.05	106.50	109.50	11.60	7.90	8.40	2.09	2.16	2.30	30.10	18.50	21.50	3.08	2.51	2.30	94.20	47.60	50.60	6.68	5.14	5.47	36.57	38.27	38.77	3.88	3.19	3.47
85	134.25	108.00	111.00	11.80	9.41	9.80	2.35	2.20	2.30	31.70	18.90	21.90	3.21	3.13	2.82	102.00	58.70	61.70	7.22	6.39	6.72	42.30	37.81	37.81	5.29	3.89	4.08
86	135.75	93.80	96.30	13.80	8.75	9.10	2.81	2.11	2.20	37.40	16.90	19.40	4.06	3.65	3.31	153.65	59.90	62.40	7.37	5.94	6.20	40.62	39.39	39.39	5.05	3.85	4.01
87	121.05	97.50	101.00	13.53	8.67	9.30	2.70	2.52	2.70	37.10	18.50	22.00	4.00	2.76	2.49	150.10	51.30	54.80	8.10	7.14	7.67	41.78	40.29	40.29	5.81	4.82	5.17
88	125.75	110.00	111.50	9.90	8.75	8.90	1.79	2.14	2.20	26.70	13.90	15.40	2.29	3.66	3.29	61.00	49.20	50.70	7.01	6.29	6.48	38.00	41.18	41.18	4.31	4.41	4.54
89	136.25	106.90	106.90	14.40	9.63	9.50	3.25	2.18	2.20	41.30	21.50	21.50	4.73	1.74	1.76	195.60	37.80	37.80	6.93	5.63	5.76	42.38	38.83	40.98	5.09	3.58	4.00

Contd.....

RIL	PH (F4)	PH (F5)	PH (F6)	SN (F4)	SNP (F5)	SNP (F6)	MN (F4)	MNP (F5)	MNP (F6)	BN (F4)	NBP (F5)	NBP (F6)	BW (F4)	BW (F5)	BW (F6)	SCYP (F4)	SCYP (F5)	SCYP (F6)	SI (F4)	SI (F5)	SI (F6)	GOT (F4)	GOT (F5)	GOT (F6)	LI (F4)	LI (F5)	LI (F6)
90	131.65	104.50	104.00	13.90	14.56	14.50	2.80	3.01	3.00	37.90	38.50	38.00	4.09	3.21	3.22	157.00	123.00	122.50	6.51	7.05	7.02	39.91	42.44	42.20	4.32	5.20	5.13
91	131.55	106.30	106.80	15.20	10.22	10.20	3.49	2.21	2.20	45.30	25.63	26.13	4.96	3.27	3.21	225.20	83.20	83.70	7.01	6.56	6.60	38.94	39.91	39.91	4.48	4.36	4.38
92	151.65	128.40	126.90	12.20	12.26	12.10	2.22	2.13	2.10	33.00	31.70	30.20	3.49	3.45	3.54	115.30	108.70	107.20	6.67	6.98	6.90	40.91	41.89	42.15	4.61	5.03	5.03
93	132.85	108.10	108.10	13.20	11.46	11.40	2.69	2.69	2.70	35.70	29.10	29.10	4.05	2.90	2.94	144.50	84.90	84.90	7.66	6.35	6.38	34.50	40.58	40.45	4.03	4.37	4.34
94	145.85	120.10	121.10	16.50	10.84	11.00	3.60	2.77	2.80	52.50	22.80	23.80	4.84	2.53	2.44	257.00	57.20	58.20	6.82	6.69	6.85	38.81	40.32	40.32	4.33	4.54	4.63
95	142.65	118.40	117.90	12.20	10.58	10.50	2.57	1.78	1.80	34.90	14.60	14.10	3.70	2.65	2.61	135.10	38.20	37.70	5.98	7.38	7.46	41.60	37.98	37.98	4.27	4.52	4.56
96	149.85	129.60	125.10	11.70	11.76	10.30	2.31	1.81	1.60	31.00	20.50	16.00	3.07	1.85	2.06	95.40	38.70	34.20	7.82	7.20	6.22	39.44	39.52	40.52	5.09	4.70	4.23
97	155.25	135.00	130.50	11.80	12.26	11.10	2.32	3.48	3.15	32.20	22.50	18.00	3.28	2.12	2.41	107.00	48.10	43.60	7.09	7.90	7.16	38.73	38.40	38.40	4.50	4.93	4.46
98	139.35	117.10	114.60	12.10	13.06	12.70	2.63	2.67	2.60	34.50	35.20	32.70	3.60	2.58	2.70	129.20	90.30	87.80	7.79	7.34	7.14	38.21	40.03	40.13	4.89	4.91	4.80
99	141.85	119.60	117.10	14.30	10.72	9.90	3.15	2.93	2.70	40.50	17.40	14.90	4.52	2.02	2.18	183.00	34.90	32.40	7.40	8.07	7.46	41.94	39.87	39.97	5.34	5.35	4.97
100	131.65	111.40	106.90	13.50	13.54	12.40	2.89	2.08	1.90	37.90	25.50	21.00	4.51	2.22	2.47	171.50	56.80	52.30	8.73	7.08	6.49	38.85	37.44	37.44	5.54	4.24	3.88
101	144.35	124.10	119.60	10.55	13.15	11.80	1.79	2.90	2.60	26.30	22.80	18.30	2.88	1.91	2.13	79.60	43.50	39.00	8.77	7.43	6.65	32.24	35.72	35.72	4.19	4.13	3.70
102	156.75	136.50	132.00	11.90	13.01	12.00	2.53	3.46	3.20	34.20	29.50	25.00	3.52	2.05	2.25	125.10	60.30	55.80	6.87	5.69	5.26	40.79	35.39	35.39	4.73	3.11	2.88
103	132.63	110.88	107.88	12.30	12.89	12.28	2.30	2.60	2.48	34.20	24.90	21.90	3.57	2.58	2.80	123.80	63.48	60.48	6.36	6.65	6.33	41.24	39.87	39.87	4.47	4.41	4.21
104	170.65	149.40	145.90	16.00	13.01	12.50	3.64	1.98	1.90	53.70	30.90	27.40	4.51	3.09	3.37	243.83	95.90	92.40	5.85	7.20	6.92	42.03	41.30	40.74	4.24	5.07	4.77
105	143.75	123.50	119.00	13.30	12.36	11.60	2.95	2.77	2.60	38.20	24.90	20.40	4.28	2.97	3.41	167.70	74.20	69.70	7.13	6.32	5.93	38.06	41.43	41.43	4.39	4.48	4.19
106	149.45	127.20	124.70	15.10	11.98	11.60	3.05	2.58	2.50	42.05	26.20	23.70	3.99	2.71	2.88	175.00	71.00	68.50	6.42	6.48	6.28	34.22	39.76	39.76	3.39	4.28	4.14
107	142.85	122.60	118.10	16.10	11.87	11.30	3.65	2.94	2.80	48.20	34.60	30.10	4.91	2.71	2.98	235.67	93.90	89.40	5.07	6.39	6.09	41.37	37.69	41.95	3.58	3.89	4.40
108	135.05	114.80	110.30	13.00	11.48	11.00	2.65	2.72	2.60	36.60	35.30	30.80	4.25	3.04	3.34	157.30	106.10	101.60	6.67	6.57	6.29	38.47	42.18	42.40	4.17	4.80	4.63
109	134.75	113.50	110.00	13.70	10.37	10.00	2.81	3.32	3.20	37.92	28.40	24.90	4.29	3.39	3.73	162.90	96.30	92.80	7.83	7.64	7.36	38.46	41.03	42.10	4.91	5.31	5.35
110	142.25	122.50	117.50	13.60	10.40	9.60	2.62	4.01	3.70	38.00	28.70	23.70	4.23	2.35	2.64	161.00	67.60	62.60	6.39	7.59	7.01	39.18	40.10	39.34	4.13	5.09	4.54
111	142.92	121.17	118.17	11.18	11.58	10.77	1.86	2.10	1.97	27.00	18.47	15.47	3.32	2.38	2.63	101.38	43.53	40.53	6.15	8.00	7.45	35.47	38.99	39.58	3.46	5.16	4.94
112	143.95	121.20	119.20	14.50	10.80	10.50	3.25	2.06	2.00	43.00	19.10	17.10	4.85	3.84	4.14	210.93	68.80	66.80	6.91	7.27	7.07	37.52	37.38	38.36	4.17	4.33	4.39

Contd.....

RIL	PH (F4)	PH (F5)	PH (F6)	SN (F4)	SNP (F5)	SNP (F6)	MN (F4)	MNP (F5)	MNP (F6)	BN (F4)	NBP (F5)	NBP (F6)	BW (F4)	BW (F5)	BW (F6)	SCYP (F4)	SCYP (F5)	SCYP (F6)	SI (F4)	SI (F5)	SI (F6)	GOT (F4)	GOT (F5)	GOT (F6)	LI (F4)	LI (F5)	LI (F6)
113	145.85	124.60	121.10	14.80	10.46	9.80	3.26	2.72	2.55	41.70	24.00	20.50	4.52	2.47	2.70	188.80	59.10	55.60	7.12	6.52	6.13	41.60	40.11	40.11	5.07	4.37	4.11
114	157.35	136.60	132.60	16.75	10.97	10.40	3.63	3.48	3.30	49.45	26.90	22.90	4.95	2.89	3.23	247.50	78.10	74.10	6.19	6.19	5.87	41.12	40.87	39.37	4.32	4.28	3.80
115	156.45	136.70	131.70	13.33	12.12	11.30	3.83	3.43	3.20	61.30	29.30	24.30	4.60	2.56	2.89	272.90	74.20	69.20	8.29	6.64	6.20	42.09	38.63	38.63	6.03	4.18	3.90
116	156.35	135.60	131.60	13.40	12.46	11.80	2.57	2.96	2.80	36.60	25.40	21.40	4.18	3.16	3.57	153.00	79.20	75.20	6.97	6.99	6.63	41.27	40.92	41.15	4.90	4.85	4.66
117	149.45	128.70	124.70	11.90	9.89	8.90	2.30	2.53	2.30	31.20	20.30	16.30	3.30	2.20	2.52	104.40	45.20	41.20	4.65	7.36	6.75	38.48	38.83	39.83	2.93	4.67	4.50
118	151.25	130.00	126.50	12.30	9.30	8.80	2.33	2.65	2.50	32.80	22.00	18.50	3.58	3.47	3.87	117.60	75.50	72.00	8.59	7.20	6.82	37.77	38.97	38.97	5.24	4.60	4.36
119	149.05	125.80	124.30	13.30	9.32	9.20	2.71	2.22	2.20	36.10	17.20	15.70	4.13	2.73	2.95	149.30	47.90	46.40	5.58	6.37	6.30	38.04	38.45	38.95	3.43	3.98	4.02
120	157.55	132.30	132.80	13.20	10.52	10.70	2.50	2.25	2.30	35.73	21.30	21.80	3.95	3.58	3.23	142.50	68.70	69.20	5.90	5.79	5.92	39.25	37.91	37.91	3.81	3.55	3.63
121	160.35	136.10	135.60	15.00	10.37	10.40	3.39	1.46	1.50	43.70	20.20	19.70	4.79	3.26	3.22	209.80	64.10	63.60	7.27	5.67	5.74	42.32	39.08	39.08	5.33	3.66	3.69
122	163.55	139.30	138.80	12.90	10.55	10.60	2.64	2.18	2.20	34.93	22.20	21.70	3.68	3.34	3.10	132.10	66.20	65.70	7.54	4.99	5.01	40.60	38.58	38.58	5.18	3.14	3.16
123	150.35	126.10	125.60	13.20	9.04	9.00	2.55	2.29	2.30	35.70	22.90	22.40	4.07	2.84	2.71	145.33	59.30	58.80	5.23	7.17	7.03	39.12	39.75	39.75	3.36	4.68	4.61
124	153.15	129.90	128.40	12.60	10.46	10.30	2.39	2.75	2.70	33.70	25.45	23.95	3.68	2.82	2.84	124.45	68.90	67.40	8.85	6.31	6.25	38.63	40.51	40.51	5.57	4.31	4.26
125	141.55	118.30	116.80	12.70	9.80	9.50	2.33	2.56	2.50	33.80	20.00	18.50	3.76	3.47	3.49	127.90	63.20	61.70	7.47	5.47	5.35	38.85	35.64	35.64	4.75	3.05	2.98
126	141.35	116.60	116.60	12.00	8.84	8.90	2.34	2.48	2.50	32.33	19.60	19.60	3.37	2.66	2.73	108.80	51.70	51.70	6.60	7.22	7.26	40.43	39.62	39.62	4.48	4.74	4.76
127	139.78	114.53	115.03	11.60	9.31	9.33	2.31	1.71	1.73	27.00	27.50	28.00	3.60	2.71	2.67	121.57	74.23	74.73	7.19	6.15	6.15	38.94	35.66	35.66	4.60	3.32	3.34
128	131.35	109.60	106.60	15.70	9.96	9.50	3.58	2.40	2.30	46.75	27.80	24.80	4.80	2.29	2.55	224.00	61.40	58.40	7.36	7.82	7.47	38.86	39.03	38.52	4.68	5.02	4.69
129	135.25	115.00	110.50	12.40	8.54	7.50	2.51	2.85	2.50	33.30	20.50	16.00	3.57	1.79	2.02	119.38	36.90	32.40	5.43	6.89	6.05	38.39	38.77	39.77	3.40	4.36	3.98
130	130.05	108.30	105.30	11.50	8.77	8.40	2.19	2.61	2.50	30.40	21.30	18.30	2.97	3.53	3.97	90.38	75.50	72.50	5.33	6.16	5.89	41.66	39.02	40.17	3.81	3.96	3.98
131	145.05	123.30	120.30	13.10	8.49	8.10	2.60	2.62	2.50	35.90	26.10	23.10	4.09	2.54	2.74	147.30	65.80	62.80	5.68	6.64	6.34	36.19	39.36	39.36	3.28	4.33	4.12
132	155.85	134.60	131.10	13.70	10.11	9.60	2.89	2.53	2.40	38.40	23.50	20.00	4.35	2.84	3.18	167.00	67.60	64.10	7.10	6.14	5.83	41.62	39.92	39.92	5.06	4.09	3.88
133	144.35	123.60	119.60	14.60	10.48	9.80	3.36	2.14	2.00	44.60	29.40	25.40	4.70	2.16	2.34	212.90	63.20	59.20	6.91	5.82	5.45	41.90	38.50	38.50	4.98	3.65	3.42
134	140.05	119.30	115.30	13.90	10.29	9.60	3.05	2.47	2.30	39.00	24.00	20.00	4.34	2.45	2.73	169.63	58.10	54.10	7.35	6.21	5.78	37.90	38.64	38.64	4.48	3.91	3.64
135	137.15	116.90	112.40	13.40	10.43	9.60	2.73	2.17	2.00	36.50	22.90	18.40	4.13	2.56	2.94	151.00	58.20	53.70	7.27	5.99	5.52	39.02	38.48	38.48	4.69	3.75	3.46

Contd.....

RIL	PH (F4)	PH (F5)	PH (F6)	SN (F4)	SNP (F5)	SNP (F6)	MN (F4)	MNP (F5)	MNP (F6)	BN (F4)	NBP (F5)	NBP (F6)	BW (F4)	BW (F5)	BW (F6)	SCYP (F4)	SCYP (F5)	SCYP (F6)	SI (F4)	SI (F5)	SI (F6)	GOT (F4)	GOT (F5)	GOT (F6)	LI (F4)	LI (F5)	LI (F6)
136	143.75	124.00	119.00	13.90	11.71	11.00	2.95	1.70	1.60	38.00	32.60	27.60	4.20	2.60	2.93	160.20	82.00	77.00	6.29	6.30	5.91	34.72	37.44	37.44	3.39	3.77	3.54
137	134.55	111.30	109.80	12.20	9.82	9.50	2.31	2.07	2.00	32.90	24.30	22.80	3.44	2.88	2.95	113.20	69.60	68.10	8.15	6.83	6.63	38.69	40.40	40.40	5.15	4.63	4.50
138	153.35	128.10	128.60	13.40	9.37	9.40	2.54	2.10	2.10	36.80	23.80	24.30	4.15	4.26	4.16	153.30	99.70	100.20	6.86	6.56	6.59	38.82	41.71	42.15	4.36	4.70	4.80
139	157.85	133.60	133.10	11.68	11.16	11.00	2.08	2.53	2.50	30.90	22.20	21.70	3.12	4.13	4.24	97.00	90.90	90.40	6.56	6.53	6.46	39.91	41.62	41.16	4.36	4.64	4.51
140	166.75	141.50	142.00	8.30	9.84	9.90	1.42	2.35	2.35	19.90	19.40	19.90	2.21	2.92	2.84	44.67	55.80	56.30	7.49	6.54	6.59	42.00	40.61	40.61	5.42	4.47	4.50
141	123.45	98.70	98.70	11.90	9.43	9.70	2.28	2.05	2.10	31.20	17.80	17.80	3.32	1.96	2.01	105.65	37.60	37.60	5.71	6.51	6.77	39.91	38.88	38.03	3.79	4.10	4.15
142	117.85	94.10	93.10	12.20	10.12	10.00	2.31	1.96	1.90	32.50	25.10	24.10	3.48	2.30	2.44	113.40	58.70	57.70	6.85	6.82	6.75	40.21	38.38	38.38	4.60	4.23	4.19
143	142.25	119.50	117.50	11.50	10.55	10.00	2.24	1.90	1.80	30.60	19.30	17.30	3.00	1.98	2.10	91.90	38.10	36.10	7.61	6.45	6.11	37.62	37.12	37.12	4.59	3.82	3.61
144	136.05	113.30	111.30	9.90	11.38	10.10	1.54	2.01	1.80	25.50	13.60	11.60	2.19	1.30	1.36	56.00	17.70	15.70	7.21	6.66	5.95	40.24	38.90	38.15	4.85	4.24	3.67
145	133.15	111.90	108.40	11.58	10.62	9.90	2.18	2.04	1.90	30.53	24.70	21.20	3.02	2.26	2.48	92.50	55.80	52.30	7.29	7.50	7.00	38.68	37.43	37.43	4.60	4.52	4.20
146	169.45	148.70	144.70	11.20	9.40	8.90	2.05	2.75	2.60	29.70	20.80	16.80	2.86	3.65	4.29	85.00	75.10	71.10	7.60	6.11	5.79	37.76	40.89	40.89	4.62	4.21	3.99
147	147.55	127.80	122.80	12.50	8.80	7.70	2.34	3.31	2.90	33.30	19.80	14.80	3.56	2.03	2.38	119.50	40.30	35.30	6.85	6.14	5.37	37.68	42.22	39.82	4.14	4.49	3.54
148	146.05	125.30	121.30	11.60	9.14	8.10	2.10	2.82	2.50	31.10	18.20	14.20	3.12	1.93	2.20	97.17	35.10	31.10	6.25	6.38	5.65	38.48	40.06	39.81	3.92	4.26	3.74
149	141.25	121.50	116.50	10.90	9.37	8.70	2.07	2.91	2.70	29.10	27.90	22.90	2.74	2.52	2.85	79.80	70.00	65.00	6.76	6.29	5.84	35.11	38.78	38.78	3.67	3.98	3.70
150	147.45	124.70	122.70	12.40	8.40	8.10	2.39	2.39	2.30	33.50	16.90	14.90	3.56	2.81	3.01	119.40	47.30	45.30	7.61	7.62	7.39	40.49	37.86	37.86	5.18	4.65	4.50
151	130.88	104.13	106.13	13.25	9.42	9.83	2.59	1.66	1.73	36.10	15.43	17.43	4.13	2.94	2.72	149.00	45.50	47.50	7.15	6.18	6.45	40.45	38.25	38.25	4.86	3.79	3.96
152	146.40	117.15	121.65	12.20	9.01	10.43	2.44	2.16	2.50	33.80	12.43	16.93	3.51	2.52	2.04	121.17	28.78	33.28	6.04	5.47	6.33	38.01	39.61	36.36	3.70	3.59	3.70
153	133.95	105.20	109.20	12.70	8.30	8.80	2.45	1.79	1.90	34.20	15.40	19.40	3.84	4.23	3.56	131.25	65.00	69.00	6.50	7.11	7.54	39.05	39.25	39.25	4.18	4.60	4.86
154	136.15	107.90	111.40	13.90	8.14	8.80	2.91	2.04	2.20	39.70	24.60	28.10	4.56	1.77	1.68	181.58	43.50	47.00	7.71	6.05	6.54	37.65	41.21	40.05	4.66	4.22	4.37
155	133.35	105.60	108.60	12.50	7.83	8.20	2.37	1.81	1.90	33.90	14.80	17.80	3.70	4.43	3.84	125.60	64.80	67.80	7.28	6.09	6.38	39.25	39.58	39.58	4.70	3.99	4.18
156	150.85	123.10	126.10	10.20	8.73	9.10	1.94	1.73	1.80	28.00	16.00	19.00	2.53	4.33	3.79	71.10	69.10	72.10	7.45	6.69	6.98	39.97	37.91	37.91	4.96	4.09	4.27
157	153.35	125.60	128.60	15.30	10.08	10.80	3.43	2.04	2.20	44.90	12.30	15.30	4.58	3.26	2.83	205.80	40.10	43.10	5.91	6.03	6.53	41.81	41.08	41.08	4.25	4.19	4.54
158	137.55	110.30	112.80	11.60	9.84	10.20	2.16	2.41	2.50	30.30	22.80	25.30	3.14	3.03	2.83	96.70	68.70	71.20	7.92	6.16	6.39	39.88	37.49	37.49	5.25	3.70	3.84

Contd.....

RIL	PH (F4)	PH (F5)	PH (F6)	SN (F4)	SNP (F5)	SNP (F6)	MN (F4)	MNP (F5)	MNP (F6)	BN (F4)	NBP (F5)	NBP (F6)	BW (F4)	BW (F5)	BW (F6)	SCYP (F4)	SCYP (F5)	SCYP (F6)	SI (F4)	SI (F5)	SI (F6)	GOT (F4)	GOT (F5)	GOT (F6)	LI (F4)	LI (F5)	LI (F6)
159	138.45	109.70	113.70	12.20	9.50	10.10	2.36	2.35	2.50	32.40	20.20	24.20	3.52	3.15	2.80	117.60	64.30	68.30	6.09	5.16	5.51	39.68	41.37	41.37	4.00	3.64	3.89
160	151.05	125.80	126.30	14.20	10.28	10.30	2.89	2.39	2.40	39.10	22.40	22.90	4.14	2.88	2.83	164.75	64.70	65.20	6.24	5.39	5.44	38.73	40.28	40.28	3.95	3.62	3.65
161	160.15	135.90	135.40	12.63	11.13	10.90	2.27	2.64	2.60	33.80	21.80	21.30	3.75	3.60	3.66	127.00	78.20	77.70	5.76	7.27	7.61	42.22	40.72	41.49	4.21	5.00	5.35
162	151.15	125.90	126.40	11.90	9.84	9.80	2.30	2.07	2.10	31.30	19.30	19.80	3.26	3.73	3.43	107.55	67.20	67.70	9.04	6.42	6.43	40.12	37.99	37.99	6.06	3.94	3.94
163	140.15	114.90	115.40	12.10	8.53	8.50	2.26	2.96	3.00	31.83	16.30	16.80	3.39	3.90	3.82	108.80	63.10	63.60	7.06	8.50	8.56	36.38	37.03	37.03	4.04	5.00	5.03
164	147.45	124.70	122.70	12.43	9.19	8.80	2.25	2.07	2.00	32.83	18.50	16.50	3.55	3.81	4.19	117.10	70.60	68.60	6.05	6.00	5.77	42.16	38.10	38.10	4.41	3.71	3.56
165	141.25	117.50	116.50	12.00	11.65	11.40	2.34	1.86	1.80	31.30	18.10	17.10	3.27	3.27	3.47	106.90	59.50	58.50	6.88	6.64	6.46	41.69	37.87	37.87	4.92	4.06	3.94
166	141.65	116.40	116.90	12.20	9.64	9.70	2.24	2.27	2.30	32.20	18.20	18.70	3.49	3.85	3.87	114.70	70.20	70.70	7.88	7.33	7.39	37.53	38.22	38.22	4.73	4.55	4.57
167	136.45	111.70	111.70	11.60	9.97	9.90	2.15	2.82	2.90	30.40	18.20	18.20	3.10	3.23	3.54	95.60	59.00	59.00	7.93	7.52	7.54	41.77	37.43	37.43	5.70	4.58	4.54
168	139.05	114.80	114.30	11.60	7.39	7.30	2.14	2.11	2.10	30.80	16.20	15.70	3.07	2.70	2.73	94.80	43.20	42.70	8.06	7.38	7.27	40.96	41.42	40.05	5.59	5.22	4.86
169	155.15	131.40	130.40	12.20	10.00	9.80	2.20	2.34	2.30	32.60	17.30	16.30	3.48	3.81	4.11	113.40	65.90	64.90	7.67	7.72	7.66	40.28	41.11	41.11	5.17	5.39	5.36
170	148.55	122.80	123.80	10.60	8.76	9.00	1.89	1.88	1.90	27.10	18.50	19.50	2.51	3.50	3.35	69.60	64.70	65.70	10.34	6.41	6.55	40.64	40.70	40.70	7.08	4.41	4.50
171	162.15	136.40	137.40	11.83	9.20	9.30	2.27	1.88	1.90	30.90	17.00	18.00	3.29	3.46	3.18	104.30	56.70	57.70	7.47	7.56	7.65	41.40	41.14	40.64	5.28	5.28	5.23
172	152.55	128.80	127.80	10.50	10.23	9.80	1.54	1.86	1.80	25.40	18.90	17.90	2.48	2.49	2.55	65.70	46.60	45.60	5.99	6.31	6.11	41.07	38.56	38.56	4.21	3.97	3.83
173	147.15	122.40	122.40	11.30	10.18	10.20	2.04	1.69	1.68	29.30	18.60	18.60	2.87	2.95	3.05	85.80	54.80	54.80	6.67	5.49	5.44	40.71	39.01	39.01	4.58	3.53	3.48
174	148.85	125.60	124.10	11.20	9.87	9.50	2.07	2.86	2.80	29.00	20.20	18.70	2.98	3.16	3.20	90.10	61.20	59.70	6.78	5.74	5.55	39.56	38.48	38.48	4.44	3.60	3.47
175	158.95	133.70	134.20	11.20	9.00	9.20	2.08	2.55	2.60	29.80	15.70	16.20	2.87	3.43	3.45	85.38	54.50	55.00	8.41	6.73	6.85	39.19	39.93	39.93	5.42	4.50	4.56
176	156.35	131.60	131.60	12.80	9.33	9.40	2.44	2.09	2.10	33.90	15.40	15.40	3.81	4.52	4.51	129.60	69.70	69.70	6.86	7.39	7.42	42.01	36.85	36.85	4.97	4.31	4.32
177	138.85	114.10	114.10	11.70	9.80	9.80	2.23	1.87	1.90	31.10	19.20	19.20	3.16	3.31	3.46	98.20	63.70	63.70	7.74	6.42	6.43	34.98	37.69	37.69	4.16	3.89	3.89
178	143.13	121.38	118.38	12.70	11.77	11.33	2.26	2.90	2.78	33.90	23.23	20.23	3.71	3.61	3.87	125.80	77.90	74.90	7.69	6.90	6.58	39.56	38.64	38.64	5.04	4.34	4.14
179	154.95	134.70	130.20	11.50	10.87	10.30	2.17	2.74	2.60	31.50	26.10	21.60	3.11	3.45	3.96	99.04	90.20	85.70	5.81	8.16	8.06	40.78	41.33	39.33	4.02	5.73	5.25
180	150.85	129.60	126.10	13.50	11.18	10.70	2.80	2.09	2.00	36.93	21.80	18.30	4.04	3.73	4.26	150.30	81.40	77.90	6.09	7.31	6.99	33.77	38.58	38.58	3.18	4.59	4.39
181	142.05	119.80	117.30	12.90	9.15	8.80	2.49	3.22	3.10	34.90	22.80	20.30	3.76	2.90	3.14	133.20	65.90	63.40	7.49	6.85	6.59	41.06	38.85	38.85	5.22	4.37	4.20

Contd.....

RIL	PH (F4)	PH (F5)	PH (F6)	SN (F4)	SNP (F5)	SNP (F6)	MN (F4)	MNP (F5)	MNP (F6)	BN (F4)	NBP (F5)	NBP (F6)	BW (F4)	BW (F5)	BW (F6)	SCYP (F4)	SCYP (F5)	SCYP (F6)	SI (F4)	SI (F5)	SI (F6)	GOT (F4)	GOT (F5)	GOT (F6)	LI (F4)	LI (F5)	LI (F6)
182	157.25	137.00	132.50	11.70	11.19	10.60	2.11	2.74	2.60	30.80	30.80	26.30	3.18	2.79	3.10	98.90	86.60	82.10	6.80	6.40	6.07	40.22	39.75	37.75	4.57	4.24	3.68
183	143.45	122.20	118.70	11.10	11.03	10.10	2.08	2.27	2.10	30.10	25.55	22.05	2.81	1.79	1.91	84.80	45.90	42.40	7.30	7.97	7.32	38.44	39.85	39.85	4.56	5.28	4.84
184	120.75	98.50	96.00	12.50	12.05	11.46	2.50	2.25	2.15	33.80	22.33	19.83	3.71	2.34	2.51	125.33	52.40	49.90	6.85	6.88	6.53	36.48	38.61	38.61	3.94	4.33	4.11
185	128.85	104.10	104.10	14.00	9.68	9.60	2.99	2.50	2.50	38.10	21.60	21.60	4.23	3.20	3.31	162.08	68.70	68.70	9.81	7.12	7.10	37.71	39.22	39.22	5.94	4.61	4.59
186	132.25	106.50	107.50	12.10	8.79	9.00	2.37	2.26	2.30	32.30	11.10	12.10	3.33	2.55	2.22	107.80	26.10	27.10	6.07	6.81	6.97	39.97	39.38	42.38	4.07	4.42	5.12
187	144.85	121.10	120.10	11.00	11.04	10.20	2.12	2.48	2.30	28.80	19.30	18.30	2.75	1.70	1.80	80.60	33.00	32.00	6.89	6.17	5.83	40.81	39.33	39.83	4.76	4.00	3.86
188	128.75	105.00	104.00	10.70	8.48	8.30	1.87	3.01	2.90	27.90	28.10	27.10	2.68	2.39	2.42	76.40	67.30	66.30	7.28	5.67	5.53	41.44	39.71	39.71	5.15	3.74	3.64
189	138.35	115.10	113.60	11.20	8.72	8.50	2.14	2.27	2.20	29.60	26.75	25.25	2.93	2.19	2.22	89.40	57.20	55.70	6.27	6.70	6.52	42.45	39.02	39.02	4.63	4.29	4.17
190	130.45	107.20	105.70	11.30	8.97	8.60	2.03	1.91	1.80	29.50	18.90	17.40	3.03	2.49	2.58	92.50	47.20	45.70	7.43	6.89	6.57	41.35	40.89	41.69	5.24	4.76	4.67
191	127.75	103.00	103.00	12.30	9.45	9.00	2.27	2.53	2.40	32.20	18.33	18.33	3.37	1.76	1.70	113.75	31.90	31.90	10.17	7.07	6.84	40.83	38.20	38.20	7.02	4.36	4.25
192	136.85	115.10	112.10	10.90	10.69	9.70	1.71	3.47	3.10	26.30	17.05	14.05	2.86	1.77	2.05	81.30	29.60	26.60	8.04	7.15	6.42	42.36	39.17	39.37	5.91	4.62	4.16
193	142.15	121.90	117.40	13.50	11.56	10.50	2.79	2.53	2.30	36.30	26.00	21.50	3.87	1.98	2.21	143.70	49.90	45.40	8.00	7.15	6.50	40.48	40.04	38.23	5.44	4.76	4.02
194	150.65	129.40	125.90	14.73	10.07	9.70	3.29	2.80	2.70	42.70	25.90	22.40	4.82	3.66	4.07	205.67	95.00	91.50	9.12	8.22	7.92	41.75	40.04	40.30	6.53	5.49	5.35
195	150.85	128.60	126.10	11.20	10.29	9.30	2.00	3.10	2.80	29.90	13.40	10.90	2.93	2.00	2.27	87.67	26.80	24.30	6.85	6.42	5.81	42.19	38.28	39.78	5.00	3.98	3.85
196	145.15	124.90	120.40	11.30	10.08	9.30	2.15	2.93	2.70	30.80	21.70	17.20	3.01	2.66	3.11	94.48	57.70	53.20	5.32	7.85	7.24	41.70	39.02	39.02	3.81	5.01	4.63
197	142.95	122.70	118.20	15.10	8.77	8.30	3.39	2.54	2.40	43.80	27.70	23.20	4.77	3.00	3.40	208.90	83.20	78.70	6.72	6.29	5.95	40.04	36.23	40.43	4.48	3.56	4.06
198	145.95	124.70	121.20	9.60	8.52	8.00	1.59	3.08	2.90	18.85	22.30	18.80	2.42	2.76	3.07	48.00	60.80	57.30	7.36	6.88	6.47	35.71	40.97	40.97	4.12	4.77	4.49
199	141.75	121.00	117.00	15.80	8.23	7.80	3.16	2.54	2.40	45.15	18.40	14.40	4.33	4.08	4.92	197.80	74.90	70.90	7.79	5.97	5.65	40.50	40.63	40.63	5.31	4.08	3.87
200	136.35	114.60	111.60	10.70	8.63	7.90	2.12	2.40	2.20	29.00	19.20	16.20	2.60	1.82	1.98	75.30	36.30	33.30	5.71	6.79	6.22	39.10	38.23	39.23	3.67	4.20	4.02
201	142.95	123.20	118.20	10.60	9.37	8.40	2.00	1.79	1.60	28.50	21.90	16.90	2.55	2.27	2.69	72.60	48.00	43.00	7.37	7.71	6.90	40.08	40.07	40.07	4.93	5.16	4.61
202	147.05	125.30	122.30	11.60	9.56	9.10	2.19	2.20	2.10	30.90	20.85	17.85	3.10	3.37	3.84	96.20	70.70	67.70	6.94	7.06	6.72	39.58	37.65	37.65	4.55	4.27	4.06
203	137.05	115.80	112.30	13.80	9.60	9.10	2.89	2.53	2.40	37.50	22.70	19.20	4.10	3.01	3.37	155.35	68.30	64.80	5.72	8.91	8.55	40.20	39.76	39.76	3.85	5.88	5.64
204	145.55	125.80	120.80	12.90	10.11	9.10	2.37	2.55	2.30	34.35	25.30	20.30	3.85	2.02	2.27	133.10	51.20	46.20	6.38	6.31	5.69	39.64	37.94	37.94	4.19	3.85	3.47

Contd.....

RIL	PH (F4)	PH (F5)	PH (F6)	SN (F4)	SNP (F5)	SNP (F6)	MN (F4)	MNP (F5)	MNP (F6)	BN (F4)	NBP (F5)	NBP (F6)	BW (F4)	BW (F5)	BW (F6)	SCYP (F4)	SCYP (F5)	SCYP (F6)	SI (F4)	SI (F5)	SI (F6)	GOT (F4)	GOT (F5)	GOT (F6)	LI (F4)	LI (F5)	LI (F6)
205	148.05	127.30	123.30	10.70	9.31	8.80	1.98	2.44	2.30	29.10	25.20	21.20	2.63	2.94	3.31	76.60	74.70	70.70	7.13	7.97	7.51	40.99	38.96	38.96	4.95	5.07	4.78
206	141.05	121.30	116.30	9.90	9.43	8.30	1.75	2.27	2.00	25.95	23.90	18.90	2.34	1.79	2.00	60.90	42.20	37.20	6.91	7.78	6.84	36.65	36.32	36.32	4.00	4.44	3.90
207	147.25	126.00	122.50	13.10	8.77	8.50	2.58	3.09	3.00	35.20	40.50	37.00	3.65	2.81	2.99	134.80	113.50	110.00	6.88	5.85	5.67	41.51	41.00	42.25	4.88	4.08	4.15
208	161.85	140.60	137.10	16.00	9.71	9.30	3.65	3.45	3.30	48.25	30.80	27.30	4.91	2.58	2.78	236.00	79.80	76.30	7.00	8.75	8.90	40.25	41.52	42.25	4.73	6.22	6.51
209	151.85	130.60	127.10	12.00	10.07	9.50	2.42	2.50	2.35	32.20	25.50	22.00	3.36	2.63	2.89	108.10	65.20	61.70	7.68	7.11	6.71	40.18	41.20	39.65	5.16	4.98	4.44
210	136.95	115.20	112.20	14.00	9.88	9.50	2.76	2.59	2.50	38.50	27.50	24.50	4.04	3.15	3.47	158.20	86.40	83.40	7.35	7.74	7.48	41.26	40.70	40.15	5.17	5.36	5.03
211	133.85	113.60	109.10	10.93	11.04	10.20	2.09	1.40	1.30	28.50	23.30	18.80	2.71	2.59	3.01	78.30	59.55	55.05	4.89	6.98	6.45	39.32	39.54	39.54	3.16	4.57	4.22
212	156.90	135.15	132.15	13.10	7.98	7.70	2.60	1.77	1.70	34.80	23.75	20.75	3.49	3.44	3.78	131.55	79.30	76.30	3.57	6.49	6.25	41.91	41.40	40.55	2.57	4.59	4.26
213	161.75	140.00	137.00	9.70	8.49	8.20	1.78	2.49	2.40	25.70	21.40	18.40	2.26	4.07	4.58	58.50	87.20	84.20	7.43	7.68	7.41	37.39	41.02	41.71	4.45	5.35	5.28
214	157.15	142.10	138.60	11.40	9.91	9.30	1.93	2.56	2.40	29.60	22.20	18.70	3.03	2.58	2.85	96.00	56.50	53.00	5.67	7.52	7.05	42.08	36.80	36.80	4.12	4.38	4.11
215	129.95	108.20	105.20	12.40	7.53	7.20	2.26	3.03	2.90	32.90	20.80	17.80	3.48	3.14	3.51	119.65	66.20	63.20	7.68	6.08	5.81	42.43	40.34	39.19	5.66	4.11	3.75
216	158.75	137.00	134.00	11.70	9.29	8.90	2.15	2.09	2.00	30.40	19.60	16.60	3.11	3.92	4.35	98.30	74.00	71.00	8.36	6.95	6.64	39.00	39.93	39.93	5.34	4.55	4.36
217	152.15	127.90	127.40	12.30	8.88	8.80	2.28	2.09	2.10	33.30	16.60	16.10	3.53	3.78	3.74	117.50	60.80	60.30	7.71	4.90	4.88	32.35	39.81	38.66	3.69	3.23	3.08
218	145.25	121.00	120.50	14.05	8.60	8.60	2.85	1.78	1.80	40.00	16.20	15.70	3.67	3.72	3.69	155.60	58.60	58.10	6.95	6.28	6.30	40.98	39.33	39.33	4.82	4.07	4.08
219	139.25	112.50	114.50	12.93	7.39	7.70	2.44	2.19	2.30	34.70	15.00	17.00	3.92	3.01	2.78	136.10	45.20	47.20	5.12	4.74	4.95	41.57	40.75	40.75	3.64	3.26	3.41
220	136.45	109.70	111.70	12.40	7.43	7.70	2.36	1.93	2.00	32.90	16.30	18.30	3.57	3.50	3.22	119.70	56.70	58.70	6.38	5.80	6.01	40.25	40.24	40.24	4.30	3.90	4.04
221	149.95	122.70	125.20	10.90	9.16	9.50	2.00	2.22	2.30	28.30	17.10	19.60	2.74	3.77	3.44	79.40	64.40	66.90	5.70	6.16	6.39	41.51	37.89	37.89	4.03	3.76	3.89
222	138.35	113.60	117.10	14.10	7.98	8.45	3.08	2.74	2.90	40.05	14.40	17.90	4.56	4.25	3.54	182.40	59.60	63.10	5.99	6.36	6.74	40.42	39.17	39.17	4.06	4.10	4.34

PH= plant height (cm), MNP= number of monopodia per plant, SNP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value (µg/inch), UI = Uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).

Appendix IIIb: Phenotypic observation on fibre quality traits in F₅ and F₆ segregating population delivered from intraspecific hybridization between RHAP 12 × RHAP 15 of *G. hirsutum*

No. of lines	UHML (F5)	UHML (F6)	FS (F5)	FS (F6)	Mic (F5)	Mic (F6)	UI (F5)	UI (F6)	MR (F5)	MR (F6)	EL (F5)	EL (F6)
1	26.65	26.45	25.23	22.33	3.13	3.07	75.60	87.60	0.44	0.43	5.00	6.50
2	24.35	22.35	23.63	22.63	3.59	3.64	78.40	79.80	0.52	0.52	5.10	5.70
3	25.00	30.90	24.60	29.90	3.45	3.19	80.00	94.40	0.57	0.54	4.50	6.20
4	25.10	22.50	24.80	25.10	3.86	3.69	76.40	80.70	0.64	0.61	4.70	5.70
5	26.50	23.70	27.30	25.40	3.26	3.49	81.90	87.10	0.54	0.58	5.00	5.80
6	22.50	24.30	22.60	25.60	4.10	3.75	85.20	80.80	0.68	0.62	5.00	5.60
7	24.70	25.40	24.60	25.00	3.49	3.72	80.80	76.20	0.58	0.62	4.10	5.40
8	27.30	22.90	24.70	25.00	3.86	3.55	73.00	81.50	0.64	0.59	4.50	5.70
9	24.80	21.10	25.20	22.90	4.12	3.41	73.80	78.30	0.68	0.57	4.80	5.90
10	23.65	23.85	23.73	25.13	3.51	3.29	77.80	58.40	0.50	0.47	4.40	5.70
11	25.70	22.80	25.10	22.90	3.71	3.47	76.00	83.10	0.62	0.58	4.80	5.70
12	26.10	22.30	24.60	22.80	4.11	3.17	77.20	81.40	0.68	0.53	4.50	6.00
13	29.60	29.60	21.40	29.40	2.41	2.41	81.60	81.60	0.40	0.40	6.20	6.20
14	27.80	24.40	26.10	25.20	2.84	3.05	71.10	81.50	0.47	0.51	4.40	5.50
15	26.10	26.20	25.10	29.10	3.13	2.57	76.60	85.30	0.52	0.43	4.70	6.00
16	26.60	22.70	26.40	25.40	3.23	3.68	78.70	80.80	0.54	0.61	5.10	5.50
17	28.65	27.75	26.03	25.53	2.54	2.87	73.40	83.00	0.34	0.40	4.80	5.80
18	26.90	24.60	28.80	25.80	2.26	2.85	77.50	79.90	0.38	0.47	5.20	5.60
19	27.60	24.90	28.10	25.40	2.92	3.04	79.50	80.80	0.49	0.50	5.00	5.80
20	24.10	21.80	25.10	22.90	2.73	2.83	82.40	87.30	0.45	0.47	4.30	5.40
21	27.40	25.20	28.30	25.60	3.27	4.05	80.00	82.90	0.54	0.67	5.00	5.80

Contd.....

No. of lines	UHML (F5)	UHML (F6)	FS (F5)	FS (F6)	Mic (F5)	Mic (F6)	UI (F5)	UI (F6)	MR (F5)	MR (F6)	EL (F5)	EL (F6)
22	26.10	26.10	21.70	25.70	2.86	2.86	80.40	80.40	0.48	0.48	6.00	6.00
23	26.90	26.90	26.40	30.00	3.66	3.66	78.00	78.00	0.61	0.61	5.00	5.00
24	27.10	20.40	24.60	25.00	4.11	3.25	79.90	83.60	0.68	0.54	4.40	5.40
25	25.30	24.20	26.20	22.80	3.69	2.99	73.00	78.30	0.61	0.50	5.80	6.00
26	26.80	26.70	25.30	22.60	3.75	3.39	73.40	69.30	0.62	0.56	4.70	6.60
27	24.90	24.40	26.10	29.20	3.70	3.04	75.20	82.60	0.61	0.50	4.80	5.00
28	30.80	26.10	28.90	29.20	3.28	3.13	74.30	80.30	0.54	0.52	5.40	6.60
29	28.30	25.60	28.60	25.30	2.96	2.82	77.80	80.30	0.49	0.47	6.20	5.10
30	27.50	22.80	26.10	22.80	3.18	3.20	75.40	78.20	0.53	0.53	4.60	5.10
31	27.40	23.40	27.10	25.10	2.66	3.24	75.30	77.20	0.44	0.54	4.90	4.90
32	26.15	23.35	25.23	25.23	3.15	3.74	75.50	77.90	0.44	0.54	4.70	4.70
33	26.00	25.60	27.10	25.30	3.54	3.47	76.80	75.60	0.59	0.58	5.00	4.70
34	26.40	24.00	28.00	25.10	3.42	3.42	77.70	72.10	0.57	0.57	5.10	4.80
35	28.90	27.30	28.10	29.40	3.22	3.52	76.00	73.30	0.53	0.58	4.80	4.90
36	26.00	24.80	25.30	22.70	3.37	4.29	75.40	75.80	0.56	0.71	4.50	4.80
37	25.00	25.70	25.00	25.70	3.34	4.09	78.30	76.50	0.55	0.68	4.60	4.50
38	27.80	24.60	27.30	25.50	3.04	3.78	74.00	75.80	0.50	0.63	4.90	4.90
39	25.40	23.80	25.40	22.80	3.99	4.26	78.00	77.70	0.66	0.71	4.80	4.90
40	26.55	26.55	28.63	30.63	3.52	3.52	82.10	82.10	0.50	0.50	5.40	5.40
41	26.50	25.30	28.40	25.30	3.23	3.98	77.30	73.10	0.54	0.66	5.30	5.10
42	30.30	26.90	28.90	29.10	3.13	3.81	72.20	73.10	0.52	0.63	5.50	5.00
43	26.90	24.30	25.40	25.40	3.47	4.19	77.90	78.70	0.58	0.70	5.00	5.00
44	29.10	26.80	29.00	25.90	3.14	3.42	75.70	78.00	0.52	0.57	5.30	5.30

Contd.....

No. of lines	UHML (F5)	UHML (F6)	FS (F5)	FS (F6)	Mic (F5)	Mic (F6)	UI (F5)	UI (F6)	MR (F5)	MR (F6)	EL (F5)	EL (F6)
45	25.85	25.15	25.23	25.03	3.31	3.84	76.80	73.50	0.47	0.56	5.50	4.70
46	26.60	24.00	27.20	25.60	3.29	3.13	76.70	69.80	0.55	0.52	5.00	5.50
47	26.45	24.35	26.23	29.43	3.55	3.35	71.20	78.20	0.51	0.48	4.70	5.00
48	25.40	26.00	26.30	25.60	2.95	3.66	78.50	76.00	0.49	0.61	4.80	4.80
49	26.30	27.20	26.00	29.10	3.41	3.85	79.40	75.50	0.57	0.64	4.70	5.50
50	27.75	26.75	28.53	28.93	3.14	3.50	74.90	75.40	0.44	0.50	4.90	4.90
51	25.80	24.50	27.00	22.80	3.56	3.59	77.50	75.10	0.59	0.60	4.80	4.70
52	25.70	26.00	25.40	29.30	3.60	3.40	76.80	74.00	0.60	0.56	4.20	5.20
53	27.90	26.10	30.80	25.70	4.09	4.39	82.90	78.60	0.68	0.73	5.50	5.50
54	26.40	26.40	24.90	25.90	4.25	3.12	76.60	78.80	0.71	0.52	4.50	4.60
55	25.05	25.05	28.43	25.13	3.47	3.31	81.70	75.80	0.50	0.47	5.00	4.90
56	26.90	26.90	25.00	25.10	3.55	3.74	74.80	70.60	0.59	0.62	4.40	4.40
57	24.65	24.65	25.83	28.83	4.03	3.89	74.50	79.70	0.59	0.57	4.90	5.20
58	23.80	23.80	27.10	25.10	3.63	3.77	76.60	74.50	0.60	0.63	5.10	5.10
59	26.80	25.40	27.10	25.90	4.13	3.46	78.90	76.40	0.69	0.57	4.90	5.20
60	25.45	24.35	27.03	25.43	3.51	3.45	79.50	75.90	0.50	0.49	4.80	4.90
61	26.10	24.80	28.50	25.70	3.12	3.26	78.20	75.00	0.52	0.54	5.20	5.20
62	25.30	22.90	26.00	22.70	2.94	3.15	76.70	78.10	0.49	0.52	4.50	4.40
63	27.20	27.20	27.20	29.30	3.10	3.16	72.00	78.80	0.51	0.52	4.90	5.20
64	27.30	26.40	25.40	25.90	3.34	2.78	65.90	69.60	0.55	0.46	4.40	4.70
65	24.75	26.55	25.13	28.93	2.88	4.14	74.10	75.50	0.40	0.61	4.20	5.10
66	22.90	24.90	24.50	25.20	3.49	4.09	58.80	74.70	0.58	0.68	4.40	5.00
67	28.40	28.50	26.30	29.30	3.32	3.58	74.80	75.40	0.55	0.59	4.30	5.30

Contd.....

No. of lines	UHML (F5)	UHML (F6)	FS (F5)	FS (F6)	Mic (F5)	Mic (F6)	UI (F5)	UI (F6)	MR (F5)	MR (F6)	EL (F5)	EL (F6)
68	22.60	22.40	24.90	22.80	3.62	3.86	49.90	77.30	0.60	0.64	4.40	4.70
69	25.10	25.20	26.20	22.90	3.89	3.31	76.70	73.30	0.65	0.55	4.50	4.70
70	27.60	22.50	27.00	22.80	3.37	3.15	77.40	76.10	0.56	0.52	5.70	4.50
71	26.20	24.90	28.10	25.40	3.27	3.05	79.20	77.80	0.54	0.51	5.20	5.00
72	28.90	24.90	26.10	25.00	3.69	3.36	64.70	75.00	0.61	0.56	4.60	4.80
73	18.90	24.40	28.20	22.90	3.20	2.73	70.00	72.80	0.53	0.45	5.10	4.70
74	20.40	23.40	28.30	25.20	3.87	2.89	56.30	72.80	0.64	0.48	5.00	4.90
75	22.30	23.40	24.60	22.90	3.82	3.03	80.40	72.50	0.63	0.50	4.50	4.80
76	25.20	25.60	26.20	25.40	4.06	3.58	82.50	76.10	0.67	0.59	4.60	4.80
77	21.40	23.50	24.50	22.70	3.59	3.76	71.90	72.30	0.60	0.62	4.60	4.60
78	26.15	26.45	26.93	25.53	3.00	2.72	74.00	73.10	0.42	0.37	5.00	4.80
79	26.00	23.80	28.20	22.80	3.82	3.62	77.40	71.70	0.63	0.60	5.30	4.80
80	28.30	23.80	29.40	25.40	3.65	3.63	79.00	77.50	0.61	0.60	5.70	4.50
81	25.40	24.10	24.60	22.90	3.96	3.52	63.90	75.00	0.66	0.58	4.90	4.90
82	27.45	24.05	25.93	24.83	3.73	3.67	58.50	73.20	0.54	0.53	5.80	5.00
83	28.10	22.90	24.70	22.80	3.42	3.74	89.00	72.00	0.57	0.62	5.80	4.80
84	28.10	23.30	24.90	22.70	3.50	3.81	81.80	69.50	0.58	0.63	4.80	4.70
85	25.45	22.35	23.63	22.53	3.28	3.66	71.40	69.00	0.46	0.53	4.70	4.60
86	29.30	27.40	26.20	25.40	3.16	3.38	83.30	76.50	0.52	0.56	5.30	4.60
87	26.85	25.15	24.63	25.13	3.25	3.89	84.00	70.70	0.46	0.57	4.90	4.40
88	29.60	25.90	25.00	25.90	3.55	3.78	82.90	76.30	0.59	0.63	4.90	5.20
89	29.10	25.20	24.70	25.50	3.45	3.74	78.60	75.20	0.57	0.62	5.10	5.10
90	28.40	28.40	23.90	29.90	4.26	4.26	77.00	77.00	0.71	0.71	4.80	4.80

Contd.....

No. of lines	UHML (F5)	UHML (F6)	FS (F5)	FS (F6)	Mic (F5)	Mic (F6)	UI (F5)	UI (F6)	MR (F5)	MR (F6)	EL (F5)	EL (F6)
91	28.90	26.10	25.30	25.20	3.84	3.61	82.00	75.00	0.64	0.60	5.20	5.00
92	29.80	24.90	25.10	25.10	3.85	3.54	78.60	72.50	0.64	0.59	5.00	5.10
93	27.65	26.05	24.43	28.83	3.78	3.96	83.90	75.90	0.55	0.58	4.90	5.90
94	28.10	25.10	24.70	25.10	3.83	3.83	84.20	79.30	0.64	0.64	5.00	5.00
95	29.70	25.60	25.30	25.90	3.86	3.53	81.00	73.70	0.64	0.59	5.30	5.50
96	30.10	25.90	25.40	25.40	3.11	3.35	86.70	68.00	0.52	0.56	5.30	4.70
97	30.90	27.50	26.20	25.70	3.70	3.50	83.80	75.10	0.61	0.58	5.30	5.00
98	29.35	24.75	24.93	25.33	3.70	3.55	82.00	72.80	0.53	0.51	5.20	5.10
99	29.40	26.40	25.20	25.50	3.46	3.68	84.10	71.60	0.57	0.61	5.10	5.00
100	28.80	25.90	25.10	29.00	3.01	3.24	85.70	78.40	0.50	0.54	5.30	5.80
101	31.90	28.30	26.40	29.80	3.29	3.22	78.00	74.00	0.55	0.53	5.60	5.50
102	29.60	24.10	25.10	25.20	3.18	3.81	84.00	78.30	0.53	0.63	5.10	5.00
103	28.80	25.60	24.90	25.50	3.58	3.69	83.00	72.00	0.59	0.61	4.80	4.50
104	29.55	25.25	25.23	25.73	3.74	3.64	83.80	73.80	0.54	0.52	5.10	5.00
105	29.40	22.60	24.80	22.70	4.23	3.52	74.10	75.50	0.70	0.58	5.30	5.10
106	30.70	25.60	26.00	25.30	3.36	3.64	81.80	77.20	0.56	0.60	5.20	5.20
107	28.60	23.50	24.90	22.70	3.86	4.68	83.00	75.80	0.64	0.78	5.00	5.20
108	27.75	23.55	24.63	24.93	3.84	4.21	85.70	75.00	0.56	0.62	5.00	5.20
109	29.35	24.55	25.13	25.23	3.75	4.22	82.30	72.60	0.54	0.62	5.30	5.00
110	29.70	25.80	25.10	25.30	3.89	3.84	79.30	76.40	0.65	0.64	5.70	5.20
111	27.10	25.40	25.30	29.20	3.24	3.51	85.90	78.80	0.54	0.58	5.30	5.60
112	28.10	24.30	24.80	25.00	3.04	3.39	82.30	71.00	0.50	0.56	5.10	4.60
113	26.70	24.60	23.80	22.90	3.84	4.02	80.70	72.50	0.64	0.67	5.00	4.90

Contd.....

No. of lines	UHML (F5)	UHML (F6)	FS (F5)	FS (F6)	Mic (F5)	Mic (F6)	UI (F5)	UI (F6)	MR (F5)	MR (F6)	EL (F5)	EL (F6)
114	27.20	24.60	24.80	22.80	3.58	3.61	83.60	71.90	0.59	0.60	5.00	4.50
115	26.80	23.90	24.60	22.80	3.70	4.07	90.30	73.20	0.61	0.68	5.80	4.70
116	27.80	24.90	25.10	25.20	3.26	3.90	82.50	74.80	0.54	0.65	5.00	4.70
117	28.45	24.35	24.73	22.73	3.42	3.33	81.10	71.30	0.49	0.47	5.00	4.70
118	28.00	24.00	24.80	22.80	3.82	3.88	82.00	75.60	0.63	0.64	5.20	4.80
119	27.60	25.10	24.60	25.60	3.73	3.69	85.00	74.00	0.62	0.61	5.00	5.10
120	27.20	23.60	24.60	22.70	3.92	3.51	82.90	71.10	0.65	0.58	4.80	4.50
121	29.30	23.30	24.80	22.80	3.81	3.63	79.20	72.10	0.63	0.60	5.10	4.50
122	27.30	23.20	24.80	22.60	3.64	3.59	58.10	74.00	0.60	0.60	5.00	4.80
123	26.40	24.40	24.50	22.80	3.63	3.97	60.40	74.00	0.60	0.66	5.00	4.90
124	25.15	23.55	23.73	22.73	3.22	3.57	88.10	73.90	0.45	0.51	5.10	5.20
125	25.40	24.00	24.70	22.80	3.45	2.84	77.60	73.40	0.57	0.47	5.40	4.50
126	26.30	23.30	24.80	22.80	3.80	4.17	83.30	72.30	0.63	0.69	5.60	4.70
127	26.30	24.20	23.70	22.90	3.15	3.31	64.50	76.80	0.52	0.55	5.90	4.60
128	26.90	25.60	25.00	25.40	3.41	3.60	72.10	74.80	0.57	0.60	6.00	4.90
129	24.20	23.90	23.80	22.80	3.66	4.00	81.20	75.60	0.61	0.66	5.90	5.40
130	23.90	24.30	23.80	22.60	4.24	3.67	72.80	73.30	0.61	0.61	5.90	4.20
131	27.30	22.60	24.50	22.60	3.80	4.02	78.50	72.00	0.63	0.67	5.90	4.30
132	27.80	23.20	24.70	22.70	3.79	3.94	78.60	74.50	0.63	0.65	6.10	4.80
133	27.20	24.90	24.60	25.40	3.07	3.17	81.50	75.90	0.51	0.53	5.90	5.00
134	26.70	24.50	24.60	25.40	3.04	3.70	77.30	75.30	0.50	0.61	5.80	5.00
135	25.70	23.30	24.50	22.90	3.24	3.15	80.00	75.10	0.54	0.52	5.90	5.00
136	28.20	26.50	25.10	25.20	3.42	3.76	87.00	74.20	0.57	0.62	6.10	5.30

Contd.....

No. of lines	UHML (F5)	UHML (F6)	FS (F5)	FS (F6)	Mic (F5)	Mic (F6)	UI (F5)	UI (F6)	MR (F5)	MR (F6)	EL (F5)	EL (F6)
137	25.60	24.70	23.90	25.20	3.77	3.54	81.00	77.10	0.63	0.59	5.80	5.10
138	25.20	24.80	23.80	25.10	4.55	3.69	80.30	81.30	0.76	0.61	5.80	4.50
139	25.85	23.55	24.33	25.33	3.76	3.70	85.00	80.70	0.54	0.53	6.00	5.50
140	28.10	25.90	24.90	29.10	3.27	3.07	90.50	76.00	0.54	0.51	6.10	5.50
141	29.80	26.00	25.10	25.60	3.36	2.27	83.00	70.80	0.56	0.38	6.30	5.20
142	28.10	26.20	24.60	25.30	3.24	2.77	79.40	72.20	0.54	0.46	5.90	5.60
143	26.80	25.10	25.00	25.20	2.92	3.26	95.30	74.50	0.49	0.54	6.20	5.10
144	28.60	25.60	24.90	25.90	2.44	2.16	81.60	77.30	0.41	0.36	6.00	5.00
145	29.00	27.90	24.80	29.20	3.29	3.16	84.30	73.50	0.55	0.52	5.90	5.00
146	26.75	23.55	24.43	22.63	3.27	3.36	78.30	75.90	0.46	0.48	6.00	5.00
147	25.90	23.40	23.90	22.80	2.90	3.49	76.10	74.90	0.48	0.58	5.90	4.60
148	26.70	24.20	24.60	25.00	2.52	4.22	80.70	77.90	0.42	0.70	5.90	4.80
149	28.60	25.90	24.90	25.30	3.05	3.09	87.90	76.50	0.51	0.51	6.00	4.80
150	28.80	24.60	24.50	25.20	3.58	3.72	88.20	77.80	0.59	0.62	6.00	5.00
151	29.00	26.10	25.20	25.30	2.78	3.15	87.80	76.00	0.46	0.52	6.10	5.60
152	24.80	23.40	23.90	22.80	3.68	3.28	72.20	81.70	0.61	0.54	5.80	4.80
153	26.50	23.80	23.80	25.00	4.51	3.77	77.30	71.30	0.75	0.63	5.90	4.20
154	26.10	23.10	23.80	25.30	3.54	3.48	79.30	75.10	0.59	0.58	5.80	4.80
155	24.40	22.00	23.70	22.60	4.21	4.63	78.30	76.00	0.70	0.77	5.80	4.80
156	26.60	25.90	24.80	25.40	4.05	4.34	86.20	76.10	0.67	0.72	6.00	4.80
157	27.30	25.10	23.90	25.40	3.65	3.83	72.00	73.90	0.61	0.64	5.90	4.90
158	24.70	25.00	23.80	25.10	3.35	3.74	72.30	74.60	0.56	0.62	5.70	4.40
159	25.10	23.90	23.70	22.80	3.32	3.92	73.90	74.50	0.55	0.65	5.80	4.60

Contd.....

No. of lines	UHML (F5)	UHML (F6)	FS (F5)	FS (F6)	Mic (F5)	Mic (F6)	UI (F5)	UI (F6)	MR (F5)	MR (F6)	EL (F5)	EL (F6)
160	27.30	25.30	23.90	25.50	3.41	4.18	80.20	77.00	0.57	0.69	5.80	4.80
161	23.85	24.05	23.53	22.73	3.85	4.25	70.50	71.00	0.56	0.63	5.90	5.00
162	25.80	26.00	23.80	25.60	3.58	3.42	85.80	81.00	0.59	0.57	6.30	4.80
163	25.20	25.40	23.90	25.30	3.60	3.40	77.80	76.50	0.60	0.56	5.80	4.90
164	27.05	24.15	24.43	25.23	3.32	3.65	82.80	75.50	0.47	0.53	6.00	4.80
165	25.60	24.80	23.80	25.10	3.84	4.05	78.30	76.60	0.64	0.67	5.80	4.80
166	26.15	24.85	24.33	25.43	3.70	3.51	79.60	72.50	0.53	0.50	5.80	4.50
167	26.20	23.30	24.50	22.90	4.14	4.30	79.40	73.40	0.69	0.71	5.80	4.70
168	25.70	26.10	23.90	25.70	3.76	3.78	84.80	75.80	0.62	0.63	5.90	5.00
169	24.10	25.90	23.90	25.60	3.87	3.72	87.40	72.10	0.64	0.62	6.00	4.50
170	27.10	26.00	24.50	25.50	3.35	3.45	81.30	76.50	0.56	0.57	5.80	5.00
171	26.70	26.20	24.70	25.60	3.54	3.93	73.30	74.80	0.59	0.65	6.10	5.00
172	28.05	24.85	24.73	25.23	3.18	3.16	68.10	73.20	0.45	0.44	6.30	4.50
173	26.30	26.30	24.60	29.20	3.62	3.32	59.40	74.90	0.60	0.55	6.00	5.10
174	26.40	24.40	24.70	25.10	3.31	3.06	79.20	71.80	0.55	0.51	6.00	4.70
175	26.35	25.05	24.43	25.13	3.49	3.53	83.40	77.50	0.50	0.51	6.00	5.20
176	29.30	27.00	24.90	25.60	3.55	4.02	85.20	75.40	0.59	0.67	6.30	4.50
177	25.05	23.75	24.63	22.63	3.33	3.68	83.00	74.60	0.47	0.53	6.10	5.40
178	27.00	24.50	24.80	25.60	3.54	4.39	79.30	74.10	0.59	0.73	6.00	4.70
179	27.30	25.90	25.30	25.90	3.64	3.71	94.10	77.90	0.60	0.62	6.30	4.90
180	24.75	25.55	23.73	25.43	3.51	3.44	81.80	75.60	0.50	0.49	5.90	4.90
181	25.80	24.20	23.90	25.10	3.82	3.62	81.20	76.90	0.63	0.60	5.80	4.60
182	26.60	26.10	24.60	25.60	3.98	3.74	86.90	78.00	0.66	0.62	6.00	5.00

Contd.....

No. of lines	UHML (F5)	UHML (F6)	FS (F5)	FS (F6)	Mic (F5)	Mic (F6)	UI (F5)	UI (F6)	MR (F5)	MR (F6)	EL (F5)	EL (F6)
183	28.60	26.10	24.90	29.10	4.12	3.36	87.50	75.30	0.68	0.56	6.10	5.20
184	24.90	23.50	24.50	22.90	3.85	4.36	79.90	72.50	0.64	0.72	6.00	5.40
185	28.45	24.45	24.73	25.13	3.50	3.21	83.70	72.20	0.50	0.45	6.00	4.80
186	27.20	25.50	24.80	25.50	3.64	3.30	81.30	74.90	0.67	0.55	6.00	5.10
187	25.00	24.30	24.60	22.90	4.02	2.80	84.50	70.80	0.63	0.47	5.90	5.00
188	27.30	24.10	24.50	22.80	3.79	3.37	87.40	72.40	0.63	0.56	6.00	4.80
189	27.90	25.80	25.10	25.50	3.17	3.09	83.70	75.40	0.53	0.51	6.20	5.00
190	26.15	24.05	24.33	22.63	3.79	2.92	86.00	68.80	0.55	0.40	5.70	4.00
191	26.90	25.50	23.80	25.40	3.51	3.50	68.30	76.80	0.58	0.58	6.30	4.60
192	27.10	25.10	24.70	25.30	3.40	3.98	81.10	72.60	0.56	0.66	6.00	4.60
193	27.65	24.85	24.93	25.13	3.49	3.23	82.00	73.30	0.50	0.46	6.10	4.80
194	26.80	26.00	24.60	25.80	3.72	3.91	87.80	76.20	0.62	0.65	5.90	4.60
195	29.15	26.95	24.63	28.93	2.31	2.21	77.00	72.30	0.30	0.29	5.80	4.70
196	26.50	25.10	23.80	25.90	3.57	4.16	78.50	80.60	0.59	0.69	5.90	5.20
197	27.70	27.00	24.80	25.90	2.91	3.64	88.40	75.30	0.48	0.60	5.90	4.80
198	27.50	26.30	24.60	25.80	3.60	3.34	84.50	76.40	0.60	0.55	6.00	4.90
199	26.50	24.80	24.60	29.10	3.41	3.54	85.10	76.00	0.57	0.59	6.00	5.00
200	28.30	25.70	25.10	29.10	2.97	3.21	82.40	76.50	0.49	0.53	5.90	5.00
201	25.85	25.55	24.43	25.63	3.25	3.71	80.00	79.50	0.46	0.54	5.70	4.60
202	28.80	26.20	24.90	22.90	3.76	3.65	92.00	76.30	0.62	0.61	6.10	5.80
203	26.80	22.70	24.50	29.10	3.54	3.64	82.70	58.20	0.59	0.60	5.90	5.20
204	26.30	25.20	23.80	25.20	3.84	3.27	84.80	71.50	0.64	0.54	5.90	5.10
205	26.85	23.35	24.53	22.63	4.01	3.16	82.30	71.20	0.59	0.44	5.90	5.10

Contd.....

No. of lines	UHML (F5)	UHML (F6)	FS (F5)	FS (F6)	Mic (F5)	Mic (F6)	UI (F5)	UI (F6)	MR (F5)	MR (F6)	EL (F5)	EL (F6)
206	27.95	27.95	20.93	28.93	2.74	2.74	74.40	74.40	0.38	0.38	4.80	4.80
207	26.10	26.40	24.50	25.80	2.72	3.44	84.20	76.80	0.45	0.57	5.90	4.90
208	25.05	25.05	21.63	25.63	3.37	3.37	77.60	77.60	0.48	0.48	5.30	5.30
209	28.30	24.90	23.90	25.20	4.00	4.07	80.10	76.00	0.66	0.68	5.90	4.60
210	23.90	23.30	23.70	22.90	3.99	4.11	74.30	76.00	0.66	0.68	5.60	4.80
211	27.15	25.05	24.43	24.83	2.92	3.03	82.50	72.30	0.40	0.42	5.80	4.80
212	25.90	23.80	24.60	25.00	4.07	4.07	81.10	58.40	0.68	0.68	6.10	4.90
213	27.30	24.90	24.60	25.60	4.06	3.39	84.80	78.30	0.67	0.56	6.00	4.80
214	27.10	24.40	24.90	25.80	3.17	3.80	83.80	80.60	0.53	0.63	6.00	5.30
215	26.30	26.30	24.50	25.30	3.54	3.26	78.50	76.50	0.59	0.54	5.90	4.80
216	25.55	26.75	24.33	28.83	3.32	3.47	79.50	73.50	0.47	0.50	5.80	5.30
217	28.40	24.80	23.90	25.40	3.17	3.87	69.90	78.30	0.53	0.64	5.90	4.90
218	28.10	28.10	24.90	25.40	3.13	3.13	73.90	73.90	0.52	0.52	4.80	4.80
219	27.10	23.50	24.60	25.50	3.23	3.09	82.50	78.30	0.54	0.51	6.00	5.20
220	27.15	23.35	24.73	25.03	3.04	3.45	81.00	76.70	0.42	0.49	5.90	5.00
221	27.70	26.80	24.80	25.90	3.23	3.56	82.80	75.30	0.54	0.59	6.10	5.00
222	24.40	24.40	21.00	29.00	3.50	3.50	79.40	79.40	0.58	0.58	5.60	5.60

PH= plant height (cm), MNP= number of monopodia per plant, SNP = number of sympodia per plants, NBP = Number of bolls per plant, SCYP= seed cotton yield per plant (g), SI= seed index (g), BW = Boll weight (g), GOT = Ginning outturn (%), LI = Lint index (g), FS = Fibre strength (g/tex), UHML = Upper half mean length (mm), Mic = Micronaire value ($\mu\text{g}/\text{inch}$), UI = Uniformity index (%), MR= Maturity ratio, FEL = Fibre elongation length (%).

**RNA SEQUENCE BASED QTL MAPPING AND GENETIC
INVESTIGATION FOR SEED COTTON YIELD AND FIBRE
STRENGTH IN *Gossypium hirsutum* L.**

MAHESH R HAMPANNAVAR

2020

Dr. B. R. PATIL

Major Advisor

ABSTRACT

The *Gossypium hirsutum* L. ($2n=4x=52$) is one of the major natural fibre crop. For a better understanding of QTL governing quantitative traits, a linkage map of cotton was sought through SRAP and TRAP markers in 222 RILs of intraspecific crosses (RHAP12 and RHAP15). The 146 polymorphic SRAP and TRAP markers were localized on 18 linkage groups with genome span length of 2910.81 cM and an average distance between neighbor marker was 19.94 cM.

Using genotypic and phenotypic data in RIL population a total of 16 QTL identified on five linkage groups for nine quantitative traits with phenotypic variation (R^2) ranging from of 4.56 - 18.44 per cent. The QTLs governing fibre strength (*qFS-16-1*), seed cotton yield (*qSCYP-16-1*) and boll weight (*qBWP-3-1*) had major impact on trait expression. Majority of the QTLs on the linkage group were found in clusters.

In RIL population seed cotton yield per plant, number of bolls per plant and boll weight had high variability where as all the fibre quality traits had low PCV and GCV except micronaire value. In association study, number of bolls per plant, boll weight and number of sympodia per plant had a significant positive correlation with seed cotton yield per plant. Furthermore in path analysis the same trait had direct positive effect on seed cotton yield per plant hence direct selection through this trait will be useful.

The intergeneration correlation and regression indicated that selection of elite lines at F_5 generation was fruitful compare to at F_6 generation as significant intergeneration correlation and regression existed between both generations.

Out of 222 RILs, the maximum transgressive segregants (>20% superior over RHAP12) were observed for seed cotton yield per plant (21). Finally RIL90, RIL3, RIL63, RIL15, RIL50, RIL93, and RIL216 were found promising lines for fibre strength and seed cotton yield per plant.