

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

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COIMBATORE - 641 003

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

Thesis submitted in part fulfillment of the requirements for the degree of
DOCTOR OF PHILOSOPHY (Agriculture) in
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CERTIFICATE

This is to certify that the thesis entitled “**GENETIC STUDIES IN UPLAND COTTON (*Gossypium hirsutum* L.)**” submitted in part fulfillment of the requirements for the award of the degree of **DOCTOR OF PHILOSOPHY (AGRICULTURE)** in **PLANT BREEDING AND GENETICS** to the Tamil Nadu Agricultural University, Coimbatore, is a record of *bonafide* research work carried out by **Mrs. K.S. USHARANI** under my supervision and guidance and that no part of this thesis has been submitted for the award of any other degree, diploma, fellowship or other similar titles or prizes. However, part of the thesis work has been published in peer reviewed scientific journal of national /international repute (copy enclosed).

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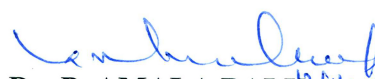
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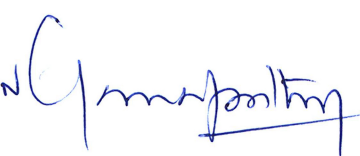

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(K.S. USHARANI)

Abstract

ABSTRACT
GENETIC STUDIES IN UPLAND COTTON
(*Gossypium hirsutum* L.)

By
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Degree : **Doctor of Philosophy in Plant Breeding and Genetics**
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2014

An investigation was carried out at Department of Cotton, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, during 2012-2014 to investigate the diallel analysis and also to assess the association between molecular markers with yield and fibre quality traits. A total of nine parents viz., Suraj, Surabhi, Khandwa 2, Anjali, KC 2, KC 3, MCU 5, MCU 7 and G.Cot 16 were selected as experimental materials and subjected to diallel analysis using the model I, method I to study the combining ability and gene action, heterosis, genetic components of variation and graphical analysis and to suggest suitable breeding strategies to improve fourteen important traits such as days to first boll bursting, plant height, number of sympodial branches per plant, number of bolls per plant, boll weight, single plant yield, ginning outturn, lint index, seed index, 2.5% span length, bundle strength, micronaire value, uniformity ratio and elongation per cent.

The analysis of variance had shown highly significant differences due to genotypes for all the traits indicating the presence of sufficient variability in the experimental materials.

The analysis of variance for combining ability revealed that the variances for the GCA were larger than that of SCA for all the traits except the number of bolls per plant indicating the preponderance of additive action which could be exploited for the improvement of these traits by mass selection or pedigree breeding.

Based on *per se* performance and *gca* effect MCU 5, Anjali and Surabhi were identified as good parents and hence suggested for further recombination breeding programme. Three hybrids namely MCU 5 x MCU 7, Anjali x MCU 5 and KC 2 x MCU 5 were found to be superior for yield and fibre quality traits based on *per se* performance, *sca* effect and standard heterosis. Hence, advancing these hybrids and effecting further selection in segregating generation would be helpful to develop high yielding varieties.

Genetic components of variation as suggested by Hayman (1954) indicated that additive component (D) and dominant genetic components (H_1 and H_2) were significant for a majority of characters studied. H_1 and H_2 were greater in their magnitude than the corresponding additive genetic variation (D) for all the traits except number of sympodial branches per plant, boll weight and elongation per cent. The positive F values was noted for all the traits except for the number of bolls per plant, boll weight and single plant yield which showed that there were more number of dominant alleles present in the parental lines than recessive alleles. The mean degree of dominance was found to be more than one for all the traits except for the number of sympodial branches per plant, boll weight and elongation per cent indicating over dominance. The proportion of genes with positive and negative effects in the parents was less than 0.25 for all the characters studied except for the number of bolls per plant and elongation per cent and also it was suggested that unequal mean allelic frequencies at effective loci. The ratio of dominant and recessive genes in the parents is greater than one for all the characters except for the number of bolls per plant, boll weight and single plant yield which indicated the presence of excess of dominant genes. The high estimates of heritability in narrow sense were found in micronaire value. The characters days to first boll bursting, plant height, boll weight, single plant yield, 2.5% span length and bundle strength recorded medium estimates of heritability.

Graphical analysis based on the position of the regression line showed over dominance type of gene action for all the traits studied except for days to first boll bursting, plant height, number of bolls per plant, boll weight, ginning outturn, seed index and elongation per cent.

In the present investigation, F_3 progenies derived from an intraspecific cross KC 2 and MCU 5 were evaluated for observing variation and correlation among yield components and fibre quality traits. An attempt has also been made to identify SSR markers linked to the investigated traits by associating the phenotypic data of F_3 progenies with the genotypic data of F_2 segregants. All the F_3 individuals were studied to assess the mean performance, genetic variability, heritability, genetic advance and association analysis of the traits.

Moderate GCV estimates were obtained for boll weight, micronaire value, lint index, elongation per cent, number of sympodial branches per plant and seed index. High heritability coupled with high genetic advance as percentage of mean was observed for boll weight, single plant yield, lint index and micronaire value. The directional selection for these traits could be effective for desired genetic improvement.

Seed cotton yield per plant exhibited positive association with plant height, number of sympodial branches per plant, number of bolls per plant, boll weight, lint index and seed index. Selection for these characters will help in selecting genotypes with high seed cotton yield per plant.

Out of 708 SSR primer pairs used, 12 (3.25%) SSR primer pairs yielded unambiguous, scorable polymorphic loci and they were used in genotyping of F_2 progenies. Marker-phenotypic association based on single marker analysis showed that 8 SSR markers viz., BNL 3563, BNL 1161, BNL 3623, BNL 3452, DPL 0234, DPL 0322, CIR 203 and NAU 797 exhibited a significant association with yield and fibre quality traits. Use of these markers in MAS may improve yield and fibre quality traits in cotton. MAS provide a potential for increasing selection efficiency by allowing earlier selection and reducing population size at early generations. Hence, markers identified in this study could be useful in future cotton breeding programme.

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LIST OF SYMBOLS AND ABBREVIATIONS

%	:	Percentage
AFLP	:	Amplified Fragment Length Polymorphism
ANOVA	:	Analysis of Variance
BC	:	Backcross
Bp	:	Base pair
°C	:	Degree celcius
CCI	:	Cotton Corporation of India
C.D	:	Critical Difference
Cm	:	Centimeter
cM	:	Centimorgan
CTAB	:	Cetyl Trimethyl Ammonium Bromide
Dd	:	Double Distilled
DNA	:	Deoxyribo Nucleic Acid
DHs	:	Double Haploids
dNTPs	:	Dinucleotide tri-phosphate
<i>et al.,</i>	:	And others
EtBr	:	Ethidium Bromide
ESTs	:	Expressed Sequence Tags
F₁	:	First filial generation
F₂	:	Second filial generation
F₃	:	Third filial generation
Fig.	:	Figure
G	:	Gram

GCA	:	General Combining Ability
<i>gca</i>	:	General combining ability effects
<i>G. barbadense</i>	:	<i>Gossypium barbadense</i>
<i>G. hirsutum</i>	:	<i>Gossypium hirsutum</i>
GV	:	Genotypic variance
GCV	:	Genotypic co-efficient of variation
h²	:	Heritability
HVI	:	High Volume Instrument
<i>i.e.,</i>	:	Which is to say, in other words
KCl	:	Potassium Chloride
LG	:	Linkage Group
LI	:	Lint Index
LOD	:	Logarithm of Odds
M	:	Molar
MAS	:	Marker Assisted Selection
mg	:	Milligram
MgCl₂	:	Magnesium Chloride
MIC	:	Micronaire value
ml	:	Millilitre
mM	:	Millimolar
μl	:	Microlitre
μM	:	Micromolar
ng	:	Nanogram
NaCl	:	Sodium Chloride
NCD II	:	North carolina design II

NILs	:	Near Isogenic Lines
No.	:	Number
NSy	:	Number of sympodial branches per plant
PCR	:	Polymerase Chain Reaction
PIC	:	Polymorphism Information Content
PV	:	Phenotypic variance
PCV	:	Phenotypic co-efficient of variation
QTL	:	Quantitative Trait Loci
RAPD	:	Random Amplified Polymorphic DNA
RILs	:	Recombinant inbred lines
<i>sca</i>	:	Specific combining ability effects
RBD	:	Randomized Block Design
SMA	:	Single Marker Analysis
TBE	:	Tris borate EDTA
USDA	:	United States Department of Agriculture
RFLP	:	Restriction Fragment Length Polymorphism
RIL	:	Recombinant Inbred Lines
RNase	:	Ribonuclease
rpm	:	Rotations per minute
SCA	:	Specific Combining Ability
<i>sca</i>	:	specific combining ability effects
SCAR	:	Sequence Characterized Amplified Region
SI	:	Seed Index

SPY	:	Single plant yield
SRAP	:	Sequence Related Amplified Polymorphism
SSR	:	Simple Sequence Repeat
STMS	:	Sequence-Tagged Microsatellite Site
<i>Taq DNA polymerase</i>	:	Enzyme from <i>Thermus aquaticus</i>
TBE	:	Tris Borate EDTA
TE	:	Tris EDTA
U	:	Enzyme Units
USDA	:	United States Department of Agriculture
UV	:	Ultraviolet
<i>viz.,</i>	:	Namely

Introduction

CHAPTER I

INTRODUCTION

Cotton is an important commercial and natural fibre crop of global importance and generates high employment at various stages, hence commonly called as ‘White Gold’. It provides fibre for textile industry, cellulose from its lint, oil and protein rich meal from its seed.

In 2013 - 2014, the world’s cotton production is estimated at 116.67 million bales of 480 lakh bales, which is 6.402 million bales lesser than the previous year 2012 - 2013. This is due to reduction in the area of cultivation in many countries (Anonymous, 2014a). India is the only country where all the four cultivated species viz., *Gossypium herbaceum* L., *Gossypium arboreum* L., *Gossypium hirsutum* L. and *Gossypium barbadense* L. were grown in commercial proportions.

India continued to maintain the largest area under cotton and second largest producer of cotton next to China with 35.29 per cent and 24 per cent of world cotton area and production, respectively. India also sustained the position of being the second largest consumer and exporter of cotton and it is expected to export 7.5 million bales and expected to also consume 23 million bales in 2013 - 14. In Tamil Nadu, cotton is being grown in an area of 1.39 lakh hectares producing 5 lakh bales with a productivity of 612 kg / ha (Anonymous, 2014b). It is also considered as an important commodity in the form of raw cotton, cotton yarn and other value added textile goods.

In any breeding programme, the choice of parents is an important aspect for the process of the crop improvement. Especially, in heterosis breeding, the choice of combiners plays an important role (Shakthivel, 2001). Cotton is highly amenable for both heterosis and recombination breeding. A considerable amount of heterosis had been reported in this crop (Tuteja *et al.*, 2005a). To exploit heterosis, knowledge on choosing appropriate parents with good genetic potential is very essential. The parent should possess good combining ability and wide genetic diversity for various economic traits (Kumaresan, 1995).

Combining ability studies aids in selection of suitable parents for further exploitation. In order to achieve high production and productivity, the breeder should have thorough knowledge of the genetic potential of germplasm, the nature of gene action involved in promoting heterosis for yield and combining ability of parents. Information on general and specific combining ability for yield and its components will prove very useful in selection of appropriate parents for development of hybrids (Kumar *et al.*, 2014). The genotype - environmental interaction study can provide the stable nature of varieties and hybrids.

A knowledge on genetic architecture of the varieties and the nature of gene action governing seed yield and its related attributes, besides the quality traits is a pre-requisite for deciding the breeding strategy that has to be followed for effective improvement in any crop and more so in cotton. The estimates of gene effects in crop improvement programme have a direct bearing on the choice of selection procedure to be followed to improve the quantitative characters.

Diallel analysis is a technique employed to gain information on hybrid vigour, combining ability and nature of gene action from the study of first generation itself. Among the several biometrical methods developed to identify superior parents for heterosis breeding, the diallel analysis has received a considerable attention (Khan *et al.*, 2009a).

A long term challenge faced by cotton breeders is the simultaneous improvement of yield and fibre quality to meet the demands of cotton cultivators as well as the modernized textile industries. Although fibre production has greatly increased during the past, rapid development in the modern textile industry requires cotton fibre with superior quality. Because of competition in the global economy, yarn and textile manufacturers have adopted more efficient production machinery capable of generating more products per unit of time. Thus, the widespread use of high speed spinning technology has increased the demand for raw cotton fibre with higher strength. Hence, cotton fibre strength must be improved to remain competitive with synthetic fibres and to meet the needs of new spinning and weaving methods. Besides fibre strength, fibre length and fibre fineness are the primary qualities that influences the textile processing (Kohel, 1999).

Conventional breeding methods have contributed much to the development of high yielding cotton cultivars. But, improvement of fibre quality traits still remains to be

resolved due to negative association between lint yield and fibre quality. Further, conventional breeding procedures could not make marked improvement in fibre quality characters because of lengthy time frames and low selection efficiency. The introgression of favourable alleles from allied and / or wild species is time consuming and is not always successful. Often, these attempts had resulted in poor agronomic qualities of the progeny, distorted segregation, sterility, motes formation and limited recombination due to incompatibility between the genomes (Reinisch *et al.*, 1994).

Recent developments in quantitative trait loci (QTL) mapping and marker assisted selection (MAS) offers new avenues to overcome the above said limitations. Molecular markers are employed to construct genetic linkage maps which are used to study genome structure and evolution (Waghmare *et al.*, 2005). Further, genetic linkage map can be employed to understand the genetic basis and improvement of the complex polygenic traits such as fibre quality. The identification of the stable QTLs affecting fibre traits across the generations would be useful in MAS and thus increases the efficiency of breeding program. The development of DNA markers linked to the fibre quality QTLs would allow cotton breeders to trace this very important trait in early growing stages or early segregating generations.

Among the DNA markers, advent of simple sequence repeat (SSR) or microsatellite markers have brought a new, user friendly and highly polymorphic class of genetic markers for cotton. SSRs are polymerase chain reaction (PCR) based markers, usually co-dominant, well dispersed throughout the genome and easily shared between labs via flanking primer sequence (Maroof *et al.*, 1994). Reddy *et al.* (2001) suggested that the total pool of SSRs present in the cotton genome is sufficiently abundant to satisfy the requirements of extensive genome mapping, QTL analysis and MAS for the development of highly productive *G. hirsutum* cultivars with superior fibre quality.

F₂ and F₃ population derived from different cross combinations have been used in QTL mapping of fibre quality traits. Identification of molecular markers linked to QTLs for fibre quality traits have been already reported. In intraspecific populations, more than a hundred QTLs for fibre traits were detected (Shappley *et al.*, 1998a; Ulloa and Meredith Jr., 2000; Zhang *et al.*, 2003; Wang *et al.*, 2006b; Wu *et al.*, 2009 and Liu *et al.*, 2012). Similarly, several QTLs for fibre quality traits were identified from different interspecific

populations of *G. hirsutum* and *G. barbadense* (Jiang *et al.*, 1998; Kohel *et al.*, 2001; Paterson *et al.*, 2003; Mei *et al.*, 2004; Lacape *et al.*, 2005; He *et al.*, 2007 and Wang *et al.*, 2011). The upland cotton (*G. hirsutum* L. $2n = 52$) is the most extensively cultivated species in this region among the four cultivated *Gossypium* species, representing 95 per cent of the production and it has been the target of numerous genetic studies and breeding efforts.

In this context, crosses were made between nine *G. hirsutum* genotypes in a 9 x 9 diallel mating design. F₂ and F₃ populations derived from an intraspecific cross between *G. hirsutum* var. KC 2 and *G. hirsutum* var. MCU 5 were used for QTL analysis for fibre productivity and quality traits. KC 2 is a medium duration variety with medium staple length and suitable for cultivating under rainfed black soil tract of Tuticorin, Tirunelveli and Virudhunagar districts of Tamil Nadu. It is highly resistant to jassids (*Amarasca sp.*) and exhibited medium yield. On the other hand, MCU 5 is known for its exceptionally extra-long and strong fibre quality characters with good yield potential, besides susceptible to jassids and long duration variety. Therefore, these two contrasting parents were employed to identify molecular association with yield and fiber quality traits in cotton using SSR markers and the present study was under taken with the following objectives:

- To evaluate the *per se* performance of parents and their hybrids.
- To determine the magnitude of general and specific combining ability variances and effects of different characters.
- To obtain information on the extent of heterosis to ascertain superior hybrid combination for commercial application.
- To understand the nature of gene action for yield and fibre quality characters.
- To assess the genetic variability present in F₃ population of the KC 2 x MCU 5 developed for combining fibre quality and yield traits.
- To study the character association analysis among yield, yield components and fibre quality traits.
- To assess the association between molecular markers with yield and fibre quality traits.

Review of Literature

CHAPTER II

REVIEW OF LITERATURE

The review of literature pertaining to the study is presented in the following major aspects.

1. Combining ability and gene action
2. Heterosis
3. QTL analysis

2.1. Combining ability and gene action

Selection of suitable parents for hybridization is one of the most important step in hybridization programme. Selection based on phenotypic performance alone is not a sound procedure, therefore parents should be chosen based on their genetic value. This requires knowledge on combining ability.

Combining ability refers to the ability of a parent to transmit desirable performance into its hybrid progeny or crosses. Combining ability analysis helps in evaluation of inbreds in terms of their genetic value and in selection of suitable parents for hybridization. The superior specific cross combinations can also identified by this technique. The general combining ability is the average performance of a genotype in cross combinations involving a set of other genotypes. It is specific for the set of lines and testing environment whereas, specific combining ability is the average performance of a specific cross combination expressed as deviation from the population mean (Sprague and Tatum, 1942). Combining ability of parents gives useful genetic information regarding the selection of parents based on the performance of their hybrids.

Different methods have been developed to estimate the general and specific combining abilities, in which diallel analysis has been largely followed by many workers for estimating combining ability and gene action. Some of the important studies on the combining ability in cotton and gene action are presented below.

Marani (1963) in a diallel cross analysis of three varieties of *G. hirsutum* and three varieties of *G. barbadense* observed that GCA variance was most important for

yield and its yield components in interspecific hybrids when compared to intraspecific hybrids. Young and Murray (1966) noticed that for lint yield, the specific combining ability was predominant than general combining ability indicating the predominance of non-additive gene action for lint yield.

Al-Rawi and Kohel (1969) reported epistasis for plant height, earliness, boll size and boll number in *G. hirsutum* cotton. Their studies showed that yield and its yield components were controlled by polygenes and heterosis was due to dominance or epistatic gene action.

The magnitude of GCA variance was two to four times higher than SCA variances indicating the importance of both additive and dominance genetic variance, former being more predominant for yield characters in *G. hirsutum* cotton (Singh and Gupta, 1970). Meredith *et al.* (1970) stated that in many of the crosses in upland cotton, lint yield and its components had considerable dominance effects.

Verhalen *et al.* (1971) reported that yield and its yield component characters in upland cotton were governed by dominance in the over dominance range except for lint percentage. El-Adl and Miller (1971), from a diallel analysis in *G. hirsutum* cotton, reported that GCA variance for all traits except lint percentage were significant which indicated the importance of additive genetic effects for these traits.

Meredith and Bridge (1972) in their study on gene action *G. hirsutum* cotton at four locations, reported that additive gene action predominated lint percentage, seed index, fibre strength, fibre elongation and fibre fineness. Dominance gene action was greater for boll size. Both additive and dominance gene actions were involved for lint yield and fibre length.

Baker and Verhalen (1973) who studied 45 F₁'s and 45 F₂'s in a ten parent's diallel in upland cotton could not able to detect significant epistasis for any of the traits. Additive components of variance was observed for lint yield, lint percentage and 2.5 per cent span length. It was also found that over dominance governed the lint yield, earliness, lint percentage, 50 per cent span length and uniformity ratio and partial dominance for fibre fineness. Complete dominance was indicated for 2.5 per cent span length and fibre strength.

Kadapa and Joshi (1973) stated that most of the yield and its yield component characters were governed by additive gene action in upland cotton. In a four parent diallel analysis in *G. hirsutum* cotton, Chinnadurai (1973) found that seed cotton yield was governed by non-additive gene action.

Chandramathi (1973) who studied combining ability in *G. barbadense* cotton reported that GCA and SCA variances were significant for most of the characters indicating involvement of both additive and dominance gene action. High proportion of GCA variance was noticed for plant height, number of fruiting branches and number of bolls per plant indicating that these characters were governed by additive gene action.

Omran *et al.* (1974) studied combining ability in crosses between *G. hirsutum* and *G. barbadense* parents and they reported that GCA variance was larger than SCA variance for yield and yield components. It indicated that the main components of genetic variance were additive for these characters. The main components of genetic variance for most of the fibre properties were also additive but for fibre strength, SCA variance was found to be more important.

Baker and Verhalen (1975) noticed highly significant estimates of *gca* and *sca* for fibre properties and yield components respectively. Predominant *gca* was observed for plant height and number of sympodial branches in *G. hirsutum*. Chandramathi (1976) in a nine parent diallel in *G. hirsutum* cotton found that additive and dominance (H_1) components appeared to be of equal importance in deciding seed cotton yield. The graphical analysis indicated overdominance for yield and its yield components.

Singh *et al.* (1977) noticed that additive gene action was of prime importance for number of bolls per plant and yield per plant. Malhi and Singh (1978) observed 45 F_1 's and the F_2 progenies in a half diallel mating design along with the parents at two locations. The analysis of parental data, variance and covariance of arrays over different environments indicate a significant interactions of the additive and dominance effects of the genes controlling the six agronomic characters, viz., seed cotton yield, boll number, boll size, ginning outturn, halo length and plant height.

Bharadwaj and Chaturvedi (1979) observed that seed cotton yield had recorded highly significant additive and dominance gene actions. Duplicate type of epistasis was

found for boll number, fibre length, ginning percentage, seed index and lint index while complementary type of epistasis was found for boll weight. While, Tomer *et al.* (1980) observed that additive type of gene action was predominant for yield of seed cotton, boll weight, number of bolls per plant and seeds per boll in upland cotton.

Kalsy *et al.* (1981) reported that both GCA and SCA variances were significant for yield, boll number, halo length and seed index indicating the importance of both additive and non-additive genetic factors for these characters in *G. hirsutum*. Gill and Kalsy (1981) reported epistatic gene action for seed cotton yield in *G. hirsutum* cotton. Parminder *et al.* (1982) reported that cross Jai x PK 924 involving good and poor combining ability parents, showed highest *gca* effects and high mean performance of yield per plant and number of bolls per plant.

Bains *et al.* (1982) reported significant additive effects for lint yield and seed index in *G. hirsutum* cotton. The additive variance component (D) was of larger magnitude as compared to dominance component (H). Vadne and Thombre (1982) indicated that ginning outturn was mainly under the control of additive gene action whereas, the fibre characters was under the control of dominance and over dominance gene action in *G. barbadense* cotton.

Duhoon *et al.* (1983) observed over dominance for seed cotton yield and lint index and partial dominance for ginning outturn and seed index in upland cotton. Patil and Chopde (1983) who studied combining ability in *G. hirsutum* and *G. barbadense* reported that both additive and dominance variances were important for ginning outturn. Sanyasi (1983) noticed both additive and non-additive gene action for seed index, lint index and ginning outturn in upland cotton.

Gupta and Singh (1984) reported that both additive and dominance gene effects were observed for halo length. However epistatic interactions together with predominance of dominance effects were involved in the genetical control of lint and seed index. Predominant role of dominant gene action for ginning outturn in F₁ generation and significant additive component (D) in F₂ was reported by Deshpande and Bhale (1984).

Salim *et al.* (1984) who studied combining ability in *G. barbadense* cotton observed dominance gene effects for seed cotton yield and over dominance for boll

weight and boll number. Dominance gene action was predominant for seed cotton yield, boll number, boll weight, sympodial branches and ginning outturn while additive and dominance gene action were important for plant height, monopodial branches and halo length in *G. hirsutum* cotton according to Duhoon *et al.* (1984). Mirza and Khan (1984) found that ginning percentage, staple length, fibre strength and fibre fineness were governed by over dominance with non-allelic gene interaction in upland cotton.

Khan and Khan (1985) from a 4 x 4 diallel analysis in *G. hirsutum* cotton observed that SCA variance was highly significant for seed cotton yield and seven other characters related to yield and fibre quality. A study by Lather (1985) indicated the predominance of non-additive gene effects for boll number, plant height, boll weight, number of monopodia and seed cotton yield. Additive type of genetic variances was also played significant role but at a lesser level.

Jagtap (1986) observed significant additive and non-additive gene action for seed cotton yield, boll number and boll weight, while additive gene action was predominant for halo length in upland cotton. Nadarajan (1986) reported that 2.5 per cent span length, uniformity ratio, fibre fineness, maturity coefficient, lint index, lint yield and seed index of *G. hirsutum* were governed by three types of gene action viz., additive, dominance and epistasis.

Randhawa *et al.* (1986) found that additive genetic variance was predominant for seed cotton yield, boll size and bolls per plant while additive and dominance genetic variance were in operative for plant height in upland cotton. Jagtap and Kolhe (1987) reported that both additive (D) and dominance (H_1) variance played a significant role for seed cotton yield, boll number, boll weight, ginning percentage, halo length and days to first flowering in *G. hirsutum* cotton, while additive gene action was important for lint length.

Pavasias *et al.* (1989) studied the combining ability of quantitative and yield characters in upland cotton. They reported that variance due to *gca* was greater in magnitude for all the characters than due to *sca* indicating that additive genetic variance was of more important for these characters. Dani (1989) studied the heterosis and combining ability for oil content and fibre yield and quality in four lines and their F_1 hybrids. IC 794 had the highest *gca* for oil index and lint / seed while $T_3 - 11$ had the best *gca* for fibre quality.

The cross combination G.Cot 10 x DC 1108 and Sharda x SD registered high *sca* effect for monopodial branches, while H 777 x SD and LRK 516 x BN recorded high *sca* effect for sympodial branches and plant height in the studies of Pavasia *et al.* (1989). Green and Culp (1990) observed significant additive genetic effects for 2.5 per cent span length, 50 per cent span length, uniformity ratio, yarn strength, yield and lint percentage in *G. hirsutum* cotton.

Nadarajan and Sree Rangasamy (1990) demonstrated that lint index, seed index 2.5 per cent span length, uniformity ratio and fibre fineness were governed by additive gene action indicating the early fixation of superior genotypes for these traits. For lint and maturity coefficient, both additive and non-additive gene actions were important in indicating the fixing of superior genotypes in later segregating generations.

Kategeri *et al.* (1991) studied the combining ability of seven intra-*barbadense* hybrid cottons, which were found to exhibit positive *sca* effect for seed cotton yield. Five of these seven hybrids also exhibited positive *sca* effect for boll number. Bhatade *et al.* (1992) studied the combining ability in 8 x 8 diallel cross of *G. hirsutum* cotton and reported that additive and non-additive genetic variances were important in controlling the seed cotton yield, boll number and boll weight. Preponderance of additive genetic variance was observed for halo length.

Gururajan and Basu (1992a) observed that additive components played a predominant role in the inheritance of seed cotton yield, ginning per cent and 2.5 per cent span length. Nadarajan and Sree Rangasamy (1992) reported that fibre traits viz., 2.5 per cent span length, fibre uniformity, fineness and maturity coefficient were governed by additive, dominance effects. However, non-additive gene action predominated the additive gene action.

Kategeri *et al.* (1992) reported that the SCA variance was nearly four times higher than that of GCA variance for seed cotton yield and two crosses showed a significant *sca* effect indicating presence of non-additive effects. Siddiqui and Patil (1992) studied twenty one hybrids obtained by 7 x 7 diallel cross of *G. hirsutum* strain along with their parents. Bolls per plant and earliness were under the influence of additive component while seed cotton yield was under the influence of dominance.

Tiwari *et al.* (1992) observed both additive and non-additive gene actions to be equally important in the expression of boll number and boll weight while seed cotton yield showed non-additive gene action. Bhatade and Sansar (1993) reported that four tall parents viz., PH 93, NH 210, Suman and LRA 6166 were good general combiners for seed cotton yield, boll number, boll size and seed index. Dwarf genotypes like NH 262 and NH 081 were good general combiners for halo length and ginning outturn, respectively.

Patel and Badaya (1993) studied four crosses in *G. hirsutum* cotton and observed that in the cross of G.Cot 10 x Surat, the seed cotton yield was governed by additive gene effect while in the other three crosses, it was governed by dominant gene effect. For number of bolls per plant, significant epistatic gene effect was noticed in the cross MCU 4 x Bikaneri Nerma. For average boll weight in the cross MCU 4 x Bikaneri Nerma, additive, dominance and epistatic (axd) gene effects were significantly observed. Additive gene effect played a significant role in the expression of boll weight in the cross MCU 4 x DES 2136.

Tang *et al.* (1993) estimated the combining ability for fibre properties among the pest-resistant cotton gene pools. They reported that *gca* effects were more important than *sca* effects, *gca* effects for DES 119 was significant, positive and consistent for elongation, strength, micronaire, 50 per cent span length and uniformity, except for 2.5 per cent span length.

Kolte and Thombre (1994) made a combining ability analysis in 8 x 8 diallel cross involving twenty eight hybrids along with their parents. The study revealed that three *G. hirsutum* parents MCU 5, B 1007 and PRS 72 showed the considerable *gca* for all yield components. An examination of *sca* effects in the combination involving a PRS 72 and B 1007 showed considerable *sca* effects for various yield components

Sambamurthy *et al.* (1994a) studied the combining ability of 10 x 10 diallel crosses of cotton and indicated that the variance due to general combining ability was highly significant for all traits studied except number of seeds/boll, which was significant at 5 per cent level only. The variance due to specific combining ability was significant for all the traits except number of seeds / boll.

Kalsy *et al.* (1994) through combining ability analysis, revealed that the presence of both additive and non-additive gene action for all the traits, except ginning outturn, where non-additive gene action was observed. Three parents F 414, F 505 and F 846 were found to be good general combiners for seed cotton yield per plant. Upadhyay and Verulkar (1994) evaluated combining ability for seven yield related traits in *G. hirsutum* and reported that the crosses Vikram x A-51-9 and Vikram x Bikaneri Nerma had both high mean performances and high *sca* effect for seed cotton yield per plant.

Panchal *et al.* (1994) from their study on interspecific crosses involving *G. hirsutum* and *G. barbadense* observed all three kinds of gene effects (additive, dominance and epistasis) in the inheritance of lint yield per plant, seed index and lint index. Additive and epistatic gene effects were important for inheritance of ginning percentage and number of motes per boll. Lloyd and Cynthia (1994) observed that dominance genetic variance was greater than additive genetic variance for all the fibre traits. Additive epistatic variance was detected for 2.5 per cent span length, uniformity ratio and micronaire.

Shanthi and Selvaraj (1995) reported that non-additive gene action was predominant for all the seven quantitative characters *viz.*, plant height, number of internodes, first sympodia emergence, number of sympodia per plant, number of bolls per plant, boll weight and seed cotton yield.

Combining ability of five seed parents and three pollen parents of *G. hirsutum* and their 15 hybrid crosses were estimated by Keerio *et al.* (1995). The best general combiners were S₁₂ for boll number and seed cotton yield, CYTO 127 and CYTO 130 for seed cotton yield and CRIS 74 for sympodia, boll number and seed cotton yield. The crosses S₁₂ x CYTO 127 and BH 36 x CRIS 54 had highly significant *sca* effect for boll number and seed cotton yield / plant.

Panchal *et al.* (1995) reported that the parents EL 664 and SILS 9 were good general combiners for seed cotton yield and lint index. The only cross EC 664 x SLS 9 recorded significantly high positive *sca* effect for seed cotton yield. For lint yield, like crosses EL 664 x SILS 9 and EL 664 x BS 38 recorded significant desirable *sca* effect. Only one hybrid EL664 x BS 38 showed significant positive *sca* effect for ginning percentage.

Carvalho *et al.* (1995) studied *G. hirsutum* varieties and their hybrids and observed both dominance and additive effects to be significant for yield, boll weight and earliness but dominance effects predominated. Additive effects predominated for number of bolls per plant, plant height and fibre maturity. They observed a low heritability for yield which was controlled mainly by dominant genes.

Genetic analysis of 56 F₁ hybrids derived from 8 x 8 diallel cross was done by Sayal and Sulemani (1996) utilizing data from lint percentage, seed index, lint index, staple length and seed cotton yield. All these traits studied showed dominance except seed cotton yield, which showed additive gene action. Goudar *et al.* (1996) studied combining ability in 9 x 9 diallel cross (9 parents and 36 F₁ hybrids) for seven yield components and the results indicated the predominance of additive variance for all measured traits.

Amudha and Raveendran (1997), in a combining ability analysis, disclosed that the bolls per plant, boll weight, seed cotton yield, ginning outturn, 2.5 per cent span length, fibre fineness and bundle strength were controlled by additive genes. Molik *et al.* (1997) studied combining ability of desi cotton. They reported that variance due to *gca* and *sca* were highly significant for all the traits except average boll weight, indicating the importance of both additive and non-additive gene effects. However, the additive gene effects were predominant for all the traits studied.

Malek and Shamsuddin (1998) found higher magnitude of general combining ability variance than that of specific combining ability for all the characters except bolls per plant and seed cotton yield indicating the importance of both additive and non-additive gene actions.

Additive and non-additive gene actions were important for all the traits except seed index. Dominance was ambidirectional for all the traits that were studied. Epistasis influenced the performance of number of bolls and seed cotton yield. Any form of recurrent selection may be followed for exploiting all the three types of gene action as reported by Sambamurthy (1998).

Valarmathi and Jehangir (1998) found that non-additive gene action was predominant for number of sympodia per plant, ginning outturn, uniformity ratio and

bundle strength. Additive gene action was predominant for number of bolls per plant, seed cotton yield per plant, lint index and 2.5 per cent span length. Preponderance of both additive and non-additive gene action was observed for boll weight and elongation per cent.

Gul Hassen *et al.* (1999) noticed preponderance of non-additive genetic effects for boll number, seed cotton yield, plant height, lint percentage, seed index and staple length whereas, boll weight and lint index were controlled by additive effects. Parents viz., A.U 59 and B 284 were the best general combiners. B 284 x A.U 59 had the best seed cotton yield.

Rady *et al.* (1999) evaluated ten parents and their forty five hybrid combinations for boll number, boll weight, lint percentage, seed index, seed cotton yield and lint yield. GCA, SCA and their interactions were also determined. Both GCA and SCA mean squares were highly significant for all traits, indicating the importance of both additive and non-additive genetic effects in determining the performance of these traits. GCA / SCA variance ratios revealed that additive and additive x additive types of gene actions were of greater importance in the inheritance of all traits studied, except seed index where non-additive genetic variance was of greater importance.

Shanthi and Raveendran (1999) observed MCU 9 x Awnabha to be the best specific combination for boll weight, while MCU 11 x TCH 1025 8 and TCH 1002 x Awnabha were the best specific combinations for seed cotton yield. General combining effects were highly significant for number of bolls, boll weight and yield of seed cotton but non- significant for height of main stem in the combining ability analysis done by Gul Hassen *et al.* (2000). Mean squares due to *sca* effects were highly significant for all the characters except number of bolls.

Ashraf and Ahmad (2000) reported that both additive and dominance gene effects were responsible for the inheritance of different traits, except monopodia per plant. GCA mean square values were found to be higher than those of SCA indicating the predominance of additive effects for all the traits. Banumathy and Shanthi (2000) indicated the predominance of dominant gene action in controlling most of the characters viz., yield, plant height, number of sympodia, number of bolls, boll weight, seed index, lint index, ginning percentage, fibre fineness, uniformity ratio, fibre length and fibre strength.

Bertini *et al.* (2001) studied the yield associated characters viz., number of days to flower initiation, number of bolls, boll weight, fibre yield and 100 seed weight and their gene action and found that the presence of a high magnitude of additive effects suggests that there is a potential for improving yield gains and fibre property without resorting to direct exploitation of hybrids. On the other hand, significant dominance deviations for days to first flowering initiation, number of bolls, boll weight and fibre yield indicating that breeding for hybrid varieties would result in improvements over existing varieties.

Rao and Reddy (2001) studied nine genetically and morphologically diverse parents and their 36 F₁'s and disclosed that almost all the traits except number of seeds per boll exhibited significant differences among the genotypes. Among the parents, high *gca* effects for seed cotton yield per plant and bolls per plant were recorded by Abadhita followed by LRA 5166. The cross combination between these parents also showed the high *sca* effects.

Reddy *et al.* (2002) found that additive and epistatic components were significant for bolls per plant, boll weight and seed cotton yield per plant. Manimaran (2003) observed that both additive and non-additive gene action were significant for plant height, number of sympodia per plant, number of bolls per plant, boll weight, seed cotton yield per plant, lint index, seed index, ginning outturn, 2.5 per cent span length, fibre fineness and fibre elongation percentage.

Misaka *et al.* (2003) estimated combining ability and heterosis for seed cotton yield and its three yield components namely, number of sympodia, bolls per plant and boll weight in a diallel analysis. Four *G. hirsutum* parents showed a positive and significant general combining ability effects for boll weight and seed cotton yield and negative combining ability effects for boll weight, number of sympodial bolls per plant and seed cotton yield.

Muthusamy *et al.* (2003) reported that predominant non-additive gene action was observed for all characters except 2.5 per cent span length, which was controlled by additive gene action. Ramalingam (2003) reported that epistatic dominance predominates for the character ginning outturn in a three way cross hybrid. The magnitude of dominance x dominance type of epistasis was maximum as compared to additive gene

effect. Narisi Reddy and Sathyanarayan (2003) in a diallel analysis studied ten parents and estimates of *gca* effects indicated that the parent NA 1325 was adjudged as the best general combiner for most of the fibre quality traits viz., lint index, ginning percentage, 2.5 per cent span length, micronaire, maturity coefficient and bundle length.

Saravanan *et al.* (2003) studied the inheritance pattern of quantitative characters in cotton by 7 x 7 full diallel fashion and reported that the additive component D was found to be greater than dominance component H_1 and H_2 for days to first flower and boll weight indicating the major role of additive gene effects for these characters. Plant height, number of bolls per plant, number of seeds per boll and seed cotton yield per plant showed the significant dominant effect with over dominance.

Manickam and Gururajan (2004) observed that the parents and their crosses showed the significant differences for all the characters studied except seed index in case of parents. Nimbalakar (2004) studied combining ability of desi cotton. The study revealed highly significant *gca* for all characters except average boll weight and lint index. *Sca* is highly significant for days to 50 per cent flowering, days to first boll bursting, number of sympodia per plant, number of bolls per plant, seed cotton yield and lint yield per plant.

Shimna Baskaran (2004) reported that the additive gene action predominates for anatomical traits like phloem distance, number of palisade cells and trichome density apart from boll weight, boll number, 2.5 per cent span length, micronaire, bundle strength and elongation percentage.

Saravanan (2004) reported that the parent KC 2 is good general combiner for boll weight, lint index, seed index and bundle strength, besides seed cotton yield. While SRT 1 and MCU 5 were found to be the good general combiner for 2.5 per cent span length. Iyanar *et al.* (2005) reported higher values of GCA variance than SCA variance for kapas yield, lint index, number of bolls, seed index and boll weight indicating the predominance of additive gene action in control of these characters.

Subramanian *et al.* (2005) reported that the non-additive gene action was found in characters viz., plant height, number of sympodia, days to 50 per cent flowering, days to 50 per cent boll bursting, number of bolls per plant, ginning percentage and seed cotton

yield. Verma *et al.* (2005) observed that for ginning outturn, five crosses recorded positive significant *sca* while other four crosses recorded negative significant effects.

Murtaza (2005) studied the genetic effects for boll number, boll weight and seed index in cotton by an 8 x 8 complete diallel mating system. The results showed that non-additive over dominance type of gene action governed the inheritance in number of bolls per plant and boll weight. He also reported that additive with partial dominance was operative in the inheritance of seed index in F_1 generation.

Saeed Rauf *et al.* (2006) studied combining ability analysis for seed cotton yield and other related traits in a set of diallel crosses involving five cotton genotypes of upland cotton. The parents CIM 413, NIAB 999 and ACALA 1517/C showed high GCA while the cross CIM 473 x NIAB 999 exhibited high SCA. Both the parents and its crosses could be utilized for further selection for high yield.

Subba Reddy and Nadarajan (2006) studied 8 x 8 diallel crosses in upland cotton. They observed additive type of gene action for 50 per cent flowering, number of bolls per plant, ginning outturn, lint index and oil content. Non-additive type of gene action was found in the case of plant height, number of sympodia per plant, boll weight and seed cotton yield.

Kaushik *et al.* (2006) revealed that the additive genetic variance was the most important for days to 50 per cent flowering, plant height, number of sympodia per plant, number of bolls per plant, number of seeds per boll, ginning percentage, seed index and 2.5 per cent span length. The parental lines H 1123, F 1867, LH 1861 and RS 2115 were the best general combiners for most of the traits. The hybrid LH 1836 x H 1123 exhibited the highest SCA effects coupled with high *per se* performance for plant height, number of bolls per plant, seed index and seed cotton yield.

Khan *et al.* (2007) investigated combining ability and heterosis in F_1 and F_2 in a 6 x 6 diallel cross and revealed that SCA variances were greater than GCA showing the predominance of non-additive gene action. Lint index in both generations and boll weight in F_2 's were controlled only by additive type of gene action due to maximum GCA variances.

Ilyas *et al.* (2007) studied quantitative and qualitative traits of upland cotton genotypes in a diallel fashion and revealed that only non-additive gene effects were found to be vital in inheritance of all the traits under study. The parents CIM 435, Express and Huma 15 showed high GCA, while crosses CIM 435 x Huma 15, CIM 435 x Express, LRA 5166 x Express and HUMA 15 x Express exhibited higher SCA and reciprocal effects which can be exploited for further selection of key traits.

Aguiar *et al.* (2007) studied the combining ability of 6 x 6 diallel set of crosses and they reported that the cultivars IAC 22, Antares and CD 403 for the traits seed cotton yield, lint yield, seed index and earliness showed the positive and significant *gca* effects values, which indicates superior average performance over other parents in the crosses they participated. The hybrids Delta Opal x ITA 96, Delta Opal x IAC 22, Ita 90 x Antares and Ita 90 x CD 403 showed positive significant *sca* effects for seed yield, lint yield and earliness.

Ragsdale and Smith (2007) estimated the within-boll seed yield components (seeds per boll, motes per boll, ovules per boll and seed setting efficiency) using diallel analysis of eight upland cotton genotypes. They observed that *gca* and *sca* effects for each trait, was indicating potential for improvement of seed yield components in that population.

Ali *et al.* (2008) studied the genetics of fibre quality traits in upland cotton by the procedure of 5 x 5 diallel mating system. They observed that additive component (D) was significant in all the traits and was lower in magnitude than dominant components (H_1 and H_2) of variation for fibre strength and fibre uniformity which was firmly supported by the value of $H_1 / D^{0.5}$. Dominant genes were in excess than recessive genes in their parents for all the traits except for fibre fineness.

Kalpande *et al.* (2008a) reported the significant *gca* effect for seed cotton yield and some other yield contributing characters *viz.*, number of sympodial branches, number of bolls and boll weight. Whereas significant positive *sca* effects for seed cotton yield per plant was also obtained. They concluded that both additive and non-additive genes advocate these characters.

Mohamed *et al.* (2009) observed the inheritance pattern of yield and its components of Egyptian cotton under divergent environments by 6 x 6 half-diallel set of crosses and they reported that most of the variation was attributed to the non-additive gene effects. For seed cotton yield per plant and boll weight the additive gene effects were more important under favourable conditions while under stress, the non-additive effects of the genes were more important.

The additive component of genotypic variation (D) was significant and predominant for plant height, sympodia per plant, staple length and fibre strength, while dominance effects (H_1 and H_2) were main controlling factors for monopodia per plant, number of bolls, lint percentage and seed cotton yield as reported by Ali *et al.* (2009) in five cotton cultivars through a complete diallel mating design.

Khan *et al.* (2009b) studied the inheritance pattern of fibre quality traits in upland cotton using 6 x 6 complete diallel cross and they reported that additive component (D) was found to be significant for fibre length, fibre strength, fibre fineness and uniformity ratio in F_1 and F_2 generations. Dominance components (H_1 and H_2) were also found to be significant for all the traits in F_1 's except for the fibre fineness, which is found to be insignificant for all the traits in F_2 generation. They also found that in F_1 's the additive gene action was somewhat partial, while in F_2 's all the traits were controlled by additive gene action as confirmed by average degree of dominance ($\sqrt{H_1/D} < \text{unity}$).

Ali and Awan (2009) studied the inheritance pattern of seed and lint traits in *G. hirsutum* by 5 x 5 complete diallel design and they found that additive component of variation (D) was significant and predominant for number of seeds per boll, GOT and lint index, while dominance effects (H_1 and H_2) were main controlling agents for seed weight per boll, seed index and lint yield.

The *G. barbadense* species had high GCA for fibre length, uniformity, strength and seed index. The GCA : SCA ratios for the lint index, uniformity, strength, elasticity, finess and seed index were higher than one indicating the presence of additive genetic effects for most of the characters except for fibre length (2.5 per cent) as revealed by Zangi *et al.* (2009) in sixteen interspecific cross combinations produced by a complete diallel mating system.

Deosarkar *et al.* (2009) noticed that for most of the characters, specific combining ability was found to be more predominant than general combining ability indicating the predominance of non-additive gene action for most of the traits.

Khan *et al.* (2009c) studied the genetic analysis in 6 x 6 complete diallel cross of additive (D), dominance (H) genetic components of variation in F₁ and F₂ hybrids in upland cotton. They reported that additive component (D) was found to be significant for boll weight and staple length in both generations and in F₁'s bolls per plant. Dominance components (H₁ and H₂) were also found to be significant for all the traits in F₁'s and non-significant in F₂ generation. In F₁'s the additive gene action was somewhat partial, while in F₂'s most of the traits were controlled by additive gene action.

Khan *et al.* (2009d) studied the combining ability of 6 x 6 diallel set of crosses and they reported that SCA variances were greater than GCA variances for boll weight, boll number and seed cotton yield per plant. It indicates that the main components of genetic variance were non-additive for these characters. Lint index in both F₁ and F₂ generations, and only boll weight in F₂ generation were controlled by additive type of gene action due to maximum GCA variances.

Braden *et al.* (2009) studied the combining ability for fibre length in Near-Long-Staple upland cotton of 4 x 4 half-diallel crosses and indicated that TAM 94L-25 had the highest *gca* effects for fibre length by weight, fibre length by number and upper-quartile length by weight and this would be the best parent to use in parental combinations to improve fibre length. The hybrid Fibremax 832 x Acala 1527-99 showed significant *sca* effects for fibre length by weight, fibre length by number and short fibre content by weight.

Laxman (2010) studied the combining ability for seed cotton yield and its components in desi cotton in diallel analysis. He indicated that both additive and non-additive gene effects were important for controlling seed cotton yield. Smith *et al.* (2010) studied the genetic analysis of fibre length uniformity in upland cotton by 5 x 5 half-diallel mating. They observed that GCA was highly significant for fibre length distributions.

Karademir and Gencer (2010) observed additive gene action for ginning percentage, fibre length, fibre fineness and fibre elongation properties, while non-additive

gene action was predominant for seed cotton yield, fibre strength and uniformity ratio. Ali *et al.* (2010) studied the inheritance pattern of lint yield and quality parameters of upland cotton by 5 x 5 full diallel mating design and reported that the additive gene action with partial dominance played a role in inheritance of these characters.

Jatoi *et al.* (2010) studied combining ability in intraspecific crosses of upland cotton and they reported that GCA variance was higher than SCA variance for yield and its yield components. They also found that the parent CRIS 134 was the best combiner for bolls per plant and seed cotton yield per plant. The hybrid Shahbaz x Sindh 1 showed high *sca* effects for plant height, bolls per plant and seed cotton yield per plant.

Hussain *et al.* (2010) studied the combining ability in 5 x 5 diallel cross of *G. hirsutum* cotton and reported that non-additive components played a predominant role in the inheritance of different fibre quality traits like staple length, fibre strength, fineness and uniformity. The parent CIM 707 showed the best general combining ability for staple length and fibre strength, FH 1000 for fibre fineness and LA 17801 for fibre uniformity.

Singh *et al.* (2010) studied 8 x 8 diallel cross in *G. hirsutum* and reported that higher non-additive gene action was observed for oil content, ginning outturn, 2.5 per cent span length and micronaire and preponderance of additive gene action was obtained in seed yield, boll weight, fibre elongation and oil content. Parental lines VCH (F), RS 810 and B 58 1290 were the best general combiner for seed yield and parental lines CSH 7106 and VCH (F) for oil content. The hybrids 23 ES x 23 K and F 1861 x VCH (F) showed a positive significant *sca* effects for seed yield.

The magnitude of GCA and SCA variances revealed that pre-dominance of additive as well as non-additive gene action was important for inheritance of seed cotton yield and its quality parameters as reported by Patil *et al.* (2011a). The parents BC 68-2, Surat dwarf, GSHV - 112 and 76 IH-20 were found to be good general combiners for seed cotton yield and its quality traits. The hybrids G.Cot 20 x 76 IH-20, GSHV 155 x LRA 5166, GSHV 155 x GSHV 112 and GSHV 01/1338 x GISV 218 had significant *sca* effects for seed cotton yield and its quality trait.

Ahmad *et al.* (2011) reported that number of bolls per plant is directly related to the higher seed cotton yield and they were controlled by both additive and non-additive

genes, as indicated by significant GCA and SCA mean squares. They also found that SCA variance was greater than GCA variance indicating that the non-additive gene action was more predominant than additive gene action.

Hinze *et al.* (2011) stated that GCA tended to be larger than SCA indicating that these traits are controlled primarily by additive genetic effects. They also found that line 7235 showed excellent GCA for improving the fibre quality measures of strength and length.

Khan and Hassan (2011) observed the nature and magnitude of genetic effects on morpho-yield traits in a 6 x 6 F₁ and F₂ diallel cross in upland cotton. They found that additive effects controlled lint percentage and monopodia in both generations, and plant height and sympodia in F₂. Non-additive inheritance with over-dominance controlled yield in both generations, and plant height and sympodia in F₁.

Feng *et al.* (2011) studied genetic effects of the fibre colour and quality of brown cotton by complete 5 x 5 diallel mating. They observed that the inheritability for all the traits has exceeded 50 per cent, with significant dominance effect at the 0.01 level. The additive effect of fibre colour, lint percentage, elongation and strength was also significant at the 0.01 level, reaching 85.6 per cent, 29.7 per cent, 16.1 per cent and 19.1 per cent, respectively.

Sarwar *et al.* (2011) from a 4 x 4 diallel analysis in *G. hirsutum* cotton reported that additive gene action with partial dominance for plant height, number of sympodial branches, number of bolls, yield of seed cotton, boll weight and lint percentage, whereas over dominance type of gene action for number of seeds per boll, seed index, lint index, staple length and fibre fineness.

Imran *et al.* (2012) studied the combining ability analysis for within-boll yield components of upland cotton in 5 x 5 complete diallel mating. They found that SCA variance was greater than GCA variance for bolls per plant, seeds per boll, seed density, lint per seed, boll size, seed cotton yield and lint percentage showed predominance of non-additive genes; while seed volume was controlled by additive gene action based on maximum GCA variance. Cultivar MS 39 was found to be the best general combiner for most of the traits studied.

Khan and Qasim (2012) studied the inheritance pattern of yield components in *G. hirsutum* by 5 x 5 complete diallel design and they found that additive type of gene action with partial dominance was involved in the phenotypic expression for most of the plant traits (plant height, number of sympodial branches, number of bolls, boll weight and seed cotton yield) except monopodial branches in which over-dominance type of gene action was observed.

Natera *et al.* (2012) studied *gca* and *sca* effects of six important commercial cultivars of *G. hirsutum* and their 15 F₁ hybrids respectively. They found significant differences for all traits except for seeds per boll and bolls per plant. Combining ability analysis of variance revealed the significant differences for *gca* and *sca* effects among the parents and hybrids for almost all the traits except for seed cotton yield / ha and fibre per cent for GCA and boll set, seed yield and fibre per cent for SCA. They also observed presence of additive and non-additive gene action for almost all the traits studied.

Khan (2013) studied the combining ability and genetic variability in a 6 x 6 F₁ diallel cross and found that mean squares due to GCA and SCA were highly significant for all the traits, except locules / boll for GCA. Mean squares due to GCA were higher in magnitude than SCA for majority of the traits and their inheritance was mainly governed by additive type of gene action and partially by non-additive. He also reported that the parents CIM 446, CIM 554 and CIM 496 were good general combiners and the hybrids CIM 446 x CIM 499, CIM 446 x CIM 554, CIM 496 x CIM 707 and CIM 506 x CIM 554 had significant *sca* effects for majority of the traits.

Raza *et al.* (2013) studied the inheritance pattern of some metric plant traits of upland cotton by 5 x 5 complete diallel design and they reported that additive component of genotypic variance (D) was significant and predominant for plant height, number of sympodial branches, boll weight, seed cotton yield, lint percentage, staple length, fibre strength and fibre fineness, while over dominance effects (H₁ and H₂) mainly contribute for number of bolls per plant. Partial dominance was involved for plant height, number of sympodial branches, boll weight, yield of seed cotton, lint percentage, staple length and fibre strength. The value of H₂ / 4H₁ demonstrated asymmetrical and unequal distribution of dominant genes in the parents for all the traits.

Shaukat *et al.* (2013) from a 6 x 6 diallel analysis in *G. hirsutum* cotton observed that fibre length, strength and fineness showed a high proportion of additive type of gene actions in F₁ generation because of that GCA variances were greater than SCA variance. The parents FH 207, MARVI and SB 149 were the best general combiners for fibre characters. They also found that the cross combinations viz., CRS 2007 x GR 156, CRS 2007 x MARVI, SB 149 x MARVI and VH 232 x SB 149 had higher specific combining ability and reciprocal effects for fibre quality characters.

Kumar *et al.* (2014) studied *G. hirsutum* varieties and their hybrids were observed for additive and non-additive type of gene action. All the characters were predominantly controlled by additive gene action except number of sympodial branches, single plant yield and bundle strength. The parent TCH 1726 exhibited positive and significant *gca* effect for most of the yield contributing characters. The hybrid KC₂ x TCH 1726 showed a significant *sca* effects for single plant yield and number of sympodial branches.

Ng *et al.* (2014) studied fibre quality traits with an emphasis on elongation in upland cotton by 5 x 5 half-diallel mating and they reported that GCA was greater than SCA for fibre elongation. It indicates that the main components of genetic variance were additive for this trait. The parental lines PSC 355 and Dever Line 8 was the best general combiner for fibre elongation.

Javaid *et al.* (2014) studied the inheritance of number of bolls, boll weight and seed cotton yield in *G. hirsutum* using 5 x 5 diallel analysis. The data revealed that variance due to SCA was significant for all the three traits signifying the importance of non-additive gene action. The comparison of the parents showed that NF-801-2-37 was the best general combiner for all the three traits followed by Acala-63-75. The hybrids Acala-63-75 x NF-801-2-37 for seed cotton yield and DPL-61 x NF-801-2-37 for number of bolls and boll weight showed high *sca* effects.

2.2. HETEROSIS

Heterosis refers to the superiority of F₁ hybrid in one or more characters over the parental values. Generally, positive heterosis is considered desirable, but for some characters negative heterosis is also desirable. In cotton, negative heterosis for plant height, micronaire value, maturity duration and gossypol content is desirable. Various factors that helps in commercial exploitation of heterosis includes (i) magnitude of heterosis,

(ii) high percentage of natural out crossing, (iii) flower biology and (iv) availability of male sterility system.

The term heterosis was coined by Shull (1914). Heterosis is defined as the increased vigour of the F_1 generation over the mean of the parents or over the better parents (Hayes *et al.*, 1955). Many researchers have observed heterosis for yield and other characters in cotton. Commercial exploitation of hybrid vigour in cotton has been successful in India with the release of Hybrid 4 in 1969 and Varalaxmi in 1971.

Heterosis produced by the joint effects of all the loci as the sum of their separate contributions can be represented by the formula $HF_1 = dy^2$ as described by Falconer (1981) where, 'd' is magnitude of dominance and 'y' is allelic frequency differences at a locus in the parental populations. The genetic causes involved in the expression of heterosis are dominance and non-allelic interactions (Hayes and Foster, 1976). The magnitude of heterosis can be maximized if parents are genetically diverse from each other. Parents should differ for maximum number of yield influencing loci so that F_1 exhibits the dominance effect at as many of the yield influencing loci as possible. The literatures on expression of heterosis in cotton are presented below.

Singh and Murthy (1971) reported more pronounced heterosis for number of sympodia, number of bolls and per plant yield in the hybrids developed between two locally adapted varieties and 15 genetically diverse strains. Meredith and Bridge (1972) observed that heterosis for yield was ranging from 92 to 115 per cent in F_1 and 86 to 107 per cent in F_2 and certain hybrids had better fibre properties. In a 10 x 10 diallel of *G. hirsutum* lines, Baker and Verhalen (1975) reported that estimates of mean mid parent heterosis were highest for earliness and lint yield. Mean inbreeding effects were small, but significant for lint yield, earliness and span length.

Rao *et al.* (1977) studied intra-*hirsutum* hybrids involving parents of diverse origin and reported highest heterosis for fibre weight followed by seed index, lint index, ginning outturn, fibre length and fibre strength. Patil and Sheriff (1980) observed significant heterosis for seed cotton yield, lint index and seed index in intra-*hirsutum* hybrids. The magnitude of heterosis in 45 F_1 's was studied by Phundan Singh (1982). He reported that boll weight, lint index and seed index contributes maximum to increased yield. Ginning outturn and halo length also contributed to yield but to a lesser extent.

Desai *et al.* (1982) recorded significant heterosis for seed cotton yield, fibre fineness and uniformity ratio in intra-*hirsutum* hybrids of upland cotton. Heterosis upto 13.5 per cent and heterobeltiosis upto 9.4 per cent for fibre length were noticed by Ramprakash (1982) in intraspecific hybrids of *G. hirsutum*.

El-Kadi *et al.* (1982) detected no overall heterotic effect over higher parent but recorded the overall mid parental heterosis for seed index, lint index, fibre strength in a number of hybrids and heterosis for lint yield in a few hybrids. Significant effect of inbreeding depression was obtained for lint index and fibre fineness in majority of the crosses, while only a few crosses exhibited the inbreeding depression for lint yield.

Bhatade (1983) investigated the environmental influences on the magnitude of heterosis in *G. arboreum* and reported that heterosis for different crosses was not consistent over environment. Only two crosses consistently displayed high heterosis for yield coupled with low inbreeding depression and the bolls per plant was the chief contributor to heterosis for yield. Duhoon *et al.* (1983) observed high heterosis for monopodial and sympodial branches, boll number and yield per plant and low heterosis for halo length in hybrids between nine genetically diverse varieties belonging to different eco-geographic regions.

Nadre *et al.* (1984) reported that the magnitude of heterobeltiosis for seed cotton was much higher while that of boll number was lower. They also observed very low magnitude and negative heterosis for boll size, halo length and plant height. Lather (1985) observed heterosis ranging from 3.25 to 29.97 per cent for boll weight, -46.57 to 19.43 per cent for boll number and -22.48 to 22.34 per cent for plant height.

Heterosis for plant height, seed cotton yield, bolls per plant, boll weight, ginning outturn and staple length in intraspecific hybrids of upland cotton was observed by Khan *et al.* (1986). Nadarajan (1986) studied the heterosis of various fibre properties in *G. hirsutum* and reported the heterosis of lint yield from -49.6 to 142.4 per cent, for 2.5 per cent span length from -9.0 to 119.2 per cent, for fibre fineness from -12.2 to 143.9 per cent and for maturity co-efficient from -9.4 to 105.7 per cent.

Saravanan *et al.* (1986) analysed a 10 x 10 diallel set of *G. hirsutum* crosses and reported positive heterosis over the better parent for all the characters studied. Gupta and

Singh (1987) studied heterosis and inbreeding depression in F_2 and F_3 generations for seed cotton yield, halo length, lint index and seed index. They encountered heterosis as well as inbreeding depression, for seed cotton yield to be more pronounced than that for the other three characters studied.

Tiwari *et al.* (1987) reported heterobeltiosis for yield as a consequence of heterosis for boll numbers per plant and the highest heterosis for yield over better parent was recorded as 219.5 per cent. Gunaseelan and Krisnaswami (1988) studied eight promising combinations which were made by using seven cultivars and the primitive non-cultivated races *i.e.*, palmeri and morrilli. They recorded maximum heterosis for boll number and seed cotton yield, while boll weight and ginning per cent exhibited a low degree of heterosis.

Rahman *et al.* (1989) estimated the manifestation of heterosis and heterobeltiosis for yield and its components in a 6 x 6 diallele cross. Heterosis as well as heterobeltiosis was manifested to the varying degree of magnitude in almost all the characters, yet it was maximum for the seed cotton yield per plant. Most of the crosses surpassed their better parents, which indicated the over dominance type of gene action, controlling these characters.

Kalsy and Garg (1989) observed hybrid vigour for seed cotton yield which ranged from 6.0 to 92.9 per cent over better parents. The highest heterotic effect of 92.8 per cent over the better parent was recorded by the hybrid A 218 x Grace Wichla. They also reported that heterotic effects were not marked in characters like halo length and ginning outturn as in other characters like yield per plant and bolls per plant. Positive heterosis was recorded for number of fruiting points, number of bolls per plant and seed index over both mid parental and better parental values.

Munasov *et al.* (1989) noticed that F_1 was intermediate between the parental values in hybrids from crossing American cultivars with wild forms. Heterosis was observed in some crosses only and F_2 segregation followed the typical pattern of quantitative inheritance and genetic variance increased considerably. Dever *et al.* (1990) studied the fibre properties of four *G. hirsutum* parents and 12 F_1 and their 12 F_2 's. The study revealed that when environmental influences were high, the fibre strength and standard fineness were more variable in F_2 than in F_1 .

Rathinavelu and Premsekar (1990) reported positive heterosis while studying F_1 and F_2 progenies obtained by using four parents for number of bolls per plant and seed index over parental values. Meredith (1990) reported that from yield and fibre quality evaluation in F_1 it showed significantly short fibres than parents and no differences in adaptive ability between parents and F_1 's.

Koodalingam *et al.* (1991) estimated heterosis for seven yield components in the F_1 crosses between ten *G. hirsutum* genotypes and three cultivars from Tamil Nadu. Heterosis for seed cotton yield and its components was observed in CU 112 x MCU 6 and CU 112 x P 216F. Patil *et al.* (1991) studied half diallel cross of nine genetically diverse parents of *G. hirsutum* and observed heterosis of 102.3 per cent for boll number, 51.6 per cent for boll weight and 139.3 and 169.4 per cent for seed cotton and lint yield, respectively.

Wang and Pan (1991) estimated heterosis percentage for yield and quality components in 56 populations of *G. hirsutum* and 30 F_2 populations were established by using the NCD II mating design. Lint yield, boll weight and fibre length showed heterosis in both generations, which may be the result of additive effects and slight inbreeding depression.

Dever and Gannaway (1992) studied F_2 hybrids of cotton and reported that when environmental influence was high, strength and standard fineness showed more variability in F_2 than in F_1 hybrid. They established that when original parental variability was low, the strength and standard fineness of the two parents were found to be similar, fibre variability in the F_2 hybrid was not greater than variability on a single plant in any generation.

Kategeri *et al.* (1992) tested 18 intra-*hirsutum* hybrids, in which all showed a positive heterosis over the mid parent for seed cotton yield. None of the hybrids, showed a significant heterosis over the mid parent for boll weight and number of bolls. Boll weight and seed cotton yield exhibited the inbreeding depression. Gururajan and Basu (1992b) evaluated eight synthetic cultures of medium staple cotton in a diallel cross and reported moderate heterosis for seed cotton yield per plant, ginning per cent and 2.5 per cent span length. Only one hybrid BD x LRA exhibited considerable heterosis for commercial exploitation.

Rahman *et al.* (1993) found that in almost all the characters of 6 x 6 diallel cross on upland cotton, heterosis as well as heterobeltiosis were manifested to the varying magnitudes but was maximum for lint index. Tang *et al.* (1993) reported that heterosis for yield of F₂ hybrids was a consequence of increased boll number, boll weight or a combination of both boll number and boll weight rather than the increased lint percentage.

Kalsy *et al.* (1994) observed that cross combination, F 414 x 081 involving one good general combiner as a parent and also exhibiting high *sca* effects, exhibited significantly higher (86.08 per cent) economic heterosis for seed cotton yield per plant. Bhatade and Rajeswar (1994) studied 13 x 13 diallel crosses involving diverse and elite genotypes of *G. hirsutum* for seed cotton yield. The study revealed that low to high heterobeltiosis and useful heterosis for number of bolls per plant and boll weight.

Siddiqui and Patil (1994) from their study involving intra-*hirsutum* hybrids reported -11.17 to 76.78 per cent heterosis for seed cotton yield per plant. Negative heterosis was observed for days to fifty per cent flowering which is considered as a desirable character. None of the hybrids showed significant heterotic effects over better parent. Varghese *et al.* (1995) noticed significant and positive heterosis for oil content in hybrids of upland cotton.

Kowsalya and Raveendran (1996) observed significant values for number of bolls per plant, ginning outturn, 2.5 per cent span length, fibre fineness and bundle strength. Valarmarathi (1996) encountered the expression of heterosis for more number of characters in the intra-*hirsutum* hybrids of H 22 x H 45, H 22 x HL 34, H 11 x H 12 and H11 x HL 34. Zhang (1997) observed that heterosis for bolls per plant and seed cotton yield were 10.6 and 9.6 per cent respectively in hybrids of upland cotton.

Rajagopal *et al.* (1998) evaluated four *G. hirsutum* hybrids for physiological aspects. All hybrids recorded positive heterosis over mid parent and better parent for stomatal frequency, transpiration rate, total dry matter at harvest and seed cotton yield. Sudhanshu Jain and Tiwari (1998) observed highest better parent heterosis for yield in 79 BH5-3 x WH 216 (73.1 and 37.12 per cent) followed by Reba B-50 x G.Cot 10 (66.49 and 14.84 per cent) and the standard heterosis for yield in 79 BH 5-3 x Reba B-50 (53.37 and 37.23 per cent).

Kumaresan *et al.* (1999) studied heterosis, heterobeltiosis and standard heterosis for six quantitative traits in a 6 x 6 diallel cross in cotton. The hybrid SVPR 1 x LRA 5166 was judged as the best among all the hybrids evaluated, and it showed a significant heterosis for number of bolls / plant, seed cotton yield, number of seeds / boll and boll weight. The cross MCU 7 x LRA 5166 exhibited a highly significant negative heterosis for days to first flowering.

Gul Hassen *et al.* (1999) in a diallel analysis studied 12 F₁ hybrids and reported high heterosis for seed cotton yield. Among all the hybrids B 284 x A.U 59 had the best seed cotton yield.

Khorgade *et al.* (2000) studied 7 x 7 half-diallel crosses in twenty one hybrids and found that expression was the highest for seed cotton yield per plant followed by number of bolls per plant, number of sympodia per plant and seed index. Kaynak *et al.* (2000) noticed highest production rate of lint index, seed cotton yield and days to first squaring. Earliness characteristics other than days to first squaring, days to first flowering and days to first boll opening showed positive heterosis.

Baber *et al.* (2001) studied 4 x 4 full diallel crosses of *G. hirsutum* and revealed that seed cotton yield was dependent on number of bolls per plant. Among twelve hybrids, four hybrids viz., CRIS-52 x CRIS-54, CRIS-5A x CRIS-52, CRIS-52 x CRIS-9 and CRIS-54 x CRIS-52 exhibited more than 70 per cent of all three types of heterosis. Thangaraj (2001) reported that relative heterosis was positive in all the six crosses for fibre fineness, maturity coefficient, bundle strength and fibre elongation. Panhwar *et al.* (2002) observed the highest heterosis of 69.23 per cent for boll weight over their parents followed by 64.24 per cent for seed cotton yield, 22.97 per cent for number of bolls and 19.62 per cent for number of sympodia per plant in six intraspecific hybrids.

Phudan Singh *et al.* (2003) reported that relatively moderate level of heterosis was observed for ginning outturn. Lint index was important component of lint yield per boll and also per plant, and expressed higher value of heterosis as compared to other traits. Laxman *et al.* (2003) reported that for seed cotton yield, the positive relative heterosis was ranged from 1.5 per cent to 105.7 per cent, while positive heterobeltiosis ranged from 0.27 per cent to 78.3 per cent in three way cross hybrids. Both relative heterosis and

heterobeltiosis were higher in three way hybrids than in single cross hybrids for all the characters studied except the quality traits of halo length.

Sundaravadivelu *et al.* (2005) noticed that high heterosis was also observed in F_3 crosses for plant height, number of sympodia, number of bolls, seed cotton yield, 100 seed cotton weight and lint index. Tuteja *et al.* (2005b) reported that mean performance and heterosis over check hybrid LHH 144 for seven characters of promising hybrids. The results indicated that magnitude of heterosis varied with the characters.

Giri *et al.* (2006) studied heterosis for seed cotton yield and its contributing traits in upland cotton by line x tester method. The study revealed that highest economic heterosis for seed cotton yield was observed in the hybrid HC 6 x G.Cot 12 to the tune of 50.9 per cent. SK 663 and Galmo delta type among the males and HS 6 among the females were identified as the best parents and may be used for further breeding programmes.

Aguiar *et al.* (2007) studied diallel cross of six genetically diverse parents of *G. hirsutum* and observed highest heterosis of 29.8 per cent for seed cotton yield and 32.25 per cent for lint yield. Khan *et al.* (2009d) revealed that, maximum heterosis was observed for seed cotton yield followed by boll number, boll weight and lint index. The heterosis over better parent was 3.13 to 65.63 per cent for bolls per plant, 0.75 to 24.40 per cent for boll weight, 0.82 to 115.22 per cent for seed cotton yield and 0.27 to 3.88 per cent for lint index.

Zangi *et al.* (2009) revealed that positive heterosis values were observed in intraspecific crosses for lint index and fineness, whereas for the same traits, negative heterosis values were observed in interspecific crosses. Heterosis values were positive in all combinations for fibre length and strength.

Karademir and Gençer (2010) revealed that significant and positive heterotic values were observed for seed cotton yield, fibre strength, fibre fineness, fibre elongation and ginning percentage except fibre uniformity respectively. Khan *et al.* (2010) evaluated the 6 x 6 F_1 and F_2 intra-*hirsutum* diallel hybrids and found that in F_1 's and F_2 's, the average positive heterosis was 11.54 and 4.50 per cent for seeds per boll, 3.40 and 2.41

per cent for seed index, 46.30 and 28.96 per cent for seed cotton yield and 6.04 and 1.52 per cent for cotton seed oil respectively.

Feng *et al.* (2011) studied heterosis for fibre colour and quality of brown cotton by complete 5 x 5 diallel mating. They observed that the mid parent heterosis of fibre colour was negative, which was -0.7 per cent; those of lint percentage, fibre length, uniformity and strength were 3.5 per cent, 4.2 per cent, 1.7 per cent and 2.6 per cent respectively, reaching the significant level.

Khan (2011) studied heterosis in thirty F₁ and F₂ diallel cross combinations and revealed that positive economic heterotic values were recorded as 80 per cent in F₁ hybrids for plant height, 97 per cent for sympodia, 60 per cent for boll weight, 83 per cent for bolls per plant and 60 per cent for seed cotton yield.

Patil *et al.* (2011b) found that the hybrids viz., GSHV 155 x GSHV 112, G.Cot 20 x BC 68-2, G.Cot 20 x 76 IH-20, GSHV 01/1338 x GISV 218, GSHV 155 x Surat dwarf, GSHV 01/1338 x BC 68-2 and GSHV 155 x LRA 5166 showed a significant positive standard heterosis as well as heterobeltiosis for seed cotton yield per plant, number of bolls per plant and boll weight. The crosses exhibited highest heterosis due to increase in boll number and boll weight was significantly associated with increase in yield and these crosses could be considered for exploitation of hybrid vigour.

Ashokkumar *et al.* (2013) observed that the hybrids MCU 12 x SOCC 17 and SVPR 2 x TCH 1641 for fibre elongation, MCU 12 x TCH 1644 and SVPR 2 x TCH 1646 for 2.5 per cent span length and MCU 5 x SOCC 17 and Surabhi x F 776 for bundle strength exhibited a significant positive heterotic effects.

Abro *et al.* (2014) studied heterosis and heterobeltiosis of yield and quality traits in upland cotton by line x tester method. The study revealed that crosses involving genotypes Okra and NIA - Bt exhibited superior and positive heterosis over mid parent and heterobeltiosis over better parent for yield contributing characters such as sympodial branches and bolls per plant and seed cotton yield as well.

Solanki *et al.* (2014) studied heterobeltiosis and standard heterosis of seed cotton yield and its contributing characters in upland cotton. The study revealed that the number of sympodia per plant, number of bolls per plant, boll weight and lint yield per plant were

main contributors towards increase in heterotic effects for seed cotton yield per plant over better parent. They also found that five crosses viz., G.Cot-12 x H 1316 (35.27 per cent), 76 IH 20 x GBHV 170 (33.67 per cent), LRA 5166 x GJHV 503 (24.39 per cent), 76 IH 20 x BS 27 (23.04 per cent) and G.Cot-12 x GJHV 460 (20.95 per cent) were the best heterotic crosses over standard check for seed cotton yield per plant.

2.3. Genetic and QTL analysis for yield and fibre quality components

Plant breeders select the plants with desirable traits by looking at the phenotype. Most of these traits are polygenic with complex non-allelic and environmental interactions. Though biometrical genetics revealed the cumulative effects of the genetic loci involved in a quantitative trait, the specific locus involved could not be detected. If the quantitative traits could be resolved into individual genetic components for example, by finding DNA marker closely linked to each trait, it would be easy to manipulate them efficiently and this would help to attain the desirable results quickly and more precisely.

Morphological and physiological features of plants have been used to understand the genetic variation. Though morphological features are indicatives of the phenotype, it is also affected by environmental factors and cultural practices. There are about 145 morphological markers identified in cultivated cotton but their utility in breeding programme has remained limited because of their deleterious effects and the difficulties in accumulating multiple markers in a single genotype (Percy and Kohel, 1999). Therefore, more reliable markers such as protein, or more specifically allelic variants of several enzymes were used. But, as the number of isozymes available is limited and their expression is often restricted to a specific developmental stage of the tissues, various DNA markers have come into use of the plant breeders. With the use of molecular techniques, it would be now possible to hasten the transfer of desirable genes among varieties and to introgress novel genes from related wild species into the local and popular genotypes which would accelerate the generation of new varieties. It would also be possible to establish genetic relationships between sexually incompatible species. Thus, DNA marker technology would provide a tool to the plant breeders to select desirable plants directly on the basis of genotype instead of phenotype.

A brief review of the research findings obtained by various workers in genetic and molecular analyses in cotton is presented below under four major headings viz., genetic variability, heritability and genetic advance, association studies *i.e.*, correlation analysis and molecular marker analysis for yield and fibre quality components.

2.3.1. Studies on genetic variability

Variability presented in a crop species is of utmost importance as it provides the basis of effective selection. The total variation present in a population comprises of genotypic and environmental effects. Thus, phenotypic variability is the observable expression of a character in a population and it includes both genotypic and environmental components of variation. Its magnitude differs under different environmental conditions and variability in a population is measured by phenotypic and genotypic co-efficient of variation. Assessment of phenotypic co-efficient of variation and genotypic co-efficient of variation for the material under study is a must for formulating the plant breeding programmes, as this facilitates easier comparison of the variability for the characters. The relevant literature pertaining to variability studies with respect to cotton is reviewed here under.

GCV and PCV studies for yield and fibre quality traits in cotton

Characters	GCV (%)	PCV (%)	References
Plant height	22.72	26.78	Punitha (2001)
	11.48	11.55	Girase and Mehetre (2002)
	17.41	18.50	Dheva and Potdukhe (2002)
	12.78	13.47	Ahmad (2003)
	12.85	12.96	Preetha and Raveendran (2007)
	13.42	14.14	Venkatesan (2008)
	16.90	21.38	Santoshkumar <i>et al.</i> (2012)
	103.77	106.04	Abbas <i>et al.</i> (2013)
	10.20	17.00	Dhivya <i>et al.</i> (2014)

Characters	GCV (%)	PCV (%)	References
Number of bolls per plant	19.36	22.30	Punitha (2001)
	27.40	27.44	Girase and Mehetre (2002)
	29.84	30.17	Saeed Ahmad <i>et al.</i> (2003)
	21.60	25.90	Ganesan and Raveendran (2007)
	20.52	21.63	Preetha and Raveendran (2007)
	11.90	12.52	Venkatesan (2008)
	37.19	35.35	Dinakaran <i>et al.</i> (2012)
	27.75	29.05	Santoshkumar <i>et al.</i> (2012)
	56.50	36.58	Abbas <i>et al.</i> (2013)
	10.90	14.40	Dhivya <i>et al.</i> (2014)
Boll weight	14.47	18.89	Saeed Ahmad <i>et al.</i> (2003)
	10.88	14.31	Prasad <i>et al.</i> (2005)
	11.70	14.90	Ganesan and Raveendran (2007)
	21.81	22.71	Preetha and Raveendran (2007)
	8.46	9.00	Venkatesan (2008)
	27.21	29.26	Dinakaran <i>et al.</i> (2012)
	16.12	17.95	Santoshkumar <i>et al.</i> (2012)
	8.40	15.40	Dhivya <i>et al.</i> (2014)
Number of sympodia per plant	22.87	26.23	Punitha (2001)
	18.00	18.13	Girase and Mehetre (2002)
	31.02	31.80	Ahmad (2003)
	17.23	18.25	Preetha and Raveendran (2007)
	6.68	8.40	Venkatesan (2008)
	23.51	26.59	Santoshkumar <i>et al.</i> (2012)
	60.49	61.27	Abbas <i>et al.</i> (2013)
	12.10	14.80	Dhivya <i>et al.</i> (2014)

Characters	GCV (%)	PCV (%)	References
Seed cotton yield per plant	32.23	34.45	Punitha (2001)
	35.30	39.80	Dheva and Potdukhe (2002)
	32.91	33.90	Ahmad (2003)
	37.36	38.36	Saeed Ahmad <i>et al.</i> (2003)
	20.20	26.00	Ganesan and Raveendran (2007)
	23.75	23.94	Preetha and Raveendran (2007)
	17.79	18.49	Venkatesan (2008)
	6.23	6.59	Ali <i>et al.</i> (2009)
	26.45	26.49	Dinakaran <i>et al.</i> (2012)
	31.86	34.90	Santoshkumar <i>et al.</i> (2012)
	25.80	25.90	Dhivya <i>et al.</i> (2014)
Ginning outturn	4.64	5.69	Dheva and Potdukhe (2002)
	5.75	6.61	Ahmad (2003)
	6.22	7.03	Saeed Ahmad <i>et al.</i> (2003)
	8.37	8.43	Ganesan and Raveendran (2007)
	5.75	6.06	Preetha and Raveendran (2007)
	5.92	6.28	Venkatesan (2008)
	13.39	13.65	Dinakaran <i>et al.</i> (2012)
	9.11	9.80	Santoshkumar <i>et al.</i> (2012)
	6.00	10.70	Dhivya <i>et al.</i> (2014)
Seed index	8.56	11.76	Gururajan (2000)
	10.99	8.62	Rao and Reddy (2001)
	8.85	12.54	Dheva and Potdukhe (2002)
	10.69	12.50	Ahmad (2003)
	10.95	12.88	Prasad <i>et al.</i> (2005)
	15.52	15.50	Ganesan and Raveendran (2007)

Characters	GCV (%)	PCV (%)	References
	9.20	10.35	Preetha and Raveendran (2007)
	6.42	7.77	Venkatesan (2008)
	12.95	14.98	Santoshkumar <i>et al.</i> (2012)
	13.50	17.70	Dhivya <i>et al.</i> (2014)
Lint index	9.39	11.64	Ahmad (2003)
	17.40	18.00	Ganesan and Raveendran (2007)
	10.97	12.44	Preetha and Raveendran (2007)
	8.80	9.89	Venkatesan (2008)
	14.08	16.66	Santoshkumar <i>et al.</i> (2012)
	11.20	17.00	Dhivya <i>et al.</i> (2014)
Micronaire	50.41	4.86	Punitha (2001)
	11.07	15.03	Dheva and Potdukhe (2002)
	6.82	7.82	Ahmad (2003)
	5.64	8.34	Prasad <i>et al.</i> (2005)
	11.45	11.71	Preetha and Raveendran (2007)
	6.83	8.33	Venkatesan (2008)
	8.04	13.82	Ali <i>et al.</i> (2009)
	9.35	9.58	Dinakaran <i>et al.</i> (2012)
	8.05	10.16	Santoshkumar <i>et al.</i> (2012)
	6.37	22.22	Abbas <i>et al.</i> (2013)
2.5 per cent span length	6.04	3.46	Punitha (2001)
	5.45	7.66	Dheva and Potdukhe (2002)
	4.23	5.18	Ahmad (2003)
	2.09	3.36	Saeed Ahmad <i>et al.</i> (2003)
	6.78	6.85	Ganesan and Raveendran (2007)
	5.70	6.22	Preetha and Raveendran (2007)

Characters	GCV (%)	PCV (%)	References
	5.26	6.12	Ali <i>et al.</i> (2009)
	10.29	10.80	Dinakaran <i>et al.</i> (2012)
	5.80	6.87	Santoshkumar <i>et al.</i> (2012)
	7.90	8.00	Dhivya <i>et al.</i> (2014)
Bundle strength	7.08	7.08	Punitha (2001)
	8.50	11.04	Dheva and Potdukhe (2002)
	2.67	3.99	Ahmad (2003)
	6.73	7.13	Ganesan and Raveendran (2007)
	5.80	8.81	Venkatesan (2008)
	5.13	6.46	Ali <i>et al.</i> (2009)
	9.44	9.95	Dinakaran <i>et al.</i> (2012)
Uniformity ratio	4.18	8.52	Prasad <i>et al.</i> (2005)
	3.10	3.94	Preetha and Raveendran (2007)
	3.83	4.73	Venkatesan (2008)
	3.25	3.70	Ali <i>et al.</i> (2009)
	4.16	4.48	Dinakaran <i>et al.</i> (2012)
	3.70	5.02	Santoshkumar <i>et al.</i> (2012)
Elongation per cent	14.23	14.42	Preetha and Raveendran (2007)
	4.32	4.80	Ali <i>et al.</i> (2009)
	8.22	8.51	Dinakaran <i>et al.</i> (2012)
	11.86	13.95	Santoshkumar <i>et al.</i> (2012)

Gite *et al.* (2006) assessed 14 genotypes which includes F₂ progenies of seven crosses along with five parents and two checks. The analysis of variance showed that the genotypes differed significantly among themselves for all the characters indicating the presence of sufficient level of variability and the phenotypic and genotypic co-efficient of variation were the highest for number of monopodia per plant. There was a narrow

variation in the PCV and GCV, though the magnitude of phenotypic co-efficient of variation was higher than that of genotypic co-efficient of variation.

According to Annapurva *et al.* (2007) the analysis of variance is significant for most of the yield contributing characters. Phenotypic and genotypic correlations were significant for almost all the characters like number of bolls per plant, days to 50 per cent flowering, boll weight, yield per plant in upland cotton (*G. hirsutum* L.). Sakthi *et al.* (2007) carried out variability analysis in *G. hirsutum* accessions. The result showed that the PCV value was greater than GCV.

Hence, an assessment of variability is a pre-requisite to select desirable genotypes, revealing a wide range of mean expression for almost all the characters. Development of an effective breeding programme depends on the existence of genetic variability for various economic characters. Selection is effective only when there is enough magnitude of variability in the breeding population.

2.3.2. Heritability and genetic advance

The extent of variability of a quantitative trait transmitted to the progenies is referred as heritability. Expression of high heritability accompanied by high values of genetic advance indicates the expression of additive gene effects. Recent studies on the heritability and genetic advance for different characters in cotton are summarized below.

Heritability and genetic advance studies for yield and fibre quality traits

Characters	Heritability	GA as per cent of mean	References
Plant height	71.97	5.87	Punitha (2001)
	98.74	23.51	Girase and Mehetre (2002)
	89.84	20.86	Ahmad (2003)
	98.36	26.26	Preetha and Raveendran (2007)
	90.15	26.26	Venkatesan (2008)
	62.50	4.27	Santoshkumar <i>et al.</i> (2012)
	95.77	137.47	Abbas <i>et al.</i> (2013)
	36.20	16.30	Dhivya <i>et al.</i> (2014)

Characters	Heritability	GA as per cent of mean	References
Number of bolls per plant	97.00	60.78	Saeed Ahmad <i>et al.</i> (2003)
	55.90	22.66	Prasad <i>et al.</i> (2005)
	81.60	48.10	Ganesan and Raveendran (2007)
	89.95	40.08	Preetha and Raveendran (2007)
	90.16	23.26	Venkatesan (2008)
	99.14	76.28	Dinakaran <i>et al.</i> (2012)
	91.30	8.33	Santoshkumar <i>et al.</i> (2012)
	77.11	74.85	Abbas <i>et al.</i> (2013)
	57.20	21.80	Dhivya <i>et al.</i> (2014)
Number of sympodia per plant	0.67	19.14	Gururajan (2000)
	18.00	0.77	Rao and Reddy (2001)
	87.79	5.24	Dheva and Potdukhe (2002)
	89.08	33.49	Preetha and Raveendran (2007)
	63.33	10.95	Venkatesan (2008)
	78.20	11.30	Santoshkumar <i>et al.</i> (2012)
	97.45	80.13	Abbas <i>et al.</i> (2013)
	66.90	26.20	Dhivya <i>et al.</i> (2014)
Boll weight	58.00	22.00	Saeed Ahmad <i>et al.</i> (2003)
	61.40	18.90	Ganesan and Raveendran (2007)
	92.26	43.16	Preetha and Raveendran (2007)
	88.26	16.37	Venkatesan (2008)
	86.53	52.16	Dinakaran <i>et al.</i> (2012)
	80.60	27.49	Santoshkumar <i>et al.</i> (2012)
	29.80	12.10	Dhivya <i>et al.</i> (2014)

Characters	Heritability	GA as per cent of mean	References
Seed cotton yield per plant	98.50	123.88	Rao and Reddy (2001)
	78.67	17.36	Dheva and Potdukhe (2002)
	91.38	5.20	Ahmad (2003)
	97.00	10.00	Saeed Ahmad <i>et al.</i> (2003)
	75.40	24.56	Prasad <i>et al.</i> (2005)
	60.80	32.49	Ganesan and Raveendran (2007)
	98.40	48.53	Preetha and Raveendran (2007)
	94.49	35.24	Venkatesan (2008)
	99.69	54.41	Dinakaran <i>et al.</i> (2012)
	83.30	8.22	Santoshkumar <i>et al.</i> (2012)
	89.10	27.30	Dhivya <i>et al.</i> (2014)
Ginning outturn	95.00	14.45	Gururajan (2000)
	87.50	1.05	Rao and Reddy (2001)
	66.71	2.81	Dheva and Potdukhe (2002)
	75.55	3.49	Ahmad (2003)
	78.00	11.00	Saeed Ahmad <i>et al.</i> (2003)
	98.60	17.11	Ganesan and Raveendran (2007)
	90.13	11.28	Preetha and Raveendran (2007)
	88.86	11.50	Venkatesan (2008)
	96.34	27.09	Dinakaran <i>et al.</i> (2012)
	86.40	5.75	Santoshkumar <i>et al.</i> (2012)
	31.60	9.00	Dhivya <i>et al.</i> (2014)
Seed index	56.00	13.72	Gururajan (2000)
	98.90	1.55	Rao and Reddy (2001)
	76.76	1.14	Dheva and Potdukhe (2002)
	73.08	1.59	Ahmad (2003)

Characters	Heritability	GA as per cent of mean	References
	97.30	30.95	Ganesan and Raveendran (2007)
	78.80	16.80	Preetha and Raveendran (2007)
	68.26	10.93	Venkatesan (2008)
	74.80	16.82	Santoshkumar <i>et al.</i> (2012)
	58.00	27.10	Dhivya <i>et al.</i> (2014)
Lint index	76.00	23.03	Gururajan (2000)
	97.30	1.13	Rao and Reddy (2001)
	65.19	0.69	Dheva and Potdukhe (2002)
	65.12	0.67	Ahmad (2003)
	93.70	34.70	Ganesan and Raveendran (2007)
	79.28	16.15	Venkatesan (2008)
	71.40	24.00	Santoshkumar <i>et al.</i> (2012)
	43.90	19.60	Dhivya <i>et al.</i> (2014)
Micronaire	66.70	0.58	Rao and Reddy (2001)
	52.40	0.49	Dheva and Potdukhe (2002)
	75.31	0.42	Ahmad (2003)
	95.53	23.05	Preetha and Raveendran (2007)
	67.24	11.53	Venkatesan (2008)
	95.17	18.79	Dinakaran <i>et al.</i> (2012)
	62.80	18.07	Santoshkumar <i>et al.</i> (2012)
	8.21	8.43	Abbas <i>et al.</i> (2013)
2.5 per cent span length	66.72	1.96	Ahmad (2003)
	38.00	2.00	Saeed Ahmad <i>et al.</i> (2003)
	60.30	10.25	Prasad <i>et al.</i> (2005)
	98.00	13.81	Ganesan and Raveendran (2007)
	84.19	10.78	Preetha and Raveendran (2007)
	7.10	0.92	Venkatesan (2008)
	90.70	20.19	Dinakaran <i>et al.</i> (2012)
	71.20	5.21	Santoshkumar <i>et al.</i> (2012)
	96.20	20.40	Dhivya <i>et al.</i> (2014)

Characters	Heritability	GA as per cent of mean	References
Bundle strength	44.80	0.76	Ahmad (2003)
	89.00	13.09	Ganesan and Raveendran (2007)
	84.74	10.97	Preetha and Raveendran (2007)
	43.34	7.87	Venkatesan (2008)
	89.89	18.44	Dinakaran <i>et al.</i> (2012)
	67.80	6.61	Santoshkumar <i>et al.</i> (2012)
Uniformity ratio	61.86	5.02	Preetha and Raveendran (2007)
	65.81	6.41	Venkatesan (2008)
	86.18	7.96	Dinakaran <i>et al.</i> (2012)
	54.10	3.09	Santoshkumar <i>et al.</i> (2012)
Elongation per cent	97.35	28.93	Preetha and Raveendran (2007)
	93.38	16.37	Dinakaran <i>et al.</i> (2012)
	72.30	16.48	Santoshkumar <i>et al.</i> (2012)

One hundred and twenty nine cotton accessions (*Gossypium* spp.) were subjected to its genetic variability and correlation analysis (Do-Thi-Ha-An *et al.*, 2008). High heritability coupled with high genetic advance as percentage of mean was observed for single plant yield, plant height, sympodia per plant, number of bolls per plant, boll weight, seed index, lint index, micronaire and bundle strength indicating that these traits are under the control of additive gene action. High heritability coupled with low genetic advance was observed for days to first flowering, 2.5 per cent span length and ginning outturn. This suggests that these characters were controlled by non-additive gene action.

2.3.3. Association analysis

2.3.3.1. Correlation studies

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

Seed cotton yield and fibre quality traits are controlled by polygenes and are highly influenced by environment. Selection merely based on yield is not effective. Correlation studies will establish the extent of association between yield and its yield

components, which forms the basis for selection of genotypes for effective improvement. Unfavourable association between the desired attributes under selection may limit genetic advance. Hence, a sound knowledge on association between the yield with yield components and fibre quality traits are essential for planning an effective selection programme. Correlation for yield with yield contributing traits and fibre quality traits in cotton in the literature is presented below.

Correlation of yield components and fibre quality traits on seed cotton yield

Character	Association with yield	References
Plant height	Positive	Swati Bharad <i>et al.</i> (1999), Echekwu (2001), Rao <i>et al.</i> (2001), Percy <i>et al.</i> (2006), Kulkarni <i>et al.</i> (2007), Leela Pratap <i>et al.</i> (2007) and Kalpande <i>et al.</i> (2008b), Rasheed <i>et al.</i> (2009), Thiyagu <i>et al.</i> (2010), Rao and Gopinath (2013), Tamilselvam <i>et al.</i> (2013) and Gul <i>et al.</i> (2014)
	Negative	Annapurve <i>et al.</i> (2007), Sakthi <i>et al.</i> (2007), Do-Thi-Ha-An <i>et al.</i> (2008) and Reddy and Reddy (2008)
Number of sympodia per plant	Positive	Manimaran (1999), Afiah and Ghoneim (2000), Rao <i>et al.</i> (2001), Gite <i>et al.</i> (2006), Sharma <i>et al.</i> (2006), Annapurve <i>et al.</i> (2007), Basbag and Gencer (2007), Kulkarni <i>et al.</i> (2007), Leela Pratap <i>et al.</i> (2007), Sakthi <i>et al.</i> (2007) and Kalpande <i>et al.</i> (2008b), Thiyagu <i>et al.</i> (2010), Rao and Gopinath (2013), Tamilselvam <i>et al.</i> (2013) and Gul <i>et al.</i> (2014)
	Negative	Reddy and Reddy (2008)
Number of bolls per plant	Positive	Murthy (1997), Manimaran (1999), Afiah and Ghoneim (2000), Rao <i>et al.</i> (2001), Baloch <i>et al.</i> (2001), Iqbal <i>et al.</i> (2006), Sambamurthy and Chamundeswari (2006), Sharma <i>et al.</i> (2006), Basbag and Gencer (2007), Aguado <i>et al.</i> (2008), Ahuja <i>et al.</i> (2008) and McCarty <i>et al.</i> (2008), Rasheed <i>et al.</i> (2009), Thiyagu <i>et al.</i> (2010), Dinakaran <i>et al.</i> (2012), Rao and Gopinath (2013) and Gul <i>et al.</i> (2014)
Boll weight	Positive	Valarmathi (1996), Sultan <i>et al.</i> (1999), Afiah and Ghoneim (2000), Hussain <i>et al.</i> (2000), Altaher and Singh (2003), Gite <i>et al.</i> (2006), Preetha and Raveendran (2007), Sakthi <i>et al.</i> (2007) and McCarty <i>et al.</i> (2008), Thiyagu <i>et al.</i> (2010), Dinakaran <i>et al.</i> (2012) and Rao and Gopinath (2013)

Character	Association with yield	References
	Negative	Baloch <i>et al.</i> (2001), Iqbal <i>et al.</i> (2006) and Ahuja <i>et al.</i> (2008)
Number of seeds per boll	Positive	Annapurve <i>et al.</i> (2007)
Ginning outturn	Positive	Choudhary <i>et al.</i> (1988), Krishna Rao and Mary (1990), Swati Bharad <i>et al.</i> (1999), Ahmad and Azhar (2000), Percy <i>et al.</i> (2006), Annapurve <i>et al.</i> (2007) and Ahuja <i>et al.</i> (2008) and Rao and Gopinath (2013)
	Negative	Giri and Upadhyay (1980), Aher <i>et al.</i> (1989), Altaher and Singh (2003), Iqbal <i>et al.</i> (2006), Sambamurthy and Chamundeswari (2006), Basbag and Gencer (2007) and Preetha and Raveendran (2007), Thiyagu <i>et al.</i> (2010) and Dinakaran <i>et al.</i> (2012)
Lint index	Positive	Sambamurthy <i>et al.</i> (1995b), Valarmathi (1996), Manimaran (1999), Echekwu (2001), Kulkarni <i>et al.</i> (2007) and Do-Thi-Ha-An <i>et al.</i> (2008), Rasheed <i>et al.</i> (2009), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
	Negative	Sambamurthy and Chamundeswari (2006), Leela Pratap <i>et al.</i> (2007) and Khan <i>et al.</i> (2011)
Seed index	Positive	Tomar and Singh (1992), Sambamurthy <i>et al.</i> (1995a), Do-Thi-Ha-An <i>et al.</i> (2008), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
	Negative	Leela Pratap <i>et al.</i> (2007), Rasheed <i>et al.</i> (2009)
2.5 per cent span length	Positive	Ahmad and Azhar (2000), Hussain <i>et al.</i> (2000), Basbag and Gencer (2007), Sakthi <i>et al.</i> (2007), Thiyagu <i>et al.</i> (2010) and Dinakaran <i>et al.</i> (2012)
	Negative	Kumar <i>et al.</i> (1992), Valarmathi (1996), Swati Bharad <i>et al.</i> (1999), Percy <i>et al.</i> (2006) and Ahuja <i>et al.</i> (2008) and Rao and Gopinath (2013)
Bundle strength	Positive	Swati Bharad <i>et al.</i> (1999), Altaher and Singh (2003), Azhar <i>et al.</i> (2004), Percy <i>et al.</i> (2006), Basbag and Gencer (2007), Reddy and Reddy (2008), Thiyagu <i>et al.</i> (2010) and Dinakaran <i>et al.</i> (2012)

Character	Association with yield	References
	Negative	Valarmathi (1996), Rao <i>et al.</i> (2001), Ahuja <i>et al.</i> (2008) and Rao and Gopinath (2013)
Micronaire	Positive	Altaher and Singh (2003), Azhar <i>et al.</i> (2004), Percy <i>et al.</i> (2006) and Sakthi <i>et al.</i> (2007), Dinakaran <i>et al.</i> (2012) and Rao and Gopinath (2013)
	Negative	Leela Pratap <i>et al.</i> (2007), Thiyagu <i>et al.</i> (2010), Reddy and Reddy (2008) and Rasheed <i>et al.</i> (2009)
Uniformity ratio	Positive	Altaher and Singh (2003) and Percy <i>et al.</i> (2006), Basbag and Gencer (2007), Leela Pratap <i>et al.</i> (2007) and Preetha and Raveendran (2007)
	Negative	Sakthi <i>et al.</i> (2007), Thiyagu <i>et al.</i> (2010), Dinakaran <i>et al.</i> (2012) and Rao and Gopinath (2013)
Elongation percentage	Positive	Basbag and Gencer (2007) and Thiyagu <i>et al.</i> (2010)
	Negative	Percy <i>et al.</i> (2006), Preetha and Raveendran (2007), Sakthi <i>et al.</i> (2007), Dinakaran <i>et al.</i> (2012) and Rao and Gopinath (2013)

Inter correlation among yield components and fibre quality traits

Characters	Direction of association	References
Days to first flowering with		
Plant height	Negative	Altaher and Singh (2003)
Number of sympodia per plant	Negative	Do-Thi-Ha-An <i>et al.</i> (2008)
Number of bolls per plant	Positive	Do-Thi-Ha-An <i>et al.</i> (2008)
	Negative	Leela Pratap <i>et al.</i> (2007)
Boll weight	Negative	Altaher and Singh (2003) and Leela Pratap <i>et al.</i> (2007)
Number of seeds per boll	Positive	Annapurve <i>et al.</i> (2007)
Ginning outturn	Positive	Gite <i>et al.</i> (2006)
	Negative	Kulkarni <i>et al.</i> (2007)

Characters	Direction of association	References
Lint index	Negative	Leela Pratap <i>et al.</i> (2007)
Seed index	Negative	Kalpande <i>et al.</i> (2008b)
2.5 per cent span length	Positive	Do-Thi-Ha-An <i>et al.</i> (2008)
	Negative	Kulkarni <i>et al.</i> (2007)
Bundle strength	Positive	Do-Thi-Ha-An <i>et al.</i> (2008)
Micronaire	Positive	Leela Pratap <i>et al.</i> (2007)
	Negative	Altaher and Singh (2003) and Preetha and Raveendran (2007)
Uniformity ratio	Positive	Leela Pratap <i>et al.</i> (2007)
	Negative	Preetha and Raveendran (2007)
Plant height with		
Number of sympodia per plant	Positive	Swati Bharad <i>et al.</i> (1999), Leela Pratap <i>et al.</i> (2007), Sakthi <i>et al.</i> (2007) and Do-Thi-Ha-An <i>et al.</i> (2008) and Rao and Gopinath (2013)
Number of bolls per plant	Positive	Sharma <i>et al.</i> (2006) and Preetha and Raveendran (2007), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
Boll weight	Positive	Dedaniya and Pethani (1994), Swati Bharad <i>et al.</i> (1999), Altaher and Singh (2003), Gite <i>et al.</i> (2006) and Leela Pratap <i>et al.</i> (2007), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
	Negative	Tamilselvam <i>et al.</i> (2013)
Number of seeds per boll	Positive	Kalpande <i>et al.</i> (2008b)
Ginning outturn	Negative	Altaher and Singh (2003), Rasheed <i>et al.</i> (2009), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)

Characters	Direction of association	References
Lint index	Negative	Leela Pratap <i>et al.</i> (2007) and Rasheed <i>et al.</i> (2009)
Seed index	Positive	Altaher and Singh (2003) and Sakthi <i>et al.</i> (2007), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
	Negative	Leela Pratap <i>et al.</i> (2007) and Rasheed <i>et al.</i> (2009)
2.5 per cent span length	Positive	Dedaniya and Pethani (1994)
Bundle strength	Negative	Do-Thi-Ha-An <i>et al.</i> (2008)
	Positive	Altaher and Singh (2003), Basbag and Gencer (2007) and Thiyagu <i>et al.</i> (2010)
Micronaire	Negative	Do-Thi-Ha-An <i>et al.</i> (2008) and Rao and Gopinath (2013)
	Positive	Dedaniya and Pethani (1994), Altaher and Singh (2003) and Rao and Gopinath (2013)
Uniformity ratio	Negative	Rasheed <i>et al.</i> (2009) and Thiyagu <i>et al.</i> (2010)
	Negative	Sakthi <i>et al.</i> (2007) and Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
Number of sympodia per plant with		
Number of bolls per plant	Positive	Swati Bharad <i>et al.</i> (1999), Gururajan (2000), Amir <i>et al.</i> (2002), Gite <i>et al.</i> (2006), Leela Pratap <i>et al.</i> (2007) and Kalpande <i>et al.</i> (2008b), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
Boll weight	Positive	Dedaniya and Pethani (1994), Altaher and Singh (2003), Sharma <i>et al.</i> (2006) and Sakthi <i>et al.</i> (2007) and Rao and Gopinath (2013)
	Negative	Leela Pratap <i>et al.</i> (2007), Rasheed <i>et al.</i> (2009) and Thiyagu <i>et al.</i> (2010)

Characters	Direction of association	References
Number of seeds per boll	Positive	Annapurve <i>et al.</i> (2007)
	Negative	Leela Pratap <i>et al.</i> (2007) and Thiyagu <i>et al.</i> (2010)
Ginning outturn	Positive	Annapurve <i>et al.</i> (2007), Do-Thi-Ha-An <i>et al.</i> (2008), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
	Negative	Altaher and Singh (2003), Kulkarni <i>et al.</i> (2007) and Sakthi <i>et al.</i> (2007)
Lint index	Positive	Sharma <i>et al.</i> (2006), Sakthi <i>et al.</i> (2007), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
Seed index	Positive	Altaher and Singh (2003), Do-Thi-Ha-An <i>et al.</i> (2008), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
2.5 per cent span length	Positive	Sakthi <i>et al.</i> (2007) and Thiyagu <i>et al.</i> (2010)
	Negative	Kalpande <i>et al.</i> (2008b) and Rao and Gopinath (2013)
Bundle strength	Positive	Altaher and Singh (2003) and Thiyagu <i>et al.</i> (2010)
	Negative	Do-Thi-Ha-An <i>et al.</i> (2008) and Rao and Gopinath (2013)
Micronaire	Positive	Altaher and Singh (2003), Do-Thi-Ha-An <i>et al.</i> (2008) and Rasheed <i>et al.</i> (2009)
	Negative	Leela Pratap <i>et al.</i> (2007), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
Uniformity ratio	Negative	Preetha and Raveendran (2007), Sakthi <i>et al.</i> (2007) and Thiyagu <i>et al.</i> (2010)
Elongation percentage	Positive	Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
	Negative	Sakthi <i>et al.</i> (2007)

Characters	Direction of association	References
Number of bolls per plant with		
Boll weight	Positive	Sharma <i>et al.</i> (2006), Kalpande <i>et al.</i> (2008b), McCarty <i>et al.</i> (2008) and Rasheed <i>et al.</i> (2009)
	Negative	Iqbal <i>et al.</i> (2006) and Sambamurthy and Chamundeswari (2006), Thiyagu <i>et al.</i> (2010), Dinakaran <i>et al.</i> (2012) and Rao and Gopinath (2013)
Number of seeds per boll	Positive	Annapurve <i>et al.</i> (2007)
	Negative	Thiyagu <i>et al.</i> (2010)
Ginning outturn	Positive	Ahmad and Azhar (2000), Dinakaran <i>et al.</i> (2012) and Rao and Gopinath (2013)
	Negative	Dedaniya and Pethani (1994), McCarty <i>et al.</i> (2008) and Thiyagu <i>et al.</i> (2010)
Lint index	Positive	Sharma <i>et al.</i> (2006), Leela Pratap <i>et al.</i> (2007), Rasheed <i>et al.</i> (2009) and Rao and Gopinath (2013)
	Negative	Sambamurthy and Chamundeswari (2006) and Thiyagu <i>et al.</i> (2010)
Seed index	Positive	Altaher and Singh (2003) and Kalpande <i>et al.</i> (2008b) and Thiyagu <i>et al.</i> (2010)
	Negative	Sambamurthy and Chamundeswari (2006), Rasheed <i>et al.</i> (2009) and Rao and Gopinath (2013)
2.5 per cent span length	Positive	Ahmad and Azhar (2000), Basbag and Gencer (2007), Thiyagu <i>et al.</i> (2010) and Dinakaran <i>et al.</i> (2012)
	Negative	Sambamurthy and Chamundeswari (2006), Kalpande <i>et al.</i> (2008b) and Rao and Gopinath (2013)

Characters	Direction of association	References
Bundle strength	Positive	Altaher and Singh (2003), Do-Thi-Ha-An <i>et al.</i> (2008), Rasheed <i>et al.</i> (2009), Thiyagu <i>et al.</i> (2010) and Dinakaran <i>et al.</i> (2012)
	Negative	Rao and Gopinath (2013)
Micronaire	Positive	Ahmad and Azhar (2000), Sakthi <i>et al.</i> (2007) and Rasheed <i>et al.</i> (2009),
	Negative	Dedaniya and Pethani (1994), Leela Pratap <i>et al.</i> (2007), Do-Thi-Ha-An <i>et al.</i> (2008), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
Boll weight with		
Number of seeds per boll	Positive	Sambamurthy <i>et al.</i> (1995a), Annapurve <i>et al.</i> (2007), Kalpande <i>et al.</i> (2008b) and Thiyagu <i>et al.</i> (2010)
Ginning outturn	Positive	Dedaniya and Pethani (1994), Sambamurthy and Chamundeswari (2006), Annapurve <i>et al.</i> (2007), Rasheed <i>et al.</i> (2009) and Thiyagu <i>et al.</i> (2010)
	Negative	McCarty <i>et al.</i> (2008), Dinakaran <i>et al.</i> (2012) and Rao and Gopinath (2013)
Lint index	Positive	Sambamurthy <i>et al.</i> (1995a), Sharma <i>et al.</i> (2006), Kulkarni <i>et al.</i> (2007), Sakthi <i>et al.</i> (2007), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
	Negative	Leela Pratap <i>et al.</i> (2007) and Rasheed <i>et al.</i> (2009)
Seed index	Positive	Sambamurthy <i>et al.</i> (1995a), Swati Bharad <i>et al.</i> (1999), Altaher and Singh (2003), Annapurve <i>et al.</i> (2007), Preetha and Raveendran (2007) and Do-Thi-Ha-An <i>et al.</i> (2008), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
	Negative	Leela Pratap <i>et al.</i> (2007)

Characters	Direction of association	References
2.5 per cent span length	Positive	Ahmad and Azhar (2000), Sambamurthy and Chamundeswari (2006), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
Bundle strength	Positive	Altaher and Singh (2003), Hinze <i>et al.</i> (2011) and Rao and Gopinath (2013)
	Negative	Preetha and Raveendran (2007), Rasheed <i>et al.</i> (2009), Thiyagu <i>et al.</i> (2010) and Dinakaran <i>et al.</i> (2012)
Micronaire	Positive	Ahmad and Azhar (2000), Preetha and Raveendran (2007), Rasheed <i>et al.</i> (2009), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
Elongation percentage	Negative	Leela Pratap <i>et al.</i> (2007) and Dinakaran <i>et al.</i> (2012)
	Positive	Preetha and Raveendran (2007) and Rao and Gopinath (2013)
	Negative	Thiyagu <i>et al.</i> (2010) and Dinakaran <i>et al.</i> (2012)
Number of seeds per boll with		
Ginning outturn	Positive	Sambamurthy <i>et al.</i> (1995a), Leela Pratap <i>et al.</i> (2007) and Thiyagu <i>et al.</i> (2010)
	Negative	Kalpande <i>et al.</i> (2008b) and Thiyagu <i>et al.</i> (2010)
Lint index	Positive	Sambamurthy <i>et al.</i> (1995a) and Leela Pratap <i>et al.</i> (2007)
Seed index	Positive	Leela Pratap <i>et al.</i> (2007) and Hinze <i>et al.</i> (2011)
2.5 per cent span length	Positive	Leela Pratap <i>et al.</i> (2007)
Uniformity ratio	Negative	Leela Pratap <i>et al.</i> (2007) and Thiyagu <i>et al.</i> (2010)

Characters	Direction of association	References
Ginning outturn with		
Lint index	Positive	Sumathi and Nadarajan (1995), Hussain <i>et al.</i> (1998), Ahmad and Azhar (2000), Leela Pratap <i>et al.</i> (2007), Sakthi <i>et al.</i> (2007) and Do-Thi-Ha-An <i>et al.</i> (2008), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
Seed index	Positive	Ulloa (2006) and Hinze <i>et al.</i> (2011)
	Negative	Jagtap and Kolhe (1984), Altaher and Singh (2003), Annapurve <i>et al.</i> (2007), Preetha and Raveendran (2007), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
2.5 per cent span length	Positive	Altaher and Singh (2003), Sambamurthy and Chamundeswari (2006) and Annapurve <i>et al.</i> (2007)
	Negative	Basbag and Gencer (2007), Preetha and Raveendran (2007), Do-Thi-Ha-An <i>et al.</i> (2008), Kalpande <i>et al.</i> (2008b), Thiyagu <i>et al.</i> (2010), Dinakaran <i>et al.</i> (2012) and Rao and Gopinath (2013)
Bundle strength	Positive	Leela Pratap <i>et al.</i> (2007), Rasheed <i>et al.</i> (2009) and Rao and Gopinath (2013)
	Negative	Altaher and Singh (2003), Basbag and Gencer (2007), Thiyagu <i>et al.</i> (2010) and Dinakaran <i>et al.</i> (2012)
Micronaire	Positive	Ahmad and Azhar (2000), Percy <i>et al.</i> (2006) and Do-Thi-Ha-An <i>et al.</i> (2008), Thiyagu <i>et al.</i> (2010), Dinakaran <i>et al.</i> (2012) and Rao and Gopinath (2013)
	Negative	Leela Pratap <i>et al.</i> (2007)

Characters	Direction of association	References
Uniformity ratio	Positive	Percy <i>et al.</i> (2006), Sakthi <i>et al.</i> (2007), Thiyagu <i>et al.</i> (2010), Dinakaran <i>et al.</i> (2012) and Rao and Gopinath (2013)
	Negative	Altaher and Singh (2003), Sambamurthy and Chamundeswari (2006), Basbag and Gencer (2007) and Leela Pratap <i>et al.</i> (2007)
Elongation percentage	Positive	Preetha and Raveendran (2007)
	Negative	Thiyagu <i>et al.</i> (2010), Dinakaran <i>et al.</i> (2012) and Rao and Gopinath (2013)
Lint index with		
Seed index	Positive	Sambamurthy <i>et al.</i> (1994b), Altaher and Singh (2003) and Do-Thi-Ha-An <i>et al.</i> (2008) and Thiyagu <i>et al.</i> (2010)
Ginning outturn	Positive	Sambamurthy <i>et al.</i> (1995a)
2.5 per cent span length	Positive	Ahmad and Azhar (2000), Preetha and Raveendran (2007) and Rao and Gopinath (2013)
Bundle strength	Positive	Preetha and Raveendran (2007) and Rasheed <i>et al.</i> (2009)
	Negative	Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
Micronaire	Positive	Preetha and Raveendran (2007), Do-Thi-Ha-An <i>et al.</i> (2008), Rasheed <i>et al.</i> (2009), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
Uniformity ratio	Positive	Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
	Negative	Leela Pratap <i>et al.</i> (2007) and Sakthi <i>et al.</i> (2007)
Elongation percentage	Positive	Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
	Negative	Sakthi <i>et al.</i> (2007)

Characters	Direction of association	References
Seed index with		
Lint index	Positive	Sambamurthy <i>et al.</i> (1995a)
2.5 per cent span length	Positive	Altaher and Singh (2003), Annapurve <i>et al.</i> (2007), Do-Thi-Ha-An <i>et al.</i> (2008), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
Bundle strength	Positive	Altaher and Singh (2003), Preetha and Raveendran (2007) and Thiyagu <i>et al.</i> (2010)
Micronaire	Negative	Leela Pratap <i>et al.</i> (2007)
	Positive	Leela Pratap <i>et al.</i> (2007), Do-Thi-Ha-An <i>et al.</i> (2008), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
Uniformity ratio	Negative	Sakthi <i>et al.</i> (2007), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
Elongation percentage	Negative	Preetha and Raveendran (2007) and Sakthi <i>et al.</i> (2007)
	Positive	Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
2.5 per cent span length with		
Fibre strength	Positive	Rajarathinam <i>et al.</i> (1993), Echekwu (2001), Herring <i>et al.</i> (2004), Tuteja <i>et al.</i> (2005b), Do-Thi-Ha-An <i>et al.</i> (2008), Dinakaran <i>et al.</i> (2012) and Rao and Gopinath (2013)
	Negative	Percy <i>et al.</i> (2006)
Micronaire	Positive	Dutt <i>et al.</i> (2004)
	Negative	Rajarathinam <i>et al.</i> (1993), Swati Bharad <i>et al.</i> (1999), Altaher and Singh (2003), Ulloa (2006), Turley <i>et al.</i> (2007), Thiyagu <i>et al.</i> (2010), Dinakaran <i>et al.</i> (2012) and Rao and Gopinath (2013)

Characters	Direction of association	References
Uniformity ratio	Positive	Basbag and Gencer (2007)
	Negative	Rajarathinam <i>et al.</i> (1993), Altaher and Singh (2003), Percy <i>et al.</i> (2006), Sakthi <i>et al.</i> (2007), Thiyagu <i>et al.</i> (2010), Dinakaran <i>et al.</i> (2012) and Rao and Gopinath (2013)
Elongation percentage	Positive	Basbag and Gencer (2007) and Rao and Gopinath (2013)
	Negative	Ulloa (2006), Preetha and Raveendran (2007), Thiyagu <i>et al.</i> (2010) and Dinakaran <i>et al.</i> (2012)
Bundle strength with		
Micronaire	Negative	Singh <i>et al.</i> (1990)
Uniformity ratio	Positive	Basbag and Gencer (2007)
	Negative	Tuteja <i>et al.</i> (2005b), Leela Pratap <i>et al.</i> (2007), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
Elongation percentage	Positive	Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)
	Negative	Preetha and Raveendran (2007) and Dinakaran <i>et al.</i> (2012)
Micronaire with		
Bundle strength	Positive	Dutt <i>et al.</i> (2004), Rasheed <i>et al.</i> (2009) and Rao and Gopinath (2013)
	Negative	Singh <i>et al.</i> (1990), Leela Pratap <i>et al.</i> (2007), Do-Thi-Ha-An <i>et al.</i> (2008) and Dinakaran <i>et al.</i> (2012)
Uniformity ratio	Positive	Rajarathinam <i>et al.</i> (1993), Altaher and Singh (2003), Percy <i>et al.</i> (2006), Preetha and Raveendran (2007), Sakthi <i>et al.</i> (2007), Thiyagu <i>et al.</i> (2010) and Rao and Gopinath (2013)

Characters	Direction of association	References
Uniformity ratio with		
Elongation percentage	Positive	Preetha and Raveendran (2007), Sakthi <i>et al.</i> (2007), Thiyagu <i>et al.</i> (2010) and Dinakaran <i>et al.</i> (2012)
	Negative	Rao and Gopinath (2013)

2.3.4. Molecular marker analysis for yield and fibre quality traits

2.3.4.1. Molecular markers

Despite the success in increasing yield and its quality by conventional breeding, the process of genetic improvement for these traits remains slow since the traits are under the control of many genes. The progress in genetic improvement of polygenic traits can be hastened by exploiting the potentials of DNA markers. This approach has enormous potential to improve the efficiency and precision of conventional plant breeding and it is also popularly known as molecular breeding or marker assisted breeding. The marker assisted breeding involves use of the presence or absence of a marker as a substitute for the direct phenotypic selection to make the process of selection more efficient, reliable, time saving and cost effective (Collard *et al.*, 2005; Collard and Mackill, 2008).

DNA markers are largely used for construction of genetic linkage maps. Linkage maps are used for identifying chromosomal regions that contains genes controlling simple traits and quantitative traits using quantitative trait loci (QTL) analysis (Mohan *et al.*, 1997). Advances in the use of DNA markers to identify QTL and marker assisted selection (MAS) have shown promises for streamlining plant breeding programmes. For example, genetic maps constructed using crosses of upland cotton has led to the identification of several QTLs for fibre strength, fineness and length (Ulloa and Meredith Jr., 2000; Zhang *et al.*, 2005b). The advantage of MAS over conventional breeding is that the selection is simple than phenotypic selection and selection can be done at seedling stage itself (single plant, even a small leaf sample is enough to predict the entire gene or QTL of the particular trait) (Collard and Mackill, 2008). Thus, DNA marker technology provides a valuable tool to

the plant breeders to select the desirable plants directly on the basis of genotype rather than phenotype.

Despite this success, progress on the mapping and molecular characterization of the cotton genome is slow relative to other crop plants such as rice, maize and soybean. Partly this has been due to large size (2.2 to 2.9 Gbp) and the allopolyploid nature of the genome.

2.3.4.2. Simple Sequence Repeats (SSRs)

Wild *Gossypium* germplasm harbors many valuable traits including disease and insect resistance, stress tolerance and fibre quality attributes. DNA markers in construction of genetic maps would be useful in introgression of alien genes into cultivated species. Molecular linkage map construction has been recognized as an essential tool for plant breeding because they have the properties of neutrality, lack epistasis and are simply inherited Mendelian characters (Tanksley and McCouch, 1997). Efficient construction of genetic map requires well spaced polymorphic markers for the given parents. Hence, selection of a marker system that serves for the above purpose is the key step in MAS.

Considering the different types of molecular marker system to study the extent of polymorphism in cultivated cotton, SSR marker is the best to predict the genetic variation within cultivated diploid and tetraploid cotton (Boopathi *et al.*, 2008).

SSR or microsatellites are short, tandemly repeated DNA sequence motifs that consist of two to six nucleotide core units (Litt and Luty, 1989). They are highly abundant in eukaryotic genome but also occur in prokaryotes at lower frequencies. The regions flanking the microsatellites are generally conserved and PCR primers relative to the flanking regions are used to amplify SSR containing DNA fragments. The length of the amplified fragment will vary according to the number of repeat units (Ellegien, 1993). Further, the reproducibility of SSRs makes them efficiently used in different laboratories to produce consensus data, which make them useful for genome mapping projects in many plant species (Dietrich *et al.*, 1996; Dib *et al.*, 1996; Schmidt and Heslop, 1998). Besides, this marker had high information content, co-dominant inheritance, locus specificity and ease for automation for high throughput screening.

Thus, advent of SSR or microsatellite markers has brought a new, user-friendly and highly polymorphic class of genetic markers in cotton. The later feature is especially useful to the cultivated upland cotton due to its low intraspecific polymorphism. However, the higher development cost and effort required to obtain working SSR primers for a given species has restricted their use to only a few of the agriculturally important crops (Squirrell *et al.*, 2003).

Several methods have been pursued to develop SSR markers in cottons, including analysis of SSR-enriched small insert genomic DNA libraries (Connell *et al.*, 1998; Liu *et al.*, 2000a and b; Reddy *et al.*, 2001 and Nguyen *et al.*, 2004), SSR mining from ESTs (Qureshi *et al.*, 2004; Han *et al.*, 2004 and 2006; Park *et al.*, 2005), and large insert BAC derivation by end sequence analysis (Frelichowski Jr. *et al.*, 2006) or SSR-containing BAC subcloning (Lichtenzweig *et al.*, 2005). Currently, a total of approximately 11,000 SSRs have been developed in cotton (Blenda *et al.*, 2006; <http://www.cottonmarker.org>). Reddy *et al.* (2001) suggested that the total pool of SSRs present in the cotton genome is sufficient to satisfy the requirements of extensive genome mapping and MAS. Liu *et al.* (2000a and b) have assigned SSRs to cotton chromosomes by making use of aneuploid stocks. SSRs have been widely employed in genetic diversity analyses (Rungis *et al.*, 2005; Zhang *et al.*, 2005a; Liu *et al.*, 2006 and Lacape *et al.*, 2007) and genetic linkage maps (Zhang *et al.*, 2002; Han *et al.*, 2004 and 2006; Song *et al.*, 2005; Guo *et al.*, 2007a and b) in cotton.

SSRs have been employed to study the extent of genetic polymorphism among cotton germplasms (Liu *et al.*, 2000b; Rungis *et al.*, 2005; Bertini *et al.*, 2006; Guo *et al.*, 2007b; Lacape *et al.*, 2007; Wu *et al.*, 2007a; Boopathi *et al.*, 2008). Eventhough few of the studies revealed that low level of polymorphism within *G. hirsutum* genotypes (Liu *et al.*, 2000b and Rungis *et al.*, 2005), some of the studies clearly discriminate the evaluated germplasms (Bertini *et al.*, 2006; Guo *et al.*, 2007b; Lacape *et al.*, 2007 and Boopathi *et al.*, 2008) and phylogenic evolution of *Gossypium* species (Wu *et al.*, 2007a). However, it has been shown that use of other marker systems such as RFLP, RAPD, AFLP *etc.*, may increase the efficiency of genetic diversity analysis.

2.3.4.3. Mapping populations and its importance in MAS

The first step in linkage map construction is development of mapping population. Generally, in self pollinated species, mapping population originates from parents that are highly homozygous (inbreds). The initial step in production of mapping population is selecting two genetically divergent parents, which show clear genetic differences for one or more traits of interest(s). At the same time the divergence should not be too genetically distant so as to reduce the sterility of the progenies and segregation distortion during linkage analysis. Several different mapping population viz., F_2 , backcross (BC), recombinant inbred lines (RIL), double haploids (DHs) and near isogenic lines (NILs) have been utilized in this context. However, population type possesses its own advantages and disadvantages (McCouch and Doerge, 1995; Paterson, 1996). Hence selection of population type is critical for successful linkage mapping. Both F_2 and BC populations are the simplest types of mapping populations because they are easy to construct and requires only a short time to produce. However, F_2 and BC populations are considered to be temporary populations because they are highly heterozygous and cannot be propagated indefinitely through seeds. RILs, NILs and DHs are permanent populations because they are homozygous or 'true-breeding' lines that can be multiplied and reproduced without genetic change. Thus, there is no single population that suits for all the needs of a general linkage mapping and MAS.

F_2 is the most preferred population for preliminary mapping since it requires less time for development and can be developed with minimum efforts as compared to other populations. Further, F_2 is more powerful in detecting QTLs of additive effect, and can also be used to estimate the degree of dominance for detected QTLs. RILs, NILs and DHs may be powerful tools for consistent QTL detection in some circumstances but provide no information on dominance relationships for any QTL (Haley and Anderson, 1997). Hence, to begin with, it is advisable to use F_2 population since it is simple to produce and have above said advantages.

From the available literature on genetic linkage map, there is no specific study relating to the ideal number of individuals in a given population required to establish accurate genetic maps. The construction of linkage map requires segregating plant

population consisting of 50 to 250 individuals (Mohan *et al.*, 1997), but a larger population size is needed for high resolution fine mapping. Simulation studies performed by using F₂, BC, RILs and DHs populations with varying sample size (50 - 1000) indicated that more accurate maps were obtained for RIL and F₂ population with co-dominant markers and lowest number of individuals provided several fragmented linkage groups and inaccurate locus order (Ferreira *et al.*, 2006).

The next key factor to be considered here is selection of one or combination of marker types to cover the entire genome of the species. Restriction fragment length polymorphisms (RFLPs), random amplified polymorphic DNA (RAPD), amplified fragment length polymorphisms (AFLPs), microsatellites or simple sequence repeats (SSRs), expressed sequence tags (ESTs), and sequence related amplified polymorphism (SRAP) have been used for map construction in cotton. Semagn *et al.* (2006) have listed out various factors to be considered in selecting one or more of these marker systems to construct the genetic linkage map. Staub and Serquen (1996) reviewed the genetic information for different types of mapping populations in relation to dominant versus co-dominant markers. From these studies, it is clear that maximum genetic informations can be obtained from F₂ population, if a co-dominant marker system is used.

2.3.4.4. Cotton linkage maps

The development of molecular markers has provided various markers suitable for use in cotton research. These markers have greatly promoted the development of cotton linkage maps. As in most plant species, the early application of DNA markers in cotton genomic research has been in the form of RFLPs. It is, therefore, not surprising that the first molecular linkage map of the *Gossypium* species was constructed from an interspecific *G. hirsutum* x *G. barbadense* F₂ population based on RFLPs by Reinisch *et al.* (1994) who used to assemble 705 RFLP loci into 41 linkage groups with average spacing between markers of about 7 cM. Since then, many interspecific maps have been constructed (Ulloa *et al.*, 2000; Rong *et al.*, 2004; Lin *et al.*, 2005; Guo *et al.*, 2007b; Yu *et al.*, 2007; Lacape *et al.*, 2009 and Yu *et al.*, 2011). However, interspecific introgressions often encountered problems, such as segregation distortion (Jiang *et al.*, 2000b), suppression of recombination (Paterson *et al.*, 1990), and linkage drag (Young and Tanksley, 1998).

For this reason, many intraspecific maps of *G. hirsutum* were also constructed by several researchers (Ulloa *et al.*, 1999; Ulloa and Meredith, 2000; Zhang *et al.*, 2005b; Wang *et al.*, 2006b; Shen *et al.*, 2007; Zhang *et al.*, 2009; Lin *et al.*, 2009; Zhang *et al.*, 2012; Byers *et al.*, 2012 and Gore *et al.*, 2014) to investigate cotton genome and identify molecular markers linked to agriculturally important genes/QTLs as shown in Table 1. The well-covered intraspecific of *G. hirsutum* contains 978 SSR loci and has a full length of 4184.40 cM. Its mean distance between adjacent loci is 4.30 cM (Zhang *et al.*, 2012). The construction of genetic maps has allowed QTL studies based on these maps.

Meredith (1992), in a study of heterosis and varietal origins, reported the first RFLP evaluation in upland cotton, *G. hirsutum* L. To determine the amount of polymorphism for RFLP markers in Upland cotton, 68 individual lines from diverse genetic backgrounds were analyzed with 75 probe/enzyme combinations resulting in 179 polymorphic fragments. This large number of fragments provided sufficient evidence that genetic analyses of this type were feasible for upland cotton (Shappley *et al.*, 1993; Shappley, 1994). Five linkage groups with 12 loci provided the first genetic linkage maps constructed with molecular markers in a cross of upland cotton (Shappley, 1994; Shappley, 1996). Shappley *et al.* (1998b) also developed a genetic linkage map with 31 linkage groups in upland cotton from a cross of two *G. hirsutum* L. lines. This map was based on segregation in 96 F₂:F₃ families scored for 129 probe-enzyme combinations that resulted in 138 RFLP loci (120 in linkage groups and 18 nonlinked).

Ulloa and Meredith (2000) developed a RFLP genetic linkage map of upland cotton from 119 F_{2,3} progeny from the cross MD5678ne x Prema, and used it for QTL analysis for agronomic and fibre quality traits. The linkage map comprises 81 loci mapped to 17 linkage groups with an average distance between markers of 8.7 cM, covering 700.7 cM, or approximately 15% of the recombinational length of the cotton genome.

Zhang *et al.* (2005b) studied the genetic linkage map with 70 loci (55 SSR, 12 AFLP and 3 morphological loci) using 117 F₂ plants obtained from a cross between two upland cotton cultivars Yumian 1 and T586. The linkage map comprised of 20 linkage groups, covering 525 cM with an average distance of 7.5 cM between two

Table 1. Molecular marker based genetic linkage maps in cotton

S. No.	Species involved	Population		Markers	No. of mapped loci	Map length (cM)	Linkage group	References
		Type	Size					
1	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₂	57	RFLP	705	4675	41	Reinisch <i>et al.</i> (1994)
2	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₂	271	RFLP	261	3767	27	Jiang <i>et al.</i> (1998)
3	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂ and F _n	96	RFLP	120	865	31	Shappley <i>et al.</i> (1998a)
4	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F _{2:3}	96	RFLP	120	865	24	Shappley <i>et al.</i> (1998b)
5	<i>G. hirsutum</i> × (<i>G. sturtianum</i> <i>G. thurberi</i> , <i>G. raimondii</i>)	BC ₁ to BC ₅	192	RAPD, SSR, RFLP and AFLP	-	-	-	Bi <i>et al.</i> (1999)
6	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₂	180	RFLP	-	3664	26	Jiang <i>et al.</i> (2000b)
7	<i>G. hirsutum</i> × <i>G. barbadense</i>	F _{2:3}	118	RAPD and SSR	-	1058	28	Ulloa <i>et al.</i> (2000)
8	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F _{2:3}	119	RFLP	81	700.7	17	Ulloa and Meredith Jr., (2000)
9	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₂	171	RFLP, RAPD and SSR	-	4766	50	Kohel <i>et al.</i> (2001)
10	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₂ F _n	430 214	RFLP	-	-	-	Saranga <i>et al.</i> (2001)
11	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F _{2:3}	569	RFLP	284	1502.6	47	Ulloa <i>et al.</i> (2002)
12	<i>G. hirsutum</i> × <i>G. barbadense</i>	BC ₁ F ₁	75	AFLP, SSR and RFLP	888	4400.0	37	Lacape <i>et al.</i> (2003)

Contd.....

Table 1. Contd..

S. No.	Species involved	Population		Markers	No. of mapped loci	Map length (cM)	Linkage group	References
		Type	Size					
13	<i>G. hirsutum</i> × <i>G. barbadense</i>	F _{2:3}	214	RFLP	-	-	-	Paterson <i>et al.</i> (2003)
14	<i>G. hirsutum</i> × <i>G. anomalum</i>	F ₂ and F _n	186	SSR and RAPD	-	-	-	Zhang <i>et al.</i> (2003)
15	(<i>G. hirsutum</i> × <i>G. barbadense</i>) <i>G. hirsutum</i>	BC ₁ F ₁	140	EST-SSR	-	-	-	Han <i>et al.</i> (2004)
16	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₂	94	AFLP, SSR and RFLP	-	3287	42	Mei <i>et al.</i> (2004)
17	(<i>G. hirsutum</i> × <i>G. barbadense</i>) <i>G. hirsutum</i>	BC ₁ F ₁	75	SSR	1160	5519	31	Nguyen <i>et al.</i> (2004)
18	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₂	57	RFLP	2584	4447.9	26	Rong <i>et al.</i> (2004)
19	<i>G. trilobum</i> × <i>G. raimondii</i>	F ₂	62	RFLP	763	1493.3	13	Rong <i>et al.</i> (2004)
20	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₂ F _n	406 208	RFLP	-	-	-	Saranga <i>et al.</i> (2004)
21	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₂	110	SSR	35	531	11	Bolek <i>et al.</i> (2005)
22	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₂ and F _{2:3}	69	SSR, SRAP and RAPD	-	-	15	He <i>et al.</i> (2005)
23	<i>G. hirsutum</i> × <i>G. barbadense</i>	BC ₁ and BC ₂	200	SSR and RFLP	1306	5597	26	Lacape <i>et al.</i> (2005)
24	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₂ and F _{2:3}	69	SSR, SRAP and RAPD	566	5141.8	41	Lin <i>et al.</i> (2005)

Contd.....

Table 1. Contd..

S. No.	Species involved	Population		Markers	No. of mapped loci	Map length (cM)	Linkage group	References
		Type	Size					
25	<i>G. hirsutum</i> × <i>G. barbadense</i>	RILs	183	EST-SSR	193	1277	19 + 11 LG	Park <i>et al.</i> (2005)
26 a)	<i>G. hirsutum</i> × <i>G. barbadense</i> 7235 × TM-1	F ₂ and F _{2:3}	163	SSR	86	666.7	21	Shen <i>et al.</i> (2005)
b)	HS427-10 × TM-1	F ₂ and F _{2:3}	169	SSR	56	557.8	17	Shen <i>et al.</i> (2005)
c)	PD6992 × SM 3	F ₂ and F _{2:3}	142	SSR	73	588	22	Shen <i>et al.</i> (2005)
27	<i>G. hirsutum</i> × <i>G. tomentosum</i>	F ₂	82	SSR	589	4259.4	52	Waghmare <i>et al.</i> (2005)
28	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂ and F _{2:3}	117	SSR and AFLP	70	525	20	Zhang <i>et al.</i> (2005b)
29	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂	-	SSR	-	1,174	5	Fan <i>et al.</i> (2006)
30	<i>G. hirsutum</i> × <i>G. barbadense</i>	RILs	183	SSR	433	2126.3	46	Frelichowski Jr., <i>et al.</i> (2006)
31	(<i>G. hirsutum</i> × <i>G. barbadense</i>) <i>G. hirsutum</i>	BC ₁ F ₁	140	EST-SSR	130	-	6	Han <i>et al.</i> (2006)
32	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RILs	258	SSR	810.07	-	22	Shen <i>et al.</i> (2006)
33	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RILs	180	SSR, RAPD and SRAP	54	-	17	Wang <i>et al.</i> (2006a)
34	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RILs	180	SSR, AFLP, RAPD and SRAP	132	865.2	26	Wang <i>et al.</i> (2006b)

Contd.....

Table 1. Contd..

S. No.	Species involved	Population		Markers	No. of mapped loci	Map length (cM)	Linkage group	References
		Type	Size					
35	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RILs	76	SSR	-	42	1	Abdurakhmonov <i>et al.</i> (2007)
36	(<i>G. hirsutum</i> × <i>G. barbadense</i>) <i>G. hirsutum</i>	BC ₁ F ₁	138	EST-SSR	1790	3425.8	26	Guo <i>et al.</i> (2007b)
37	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₂ and F _{2:n}	69	SSR, SRAP, RAPD and REMAPs	1029	5472.3	26	He <i>et al.</i> (2007)
38	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RILs	207	SSR	156	1024.4	31	Shen <i>et al.</i> (2007)
39	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RILs	270	SSR	-	96.2	1	Wan <i>et al.</i> (2007)
40	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RILs	180	SSR, AFLP, RAPD and SRAP	132	865.20	26	Wang <i>et al.</i> (2007a)
41	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂	171	SSR, AFLP, RAPD and SRAPs	-	1025.1	-	Wang <i>et al.</i> (2007b)
42	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₂	186	SSR, TRAP, SRAP and AFLP	1097	4536.7	35	Yu <i>et al.</i> (2007)
43	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂	251	SSR	-	650.8	17	Guo <i>et al.</i> (2008)
44	<i>G. hirsutum</i> × <i>G. barbadense</i>	RILs	121	SSR	-	5472.3	26	He <i>et al.</i> (2008)
45	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RILs	60	ATG-AFLP	-	-	17	Lu <i>et al.</i> (2008)
46	<i>G. arboreum</i> × <i>G. arboreum</i>	F ₂	189	SSR	264	2508.71	13	Ma <i>et al.</i> (2008)
47	<i>G. hirsutum</i> (4 way cross)	-	273	SSR, EST-SSR	286	2113.3	56	Qin <i>et al.</i> (2008)

Contd.....

Table 1. Contd..

S. No.	Species involved	Population		Markers	No. of mapped loci	Map length (cM)	Linkage group	References
		Type	Size					
48	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RILs	-	SSR	-	504.05	15	Zhang <i>et al.</i> (2008)
49	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂	137	SRAP, SSR, RAPD and RGAP	471	3070.2	51	Lin <i>et al.</i> (2009)
50	<i>G. hirsutum</i> × <i>G. barbadense</i>	RILs	140	SSR and AFLP	800	2044	26	Lacape <i>et al.</i> (2009) Lacape <i>et al.</i> (2010)
51	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RILs	188	SSR	125	965	26	Wu <i>et al.</i> (2009)
52	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RILs	270	SSR and SRAP	604	3140.9	60	Zhang <i>et al.</i> (2009)
53	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₂	214	SSR and AFLP	175	2030	42	Yang <i>et al.</i> (2009)
54	<i>G. hirsutum</i> × <i>G. barbadense</i>	BC ₁ F ₁	62	SSR	57	911.6	19	Santoshkumar (2010), Urbi (2010)
55	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂	162	SSR, SNP	132	1003	33	Jenkins <i>et al.</i> (2010)
56	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RILs	2517	SSR	51	42.9	1	Chen <i>et al.</i> (2010)
57	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₂	209	SSR	82	411.6	17	Wang <i>et al.</i> (2011)
58	<i>G. hirsutum</i> × <i>G. barbadense</i>	BC, F ₂	300	SSR	164	237	17	Gutierrez <i>et al.</i> (2011)
59	<i>G. hirsutum</i> × <i>G. barbadense</i>	BC ₁	141	EST_SSR's	2316	4418.9	26	Yu <i>et al.</i> (2011)
60	<i>G. hirsutum</i> × <i>G. tomentosum</i>	BC ₃ F ₂	634	RFLP	589	1010.0	-	Zhang <i>et al.</i> (2011)

Contd.....

Table 1. Contd..

S. No.	Species involved	Population		Markers	No. of mapped loci	Map length (cM)	Linkage group	References
		Type	Size					
61	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂	136	SSR	35	273.11	12	Saeed <i>et al.</i> (2011)
62	<i>G. hirsutum</i> × <i>G. hirsutum</i>	IF ₂	171	cDNA-AFLP	-	2477.06	26	Liu <i>et al.</i> (2011)
63	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RILs	180	EST-SSR	181	941.2	38	Liu <i>et al.</i> (2012)
64	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RILs	196	SSR	190	700.9	34	Sun <i>et al.</i> (2012)
65	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RILs	188	SSR, SRAP and RAPD	388	1946.22	30	Alfred <i>et al.</i> (2012)
66	<i>G. hirsutum</i>	CP	172	SSR	978	4184.4	69	Zhang <i>et al.</i> (2012)
67	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂	299	SSR and AFLP	103	932.9	8	Chaudhary <i>et al.</i> (2013)
68	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂	-	SSR	269	1,837.8	43	Li <i>et al.</i> (2013)
69	<i>G. arboreum</i> × <i>G. arboreum</i>	F ₂	180	SSR and RAPD	45	346	10	Shaheen <i>et al.</i> (2013)
70	<i>G. hirsutum</i> × <i>G. barbadense</i>	BIL	146	SSR	392	2895	-	Yu <i>et al.</i> (2013)
71	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂	173	SSR	421	3814.3	49	Zhi <i>et al.</i> (2013)
72	<i>G. barbadense</i> × <i>G. barbadense</i>	F ₂	124	gSSR, EST-SSR, SRAP and SSCP-SNP	337	2108.34	52	Wang <i>et al.</i> (2013)
73	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F5:7 RILs	98	SSR and biallelic GBS-based SNP	841	2061.06	117	Gore <i>et al.</i> (2014)

Contd.....

Table 1. Contd..

S. No.	Species involved	Population		Markers	No. of mapped loci	Map length (cM)	Linkage group	References
		Type	Size					
74	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F _{2:3}	-	SSR	-	1273	37	Wang <i>et al.</i> (2014)
75	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂ and F _{2:3}	464	SSR	144	1273	37	Zhe <i>et al.</i> (2014)
76	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂	186	SSR and AFLP	-	-	27	Bardak <i>et al.</i> , (2015)
77	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RIL	-	SSR	1,540	2,842.06	-	Tang <i>et al.</i> , (2015)
78	<i>G. hirsutum</i> × <i>G. barbadense</i>	BC ₁	115	SSR, CIPs and TDFs	-	4,168.72	56	Yang <i>et al.</i> , (2015)

markers, or approximately 11.8% of the recombination length of the cotton genome. Wang *et al.* (2006b) constructed genetic linkage maps using SSR from 180 F_{8:9} recombinant inbred lines.

Lin *et al.* (2009) used the Sequence-related amplified polymorphism (SRAP) combined with SSRs, RAPDs and RGAPs to construct a high density genetic map for a F₂ population derived from the cross DH 962 (*G. hirsutum* accession) x Jimian 5 (*G. hirsutum* cultivar). A total of 4,096 SRAP primer combinations, 6310 SSRs, 600 RAPDs, and 10 RGAPs produced 331, 156, 17 and 2 polymorphic loci, respectively. Among the 506 loci obtained, 471 loci (309 SRAPs, 144 SSRs, 16 RAPDs and 2 RGAPs) were assigned to 51 linkage groups. Of these, 29 linkage groups were assigned to corresponding chromosomes by SSR markers with known chromosome locations. The map covered 3070.2 cM with a mean density of 6.5 cM per locus.

A three-parent composite population was developed from three cultivars to improve agronomic and economic traits by Zhang *et al.* (2012). Sixty nine linkage groups were identified that spanned 4,184.4 cM covering approximately 94.1% of the entire tetraploid cotton genome.

Zhi *et al.* (2013) presented the genetic linkage map comprising 421 loci and covering 3814.3 cM, accounting for approximately 73.35% of the cotton genome, using an F₂ population derived from cross GX1135 (P₁) x GX100-2 (P₂) of upland cotton. Forty-four of 49 linkage groups were assigned to the 26 chromosomes.

Gore *et al.* (2014) constructed an intraspecific linkage map of tetraploid cotton with 841 SSR and biallelic GBS-based SNP loci that spanned 2061.06 cM of the genome. These 841 marker loci were assembled into 117 linkage groups, of which 116 could be putatively assigned to 25 of the 26 cotton chromosomes. The tetraploid cotton genome has an estimated genetic distance of 4070 cM (Blenda *et al.*, 2012), thus the 117 linkage groups covered 50.6% of the genome.

The linkage maps so far constructed in cotton helped in determining the chromosomal location of many agronomically important characters such as yield (Saranga *et al.*, 2004; He *et al.*, 2005; Wang *et al.*, 2006a, Wang *et al.*, 2007a, Chen *et al.*, 2010, Liu *et al.*, 2011 and Liu *et al.*, 2012), fibre quality (Kohel *et al.*, 2001; Paterson *et al.*, 2003;

Lacape *et al.*, 2005; Lin *et al.*, 2005; Park *et al.*, 2005; Shen *et al.*, 2005; Frelichowski Jr. *et al.*, 2006; Wang *et al.*, 2006b; Wang *et al.*, 2007b; He *et al.*, 2008, Zhang *et al.*, 2009, Lacape *et al.*, 2010, Zhang *et al.*, 2011, Wang *et al.*, 2011, Sun *et al.*, 2012 and Zhang *et al.*, 2012), yield and fibre quality (Shappley *et al.*, 1998a and b; Ulloa and Meredith Jr., 2000; Saranga *et al.*, 2001; Mei *et al.*, 2004; Zhang *et al.*, 2005b; Shen *et al.*, 2006; He *et al.*, 2007; Shen *et al.*, 2007; Wan *et al.*, 2007, Qin *et al.*, 2008, Zhang *et al.*, 2008; Zhang *et al.*, 2009; Wu *et al.*, 2009, Chen *et al.*, 2010 and Zhang *et al.*, 2012), bacterial blight resistance and pubescence (Wright *et al.*, 1998), stomatal conductance (Ulloa *et al.*, 2000), verticillium wilt resistance gene (Bolek *et al.*, 2005) and leaf morphology (Jiang *et al.*, 2000a).

2.3.4.5. Molecular markers identified for specific traits in cotton

One of the most widely used applications of the molecular marker technology is the identification of marker linked to traits of interest without the necessity for mapping the entire genome. Martin *et al.* (1991) have described an efficient method based on the RAPD technique to isolate DNA segment linked to *Pseudomonas* resistance gene in tomato by using random primers and their near isogenic lines. Thus, markers that showed polymorphisms between the parents are likely to be linked to the gene of interest. Marker analysis has been successful in identifying markers linked to gene of interest in cotton and are summarized in Table 2.

2.3.4.6. QTL mapping for yield and fibre quality traits in cotton

In view of most measures of cotton quality and productivity are polygenic, QTL mapping is in a high priority of many research programmes. Several noteworthy findings have come out of QTL mapping for yield and fibre quality in cotton and are summarized in Table 3.

Most cotton QTLs identified so far influence fibre quality and yield (Jiang *et al.*, 1998; Yu *et al.*, 1998; Kohel *et al.*, 2001; Khan *et al.*, 1998; Shappley *et al.*, 1998a; Ulloa and Cantrell, 1998), among other agronomic traits. In *G. hirsutum* two RFLP genetic maps have been developed and used to identify QTLs for agronomic and fibre quality traits (Shappley *et al.*, 1998a; Ulloa and Meredith Jr., 2000 and Ulloa *et al.*, 2000).

Table 2. Molecular markers linked to specific traits in cotton

S. No.	Trait	Gene	Marker	Reference
1	Fertility restoration	<i>Rf1</i>	RAPD	Guo <i>et al.</i> (1998)
2	Fertility restoration	<i>Rf1</i>	RAPD	Lan <i>et al.</i> (1999)
3	Leaf nectarines	-	RAPD	Amir <i>et al.</i> (2002)
4	Fibre strength	-	SCAR	Guo <i>et al.</i> (2003)
5	Fertility restoration	<i>Rf1</i>	RAPD and SSR	Liu <i>et al.</i> (2003)
6	Fibre strength	-	RAPD and SSR	Zhang <i>et al.</i> (2003)
7	Fertility restoration	<i>Rf1</i> and <i>Rf2</i>	RAPD	Zhang and Stewart (2004)
8	Natural leaf defoliation trait	-	SSR	Abdurakhmonov <i>et al.</i> (2005)
9	Verticillium wilt resistance	<i>CM12</i> , <i>STS1</i> and <i>3147-2 locus</i>	SSR	Bolek <i>et al.</i> (2005)
10	Fertility restoration	<i>Rf1</i>	RAPD and STS	Feng <i>et al.</i> (2005)
11	Fertility restoration	<i>Rf1</i>	RAPD, STS and SSR	Yin <i>et al.</i> (2006)
12	Root knot resistance	<i>Mi2</i>	RAPD and STS	Niu <i>et al.</i> (2007)
13	Lint percentage, fibre quality and spiny bollworm resistance	-	SSR	Wan <i>et al.</i> (2007)
14	Node for first fruiting branch	-	SSR	Guo <i>et al.</i> (2008)
15	Blue disease resistance	<i>Cbd</i>	SSR	Fang <i>et al.</i> (2010)

Table 3. QTL mapping for yield and fibre quality traits in cotton

Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
1	<i>G. hirsutum</i> x <i>G. barbadense</i>	F ₂	Fibre strength	LGD02	13.3	Jiang <i>et al.</i> , 1998
				Chr.20	9.7	
				Chr.22	12.0	
			Fibre length	LGD03	14.7	
			Fibre thickness	Chr.10	12.6	
			Fibre elongation	LGA02	14.0	
				LGD03	12.3	
			Earliness	LGD04	8.1	
2	<i>G. hirsutum</i> x <i>G. hirsutum</i>	F _{2:3}	Seed index	LG4, LG11, LG14	-	Shappley <i>et al.</i> , 1998a
			Micronaire	LG6, LG7, LG9, LG10, LG11, LG14, LG17, LG19, LG20, LG24, LG24, LG25, LG27, LG28	-	
			Elongation percentage	LG4, LG6, LG7, LG10, LG11, LG14, LG15, LG16, LG17, LG18, LG19, LG20, LG21, LG24, LG25, LG27, LG28, LG30	-	

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Table 3. Contd..

Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
			Bundle strength	LG6, LG10, LG13, LG19, LG20, LG27	-	
			2.5 per cent span length	LG3, LG12, LG 16, LG17, LG28	-	
			Plant height	LG6, LG23	-	
3	<i>G. hirsutum</i> x <i>G. hirsutum</i>	F _{2:3}	Fibre strength	LG1	35.2	Ulloa and Meredith Jr., 2000
				LG6	11.3	
			Elongation percentage	LG3	15.3	
				LG9	31.6	
			2.5 per cent span length	Chr.1	11.5	
				Chr.15	44.6	
			Micronaire	Chr.1	40.0	
			Uniformity ratio	Chr.3	15.2	
				Chr.7	33.6	
			Lint yield	Chr.10	9.2	
				Chr.17	15.7	

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Table 3. Contd..

Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
4	<i>G. hirsutum</i> x <i>G. barbadense</i>	F ₂	Fibre strength	Chr.3b	15.4	Kohel <i>et al.</i> , 2001
				Chr.14b	10.4	
				Chr.15a	14.9	
				Chr.25b	23.1	
			Fibre length	Chr.4a	12.6	
				Chr.18	11.6	
				Chr.22	7.8	
			Micronaire	Chr.1a	43.9	
				Chr.2a	31.8	
				Chr.3a	40.7	
				Chr.12b	16.7	
				Chr.16	17.4	
				LGD01	21.3	
5	<i>G. hirsutum</i> x <i>G. barbadense</i>	F ₂	Fibre length	Chr.9, Chr.20, LGA01, LGA02, LGA03, LGA05	13.7	Paterson <i>et al.</i> , 2003
			Fibre elongation	Chr.5, Chr.10, Chr.15, Chr.23, LGA02, LGA03, LGD07	7.3	

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Table 3. Contd..

Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
			Bundle strength	Chr.1, Chr.4, Chr.14, Chr.17, Chr.18, Chr.20, Chr.22, Chr.23, Chr.25, LGA01, LGA02, LGA03, LGA05, LGD02, LGD03, LGD04, LGD07	17.4	
			Micronaire	Chr.2, Chr.4, Chr.5, Chr.6, Chr.9, Chr.14, Chr.15, Chr.17, Chr.20, Chr.23, Chr.25, LGA01, LGA05, LGA06, LGD01, LGD02, LGD03, LGD04, LGD05, LGD07	30.3	
6	<i>G. hirsutum</i> x <i>G. anomalum</i>	F _{2:3}	Fibre strength	Chr.10	30.0	Zhang <i>et al.</i> , 2003
7	<i>G. hirsutum</i> x <i>G. barbadense</i>	F ₂	Fibre length	Chr.4	24.0	Mei <i>et al.</i> , 2004
			Fibre elongation	Chr.9	42.0	
			Number of seeds	Chr.9	22.0	
8	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₃	Boll weight	Chr.2, Chr.9, Chr.14, Chr.25, A03, A06, D07	23.1	Saranga <i>et al.</i> , 2004
			Boll number	Chr.4, A02, D01	17.7	

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Table 3. Contd..

Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
			Seed-cotton yield	Chr.2, Chr.4, Chr.6, Chr.14, Chr.15, Chr.18, Chr.25, A02, A03, D01, D07	20.5	
9	<i>G. hirsutum</i> x <i>G. barbadense</i>	BC ₃ F ₂	Elongation percentage	Chr.1, Chr.2, Chr.5, Chr.6, Chr.12, Chr.17, Chr.18, Chr.20, Chr.22, Chr.23, Chr.26, LGA01, LGA03, LGD02, LGD08	28.0	Chee <i>et al.</i> , 2005
10	<i>G. hirsutum</i> x <i>G. barbadense</i>	F ₂ and F _{2:n}	Lint index	BNL285c ~ BNL1611a	24.3	He <i>et al.</i> , 2005
			Seed index	m3e14-850 ~ BNL162c	31.7	
				m7e3-470 ~ m3e3-480	31.3	
				JSPER280b ~ BNL3103	16.1	
			Seed cotton yield	m2e1-580 ~ S469	22.7	
				m2e7-530 ~ m3e5-580	39.9	
			Number of bolls per plant	m3e1-520 ~ m12e15-550	38.3	
				m1e1-580 ~ m9e8-500	28.6	
				JESPR17a ~ S432	28.0	

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Table 3. Contd..

Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
11	<i>G. hirsutum</i> x <i>G. barbadense</i>	BC ₁ , BC ₂ and BC ₂ S ₁	Fibre length	Chr.3, Chr.5, Chr.6, chr.10, Chr.14, Chr.18, Chr.20, Chr.23, Chr.25, Chr.26, LGA01, LGD02	14.8	Lacape <i>et al.</i> , 2005
			Fibre strength	Chr.3, Chr.5, Chr.16, Chr.18, Chr.23, Chr.28, LGA01, LGA03, LGD02	21.3	
			Elongation percentage	Chr.9, Chr.10, Chr.15, Chr.17, Chr.20, Chr.22, Chr.23, LGD08	21.3	
			Micronaire	Chr.3, Chr.4, Chr.5, Chr.6, Chr.9, Chr.10, Chr.16, Chr.18, Chr.20, Chr.22, Chr.25, LGA02, LGD03, LGD08	29.1	
12	<i>G. hirsutum</i> x <i>G. barbadense</i>	F ₂	Micronaire	LGA03	28.9	Lin <i>et al.</i> , 2005
				Chr.10	17.4	
				Chr.14	21.2	
				LGA02	16.8	
				LGD03	21.0	

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Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
			Fibre strength	LGA02	21.1	
				Chr.23	21.6	
			Fibre length	Chr.1	17.3	
				Chr.9	20.7	
				Chr.14	17.1	
				LG21	20.7	
13	<i>G. hirsutum</i> x <i>G. barbadense</i>	RILs	Fibre length	Chr.2	5.2	Park <i>et al.</i> , 2005
			Micronaire	Chr.3	14.1	
			Bundle strength	Chr.15	5.4	
				Chr.18	6.3	
			Elongation percentage	Chr.15	5.7	
				LGA01	10.9	
14	<i>G. hirsutum</i> x <i>G. barbadense</i>	F ₂ and F _{2:3}	Fibre length	Chr.7	6.3	Shen <i>et al.</i> , 2005
				Chr.23	8.6	
				Chr.25	27.2	
				LGD02	8.3	
			Micronaire	Chr.15	11.6	
				Chr.23	17.4	

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Table 3. Contd..

Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
			Fibre strength	Chr.25	21.8	
				Chr.23	11.2	
				LGD03	31.0	
			Elongation percentage	Chr.5	8.6	
				LGD03	12.6	
15	<i>G. hirsutum</i> x <i>G. hirsutum</i>	F ₂	Fibre length	Chr.6	27.4	Zhang <i>et al.</i> , 2005b
			Fibre strength	Chr.2	12.9	
				Chr.3	11.8	
			Elongation percentage	Chr.5	10.9	
				Chr.6	9.8	
			Micronaire	Chr.5	15.9	
				Chr.6	7.4	
16	<i>G. hirsutum</i> x <i>G. barbadense</i>	RILs	Elongation percentage	Chr.03	14.5	Frelichowski Jr., <i>et al.</i> , 2006
				Chr.15	5.8	
				Chr.18	11.3	
			Bundle strength	Chr.3	5.7	
				Chr.15	16.8	
				Chr.18	12.8	

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Table 3. Contd..

Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
			Micronaire	Chr.3	25.1	
				Chr.5	7.3	
				Chr.12	11.1	
				Chr.17	6.8	
			2.5 per cent span length	Chr.2	5.7	
				Chr.9	8.0	
				Chr.18	25.2	
17	<i>G. hirsutum</i> x <i>G. hirsutum</i>	RILs	Fibre length	LG02	9.42	Wang <i>et al.</i> , 2006b
				LGA10	16.6	
				LGD02	14.7	
			Bundle strength	LG05	5.0	
				LGA11	5.1	
				LGD02	6.9	
				LGD09	9.3	
			Micronaire	LGA10	10.9	
				LGD02	15.5	
				LGD06	12.9	

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Table 3. Contd..

Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
			Elongation percentage	LG07	4.9	
				LG10	5.1	
				LG11	5.6	
				LGA09	4.9	
				LGD06	9.0	
18	<i>G. hirsutum</i> x <i>G. hirsutum</i>	RILs	Lint percentage	Chr.12, Chr.18, Chr.23, Chr.26	59.0	Abdurakhmonov <i>et al.</i> , 2007
19	<i>G. hirsutum</i> x <i>G. barbadense</i>	F ₂	Lint index	Chr.17, Chr.23, LGA02, LGD08	36.8	He <i>et al.</i> , 2007
			Seed index	Chr.1, Chr.6, Chr.7, Chr.23, Chr.25, Chr.26, LGA02, LGA03	38.5	
			Seed cotton yield	Chr.7a, Chr.7b, Chr.7c, LGD02	39.0	
			Number of seeds per boll	Chr.3a, Chr.3b, Chr.5, Chr.14, Chr.18, Chr.20,	38.1	
			Fibre strength	Chr.23, LGA03a, LGA03b	37.1	

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Table 3. Contd..

Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
			Fibre length	Chr.1, Chr.6, Chr.9, Chr.14	7.6	
			Micronaire	Chr.10, Chr.14a, Chr.14b, Chr.14c, Chr.22, LGDA02, LGA03, LGD03	21.5	
20	<i>G. hirsutum</i> x <i>G. hirsutum</i>	RILs	Fibre strength	LGD06, LGD08	16.1	Shen <i>et al.</i> , 2007
			Fibre length	LGA05, LGD06, LGD09	7.71	
			Micronaire	LD06, LGD08, LGD09	10.91	
			Elongation percentage	LGA11	4.9	
			Seed index	LGD06, LGD08, LGD09	16.2	
			Number of bolls per plant	LGD08	14.1	
21	<i>G. hirsutum</i> (4 way cross)	-	Number of bolls pre plant	LGD02	10.2	Qin <i>et al.</i> , 2008
			Seed index	LGD02, LGD03	10.0	
			Fibre length	LGA11, LGD02, LGD04, LGD09, LGD13	10.3	

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Table 3. Contd..

Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
			Fibre strength	LGA10, LGA13, LGD02, LGD11, LGD13	14.0	
22	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₆	Fibre length	A01,A03,C20	20.3	He <i>et al.</i> , 2008
			Fibre uniformity	A01,A03,C9,C20	32.2	
			Fibre micronaire	C ⁿ ,C14	12.0	
			Fibre strength	A03,C3,9,14,15,22,23,D08	14.6	
			Fibre elongation	A03,C7,9,10,14,22	20.5	
23	<i>G. hirsutum</i> x <i>G. hirsutum</i>	RILs	Micronaire	Chr.3, Chr.5, Chr.13	13.3	Wu <i>et al.</i> , 2009
			2.5 per cent span length	Chr.12, Chr.13, Chr.14, Chr.20	38.6	
			Elongation percentage	Chr.14, Chr.20, Chr.26	9.7	
			Bundle strength	Chr.5, Chr.9, Chr.12, Chr.16, Chr.20, Chr.26	13.7	
24	<i>G. hirsutum</i> x <i>G. hirsutum</i>	RILs	Bundle strength	Chr.6	11.0	Zhang <i>et al.</i> , 2009
				Chr.7	31.8	
			Fibre length	Chr.6	32.9	
				Chr.7	26.5	

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Table 3. Contd..

Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
			Uniformity ratio	Chr.8	9.5	
				Chr.6	28.6	
				Chr.7	12.3	
				Chr.12	11.4	
			Micronaire	Chr.7	24.7	
				Chr.23	10.8	
			Elongation percentage	Chr.7	15.1	
				Chr.14	8.3	
25	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₆	Seed cotton yield	Chr.1, Chr.6, Chr.15	0.1	Babar <i>et al.</i> , 2009
26	<i>G. hirsutum</i> × <i>G. barbadense</i>	BC1F1	Elongation percent	Chr.19	13.4	Santoshkumar (2010) and Urbi (2010)
			2.5% span length	Chr.19	17.7	
			Micronaire	Chr.25	14.7	
27	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂	Lint percentage	Chr.26	87.1	Jenkins <i>et al.</i> , 2010

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Table 3. Contd..

Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
28	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RILS	Boll size	D08	35.0	Chen <i>et al.</i> , 2010
			Lint percnrage	D08	19.0	
29	<i>G. hirsutum</i> × <i>G. tomentosum</i>	BC ₃ F ₂	Fibre fineness	Chr.14	11.9	Zhang <i>et al.</i> , 2011
			Fibre strength	Chr.2	12.9	
30	<i>G. hirsutum</i> × <i>G. barbadense</i>	F ₂ , F _{2:3} and F ₈	Fibre length	Chr.16, Chr.25	8.1	Wang <i>et al.</i> , 2011
			Lint percentage	Chr.16, Chr.18, Chr.23	9.9	
			Fibre uniformity	Chr.02,Chr.15,Chr.16	19.9	
			Fibre micronaire	Chr.02,Chr.16, Chr.23, Chr.25	11.9	
			Fibre elongation	Chr.2, Chr.18, Chr.25	10.2	
			Fibre strength	Chr.23, Chr.24	6.8	
31	<i>G. hirsutum</i> × <i>G. hirsutum</i>	IF ₂	Boll weight	LG4, LG15, LG18	47.8	Liu <i>et al.</i> , 2011
			Lint percentage	LG1, LG2, LG3, LG4, LG7, LG9, LG11, LG13, LG15, LG16, LG17, LP19, LP26	39.8	
			Seed index	LG5, LG7, LG16, LG26	23.7	

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Table 3. Contd..

Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
			Seed-cotton yield	LG1, LG2, LG4, LG8, LG9, LG10, LG12, LG13, LG15, LG16, LG18	35.9	
			Bolls/plant	LG1, LG6, LG9, LG10, LG12, LG16, LG17, LG18, LG19, LG22	40.3	
			Lint index	LG1, LG2, LG3, LG6, LG7, LG8, LG9, LG13, LG16, LG18, LG19	36.6	
			Fruit branch number	LG2, LG3, LG4, LG7, LG9, LG13, LG15	36.7	
32	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂ and F _{2:4}	Seed-cotton yield	-	0.1	Saeed <i>et al.</i> , 2011
			Boll number	-	0.3	
			Boll weight	-	0.1	
			Plant height	-	0.5	
33	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RIL and IF ₂	Seed cotton yield	D2, D5, D8, A12	8.4	Liu <i>et al.</i> , 2012
			Lint yield	A12, D2, D8,	13.2	
			Bolls per plant	D5, D8	8.5	

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Table 3. Contd..

Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
			Seed index	A3, A5, D2, D4,	15.0	
			Lint index	A5, A7, A9, A11, A12, D2, D4, D6, D12	14.5	
			Fruit branch number	A5, A11, D2, D7,D8	16.9	
34	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RIL	Fibre strength	Chr.7, Chr.13,Chr.18, Chr.24, Chr.25	27.8	Sun <i>et al.</i> , 2012
			Fibre length	Chr.4, Chr.7, Chr.14, Chr.18, Chr.23, Chr.25	20.6	
			Micronaire	Chr.3, Chr.4, Chr.5, Chr.7, Chr.14, Chr.16, Chr.19, Chr.25	19.1	
			Uniformity ratio	Chr.4, Chr.7, Chr.13, Chr.14, Chr.25	13.4	
			Fibre elongation	Chr.4, Chr.7, Chr.13, Chr.14, Chr.15, Chr.18, Chr.25	11.5	
35	<i>G. hirsutum</i>	CP	Fibre strength	Chr.1, Chr.3, Chr.7	17.8	Zhang <i>et al.</i> , 2012
			Fibre length	Chr.3, Chr.23	9.0	
			Micronaire	Chr.7, Chr.24	15.8	
			Uniformity ratio	Chr.2, Chr.9, Chr.15, Chr.20, Chr.21	26.3	

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Table 3. Contd..

Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
			Fibre elongation	Chr.7	15.0	
36	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂	Fibre strength	Chr.2A, Chr.3A	36.03	Chaudhary <i>et al.</i> , 2013
37	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂	Bud period	C1 (A1), C10 (A10), C17 (A17), C12 (A12)/26 (D12), LG2	12.6	Li <i>et al.</i> , 2013
			Growth period	C13 (A13), C17 (D3), C24 (D8)	13.8	
			Height of first fruiting branch node	C9 (A9), C17 (D3), C25 (D6)	13.3	
38	<i>G. arboreum</i> × <i>G. arboreum</i>	F ₂	Sympodia length	Chr.16	5.0	Shaheen <i>et al.</i> , 2013
			Uniformity index	Chr.9	9.7	
			Boll weight	Chr.9	22.4	
39	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂	Fibre length	Chr.3, Chr.5, Chr.12, Chr.14	9.24	Zhi <i>et al.</i> , 2013
			Uniformity ratio	Chr.2, Chr.18	9.11	
			Fibre strength	Chr.1, Chr.8	8.91	
			Fibre elongation	Chr.4, Chr.24	10.76	

Contd.....

Table 3. Contd..

Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
40	<i>G. barbadense</i> × <i>G. barbadense</i>	F ₂	Seed cotton weight per boll	Chr.8, Chr.19, LG03	22.88	Wang <i>et al.</i> , 2013
			Lint weight per boll	Chr.15, LG03, LG09	24.90	
			Lint percentage	Chr.5, Chr.22, LG06, LG18	24.74	
			100 seeds weight	Chr.6, Chr.22, Chr.10, LG03	34.52	
			Lint index	Chr.8, Chr.10, LG31	30.34	
			Seed index	Chr.15, LG03	16.00	
			Fibre uniformity	Chr.17	13.70	
			Micronaire value	Chr.8, Chr.15, Chr.26, LG09	13.52	
			Fibre elongation	Chr.11, Chr.12, LG03	14.63	
			Fibre strength	Chr.5, Chr.18, Chr.15	19.96	
41	<i>G. hirsutum</i>	Random-mated RILs	Fibre strength	Chr.24	-	Fang <i>et al.</i> , 2014
42	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F5:7 RILs	Boll size	Chr.19	20.36	Gore <i>et al.</i> , 2014
			Lint yield	Chr.17	17.89	
			Fibre strength	Chr.11	18.14	
			2.5%-span length	Chr.25	19.36	

Contd.....

Table 3. Contd..

Sl. No.	Species involved	Population type	QTLs reported for	Chromosome number / Linkage group	Maximum phenotypic variance observed (%)	Reference
43	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F _{2:3}	Lint percentage	Chr. 3, Chr. 19, Chr. 26, Chr. 5 /Chr. 19	-	Wang <i>et al.</i> , 2014
44	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂ and F _{2:3}	Seed yield	Chr. 3, Chr. 17, Chr. 20, Chr. 2/Chr. 17	23.31	Zhe <i>et al.</i> , 2014
			Lint yield	Chr. 8, Chr. 17, Chr. 20, Chr. 24, Chr. 26, and Chr. 2/Chr. 17	35.37	
			Lint percentage	Chr. 3, Chr. 19, Chr. 26	29.55	
			Boll number	Chr.17, Chr. 20, Chr. 2/Chr. 17, LG1	42.30	
			Boll size	Chr. 18, Chr. 19, Chr. 20, Chr. 26, LG2	31.72	
			Lint index	Chr. 13, Chr. 14, Chr. 15, Chr. 19, Chr. 25, Chr. 2/Chr. 17	35.68	
			Seed index	Chr. 3, Chr. 14, Chr. 18, Chr. 19, Chr. 26	30.86	
45	<i>G. hirsutum</i> × <i>G. hirsutum</i>	RILs	Fibre strength	D 3	17.55	Zhiyuan <i>et al.</i> , 2014
			Fibre length	D 11	25.34	
46	<i>G. hirsutum</i> × <i>G. hirsutum</i>	F ₂	Fuzzless	-	-	Bardak <i>et al.</i> , 2015
47	<i>G. hirsutum</i> × <i>G. barbadense</i>	BC ₁ & BC ₁ F ₂	Fibre quality traits	-	23.73	Yang <i>et al.</i> , 2015

From the above studies, comparison of QTLs revealed poor consistency among populations. Although some QTLs were found to be located on same chromosomes in different populations, no common markers could prove that they were of the same QTL. Only a few stable and common QTLs have been reported up to now due to non-replicated experiments and difficulty in assignment of linkage groups. To identify stable QTLs for routine molecular breeding programme we need to integrate different maps of intraspecific and interspecific population and for this it is important to work with a fixed population and common set of molecular markers.

In this study, we proposed the identification of molecular association between yield and fibre quality traits with anchored SSR markers and F₂ and F₃ population which were derived from parents that were also used to produce RILs. It is believed that identification of linked molecular markers can be validated across the genotypes and environments which could be useful in increasing the efficiency of MAS. Hence, an attempt was made to identify molecular association among intraspecific F₂ and F₃ population derived from (*G. hirsutum* var. KC 2 x *G. hirsutum* var. MCU 5) which are locally well adapted varieties. Identification of linked molecular markers in this population will be much useful in the genetic improvement of local cotton varieties for yield and fibre quality traits.

Materials and Methods

CHAPTER – III

MATERIALS AND METHODS

The experiments of the present study was conducted at the laboratory of the Department of Cotton, Centre for Plant Breeding and Genetics (CPBG), Tamil Nadu Agricultural University (TNAU) and also in the experimental fields of Department of Cotton, CPBG, TNAU, Coimbatore and Cotton Research Station, Srivilliputhur during 2012-2014.

3.1. MATERIALS

The genetic materials used for this study consists of nine *Gossypium hirsutum* genotypes ($2n = 4x = 52$). These nine genotypes were used for 9 x 9 diallel mating analysis. The selfed seeds of *G. hirsutum* lines were obtained from the germplasm collection maintained at Department of Cotton, Tamil Nadu Agricultural University, Coimbatore. The parentage of genotypes are presented in Table 4. For molecular association study for yield and fibre quality traits, the F_2 seeds of KC 2 x MCU 5 were obtained from Department of Cotton, TNAU, Coimbatore. The F_2 and F_3 populations derived from an intraspecific cross of KC 2 x MCU 5 were developed and used for genotyping and phenotyping respectively for fibre productivity and quality traits.

3.2. METHODS

Methods of this experiment consist of two parts

1. Diallel analysis
2. QTL Analysis

3.2.1. Diallel analysis

i) Crossing

During winter 2012-2013, nine parents were raised in a crossing block (Plate 1 and 2). Each genotype was sown in 20 rows of 6m length in crossing block with a spacing of 90 x 45 cm. Crosses were made between parents in a 9 x 9 diallel mating design. The conventional hand emasculatation and pollination method developed by Doak

Plate 1. Parents under study



Suraj



Surabhi



Khandwa 2



Anjali



KC 2



KC 3



MCU 5



MCU 7



G.Cot 16

(1934) was followed. Emasculation of the flower buds was done in the ovule parent on the previous day evening. The entire staminal column with anthers was removed carefully along with corolla and bracts with the help of nail without any damage to ovary. Pollination was done on the next day morning by dusting the pollen grains on the stigma of ovule parent. Crossed bolls were collected separately and ginned to obtain F₁ seeds.

Table 4. List of parental material used in the study

S. No.	Parents	Pedigree
1.	Suraj	LRA 5166 (CCH 526612 x HLS 329)
2.	Surabhi	MCU 5 VT (MCU 5 x <i>G. mexicanum</i>)
3.	Khandwa 2	Indore 2 x Cotom
4.	Anjali	LRA 5166 x (Khandwa 2 x Reba B 50) BC 2
5.	KC 2	MCU 10 x KC 1
6.	KC 3	TKH 497 X KC 1
7.	MCU 5	Multiple cross derivative [(Sealand 542 x MCU 1) MCU 2) x (MCU 1 x Gatooma)]
8.	MCU 7	X-ray irradiation of X L 1143 EE
9.	G.Cot 16	TK 1 X G.Cot 10
10.	MCU 13 (Check)	It is a multiple cross derivative involving the parents of [(TCH 665 x LS 149) x (TCH 665 x TCH 21)] x (TCH 21 x EECH) x (TCH 92-7 x EECH)

ii) Hybrid Evaluation

During winter 2013-14, nine parents and seventy two hybrids were raised along with the standard check (MCU 13) in RBD with two replications for diallel method by Griffing model 1 and method 1 (Plate 3). A spacing of 90 cm between the rows and 45 cm between plants within row was adopted. Recommended agronomic practices and plant protection measures were followed as per crop production manual (TNAU and Department of Agriculture).

Plate 2. Crossing block for generating F₁s



Plate 3. Field view of experimental plot - F₁ hybrids



3.2.2. QTL Analysis

3.2.2.1. Plant materials: Parents

In this study, a cross involving KC 2 and MCU 5 were used to develop F₂ and F₃ population for QTL analysis of yield and fibre quality traits. Medium duration upland cotton, *Gossypium hirsutum* L. var. KC 2, well adapted to rainfed tract of Tamil Nadu and highly resistant to Jassids but possessing medium staple length was used as female parent. A contrasting long duration *Gossypium hirsutum* L. var. MCU 5, possessing exceptionally long and strong fibre and susceptible to sucking pests, was used as male parent (Plate 4). These two lines have also shown significant dissimilarity at molecular level and hence they were selected for mapping population development. The F₂ progenies were obtained by selfing the hybrid between the above two parents and constituted the material for the study.

3.2.2.2. Mapping population development

Three hundred and thirty seven F₂ plants were developed by selfing F₁ individuals from the intraspecific cross KC 2 x MCU 5 during winter 2011, at the Cotton Breeding Station, TNAU, Coimbatore. Of the 337 F₂ seeds sown in the field, 246 F₂ plants could be established. Hence, these 246 F₂ plants were chosen for genotyping and QTL analysis in this study during winter 2012-2013. Along with F₂ plants, five rows of each parent were grown in the field. For F₃ generation, summer sowing was carried out at Cotton Research Station, Srivilliputhur during summer 2013. Recommended agronomic practices and need based plant protection measures were followed. Each and every selected individual plant was again selfed by adopting clay smear method described by Ramanatha Iyer (1936) for advancing them to F₄ and F₅ generations for future genetic analysis.

3.2.2.3. Microsatellite marker analysis

Microsatellite analysis had the following steps;

1. Isolation of genomic DNA
2. Quantification of genomic DNA
3. Polymerase chain reaction (PCR) based amplification of genomic DNA using forward and reverse microsatellite primers

Plate 4. F₂ mapping population derived from KC 2 x MCU 5



KC 2



MCU 5



Field view of F₂ population

4. Resolution of polymorphism through 3% metaphor agarose gel electrophoresis and documenting the gel
5. Analysis and scoring of banding pattern

1. Isolation of genomic DNA

Genomic DNA was isolated from the cotton leaves of the parents and the 246 F₂ lines of KC2 x MCU5 by essentially following the procedure (Zhang and Stewart, 2000) and the quantity and quality of the DNA was checked for polymerase chain reaction (PCR).

Materials

- a. Leaf samples
- b. Extraction buffer

Tris-HCl pH 8.0	-	0.1 M
NaCl	-	1.0 M
EDTA(Na ₂ .2H ₂ O) pH 8.0	-	0.02 M
CTAB	-	2% w/v
Polyvinlypyrrolidone-40	-	2% w/v
1, 10-phenanthroline	-	1 mM
β-mercaptoethanol	-	0.2% v/v
- c. Chloroform: Isoamyl alcohol (24:1 v/v)
- d. Isopropanol
- e. Ammonium acetate 15 mM
- f. Ethanol (100%, 80% and 70%)
- g. Cleaning solution

Tris-HCl pH 8.0	-	0.05 M
EDTA pH 8.0	-	0.05 M
NaCl	-	2.05% w/v
cTAB	-	2% w/v
1, 10-phenanthroline	-	0.02% w/v

h. Low salt Tris-EDTA buffer

Tris-HCl pH 8.0	-	0.1 M
EDTA pH 8.0	-	0.02 M

Method

- One to three folded or newly unfolded young leaves (2-3g) were transferred into mortar and 500 µL of extraction buffer is also added to the mortar and grounded to homogenize the mixture.
- The mixture was transferred to 1.5 mL eppendorf tube.
- Contents were mixed by a few inversions and incubated at 65°C for 15-30 minutes.
- After incubation, equal volume of Chloroform : Isoamyl alcohol (24:1, v/v) was added and centrifuged at 12,000 rpm at 4°C for 10 minutes.
- The supernatant was then transferred to a fresh 1.5 mL tube, mixed with 0.5 mL of Isopropanol and kept at -20°C for one hour to precipitate DNA.
- The tubes were centrifuged at 12,000 rpm at 4°C for 10 minutes and the liquid phase was discarded.
- After sequential washing with 70% and 100% ethanol, the DNA pellet was completely air dried and suspended in 300 µL of low salt Tris-EDTA buffer.
- The extracted DNA was then subjected to additional cleaning procedure. Preliminary DNA solution was mixed with 0.5 mL cleaning solution and shaken for 1 to 2 h at room temperature. The solution was then centrifuged at 4°C for 5 minutes.
- After discarding the liquid phase, the DNA pellet is then washed with 0.5 mL of 80% ethanol + 15 mM ammonium acetate and 0.5 mL of 100% ethanol, sequentially. The cleaned DNA pellet was air dried, and resuspended in 300 µL of low salt Tris-EDTA buffer and stored at -20°C and used as template for PCR after dilution.

2. Quantification of genomic DNA

The quantity of extracted DNA was checked by NanoDropTM 1000 (NanoDrop Technologies, USA).

Materials

- a. Genomic DNA
- b. NanoDropTM 1000 Spectrophotometer (NanoDrop Technologies, USA)
- c. Low salt Tris-EDTA buffer
- d. Milli Q[®] water

Protocol

- The instrument was initialized with 2.0 μL of Milli Q[®] water.
- 2.0 μL of Low salt Tris-EDTA buffer was used as blank.
- 2.0 μL of unknown DNA was added to the instrument and the quantity measured as ng/ μL .
- To ensure accuracy, the quantification of each unknown sample was repeated twice.

Further, the isolated DNA was observed and checked for its intactness, homogeneity and purity by electrophoresis in 0.8 per cent agarose gel. After quantification, the final concentration of DNA was adjusted to 20 ng/ μL by using low salt Tris-EDTA buffer.

3. PCR amplification

The 708 SSR markers that span all over the cotton genome was obtained from cotton marker database (CMD) (<http://www.cottonmarker.org/>) and they were commercially synthesized and procured from 1st BASE, Singapore. dNTPs, assay buffer and *Taq* DNA polymerase were purchased from Bengaluru GeNei Ltd., Bengaluru, India.

The cocktail for PCR amplification was prepared as below:

Stock	Aliquot (μL)	Final Concentration
DNA (20 ng/μL)	2.00	40.0 ng
dNTPs (2 mM)	1.50	200.0 μM
Forward primer (100 μM)	0.03	0.2 μM
Reverse primer (100 μM)	0.03	0.2 μM
<i>Taq</i> Buffer (10X)	1.50	1X
<i>Taq</i> DNA polymerase (3U/μL)	0.15	0.5U
Sterile distilled water	9.79	
Total	15.00	

The amplification reaction was carried out in thermo cycler (Mastercycler, Eppendorf, Germany) and the programme of reaction was set as follows:

Step	Temperature (°C)	Time (Minutes)	Purpose
1	93°C	12.00	Initial denaturation
2	95°C	0.15	Denaturation
3	48°C*	0.30	Annealing
4	72°C	1.00	Extension
5	72°C	6.00	Final extension
6	4°C	∞	Hold the samples

* which varies depending on melting temperature (T_m) of each primer pairs (it was in the range of 48-55°C). Step 2-4 were repeated 40 times.

4. Metaphor Agarose gel electrophoresis

Metaphor Agarose gel electrophoresis was performed to analyze PCR amplified products.

Materials

- a. Loading dye 6X
Sucrose 40% (w/v)
Bromophenol Blue 0.25% (w/v)
- b. 10X TBE (Tris Borate EDTA buffer)
Tris Base 107.86g
Boric acid 55.03g
EDTA($\text{Na}_2 \cdot 2\text{H}_2\text{O}$) 8.32 g

Dissolved in 800 mL of distilled water and made up to 1000 mL

Protocol

- Open ends of the pyrex gel casting plate is then sealed with cello tape and placed on a horizontally levelled platform.
- 3 % agarose and 1 % metaphor agarose were added to 1X TBE buffer, mixed well and boiled till the agarose dissolved completely and cooled to lukewarm temperature. Ethidium bromide was used as a staining agent at the final concentration of 10 mg/mL.
- The gel was poured into the gel-casting tray; the combs were placed properly and the gel was allowed to solidify.
- After solidification, the combs and cello tape should be removed carefully.
- The casted gel was placed in the electrophoresis unit with wells towards the cathode and submerged with 1X TBE to a depth of about 1cm.
- The PCR products were mixed well with 5 μL of loading dye and were loaded in to the gel.
- A 100bp DNA ladder was spotted on the left end of each gel as DNA ladder.
- The gel was run at 90 Volts for 3 hours. Bands were visualized and documented using gel documentation system (AlphaImager[®] HP, Alpha Innotech Corporation, California, USA).

5. Analysis and scoring of banding pattern

i) Identification of polymorphic markers

A total of 708 SSR primer pairs (Annexure 1) were used to screen for polymorphism between the parents, KC 2 and MCU 5. Though, 23 SSRs have shown polymorphism between the parents, only, 12 SSRs produced clear, scorable and unambiguous polymorphic loci and hence, they were chosen for the purpose of genotyping F_2 individuals (Table 5).

Table 5. List of polymorphic primers

S. No	Primers	S. No	Primers	S.No	Primers	S. No	Primers
1.	BNL 4108	7.	BNL 2544	13.	NAU 828	19.	CIR 203
2.	BNL 1161	8.	BNL 3103	14.	DPL 0234	20.	CIR 295
3.	BNL 3623	9.	NAU 2035	15.	DPL 0067	21.	CIR 168
4.	BNL 2440	10.	NAU 923	16.	DPL 0322	22.	CM 0066
5.	BNL 3563	11.	NAU 797	17.	GH 132	23.	TMB 0471
6.	BNL 3452	12.	NAU 2967	18.	GH 0247	-	

ii) Genotyping of F_2 individuals

A total of 12 polymorphic SSRs were used for genotyping of 246 F_2 individuals. PCR amplification and metaphor agarose gel electrophoresis were carried out as discussed above for each SSR and gels were documented.

iii) Scoring of genotyping data

Genotyping data of all the F_2 individuals were scored against 12 SSRs. The segregation pattern of SSR markers for all the F_2 individuals were scored as co-dominant fragments. The individuals showing the banding pattern as parent 1 (KC 2) were scored as "A", as heterozygous were scored as "H", as parent 2 (MCU 5) were scored as "B" and null banding pattern were scored as "-". This genotyping data was used for QTL analysis for yield and fibre quality traits.

3.3. Phenotypic evaluation of yield and fibre quality traits

i) Diallel analysis

For diallel analysis, in each genotype, five competitive plants were chosen from each replication at random and tagged for recording observations. The average values of the observations from these five plants represented the mean of that replication.

ii) QTL analysis

For phenotypic evaluation of parents and F_3 plants, observations on plant height, number of sympodial branches per plant, number of bolls per plant, boll weight, single plant yield, ginning outturn, lint index, seed index and fiber quality traits were recorded.

3.3.1. Observations recorded

i) Yield attributes

a) Days to first boll bursting (days)

The number of days from sowing to first boll bursting in a plant was recorded in days and mean was worked out.

b) Plant height (cm)

The height of the plant from the cotyledonary node to the tip of the plant at maturity was recorded in cm.

c) Number of sympodial branches per plant

The number of sympodial branches *i.e.*, number of fruiting branches present in each plant at maturity was counted.

d) Number of bolls per plant

Number of matured bolls was counted at maturity in five randomly selected plants and the mean was worked out.

e) Boll weight (g)

Ten burst bolls in each of the five plants were collected and the kapas from the bolls are then weighed. The weight of seed cotton per boll was worked out and expressed as boll weight in gram.

f) Single plant yield (g)

The seed cotton from all the matured bolls that has been collected separately from each of the five plants was weighed and mean yield of seed cotton per plant was calculated and expressed in gram.

g) Ginning outturn (%)

One hundred seeds with fibres (kapas pooled) were taken and weighed. Then this sample was ginned by means of a power operated gin to separate the lint from the seeds. The quantity of lint obtained was then weighed and the lint outturn from the kapas sample taken was calculated and expressed as ginning outturn in percentage.

$$\text{Ginning outturn (Per cent)} = \frac{\text{Weight of the lint}}{\text{Weight of seed cotton}} \times 100$$

h) Lint index

The quantity of lint obtained from 100 seeds (kapas pooled) ginned was weighed separately and the lint index was computed using the formula given below.

$$\text{Lint index} = \frac{\text{Weight of 100 seeds} \times \text{Ginning per cent}}{100 - \text{Ginning per cent}}$$

i) Seed index

The weight of 100 seeds without fibres was weighed to find out the seed index using the formula given below.

$$\text{Seed index} = \frac{\text{Weight of seeds}}{\text{Number of seeds taken}} \times 100$$

The seed index is expressed in gram per 100 seeds.

ii) Fibre Quality traits

The seed cotton collected from each plant was ginned and the lint obtained was assessed for the following fibre quality characters. These traits were estimated by High Volume Instrument 900 Classic installed at the Department of Cotton, Tamil Nadu Agricultural University, Coimbatore.

a) 2.5 per cent span length (mm)

This is defined as the distance spanned by a specified percentage of fibre in the specimen being tested. Fibre length at 2.5 per cent span was estimated by using HVI and expressed in millimetres.

b) Bundle strength (g/tex)

Bundle strength denotes the strength of fibres. This is also referred as fibre strength or tensile strength *i.e.*, the maximum specific stress that is developed in a tensile test to rupture the fibres. It is a force that is required to break the fibre of unit linear density. Fibre strength was determined by using HVI. This parameter is expressed as gram per tex.

c) Fibre fineness (Micronaire value - µg/inch)

This is the relative measure of size, diameter and linear density of the fibres and expressed as micronaire values.

d) Uniformity ratio (%)

The ratio between 50 per cent span length to 2.5 per cent span length is called uniformity ratio of fibre length. It was estimated by using HVI and expressed in percentage.

$$\text{Uniformity ratio} = \frac{50 \text{ per cent span length}}{2.5 \text{ per cent span length}} \times 100$$

e) Elongation per cent (%)

Elongation per cent is the elongation of fibre bundle. It is a measure of the per cent increase in jaw separation of the instrument under load. This was estimated by using High Volume Instrument.

3.4. Statistical analysis

For diallel analysis, statistical analysis was carried out by using the mean values over five sample plants through INDOSTAT package.

3.4.1. Analysis of variance

The mean values recorded over five sample plants for the different characters were subjected to statistical analysis. Analysis of variance, estimation of standard error and critical difference were worked out individually for all the characters by adopting the method suggested by Panse and Sukhatme (1985).

Analysis of variance table was constructed as follows

Source	df	SS	MS	Expectation
Replications	r-1	SS_r	M_r	$\sigma_e^2 + g \sigma_r^2$
Genotypes	g-1	SS_g	M_g	$\sigma_e^2 + r \sigma_g^2$
Error	(r-1) (g-1)	SS_e	M_e	σ_e^2
Total	(rg-1)			

Where,

r	=	number of replications
g	=	number of genotypes
SS_r	=	sum of squares for replications
SS_g	=	sum of squares for genotypes
SS_e	=	sum of squares for error
M_r	=	mean squares for replications
M_g	=	mean squares for genotypes
M_e	=	mean squares for error
σ_e^2	=	error variance
σ_g^2	=	genotypic variance
σ_r^2	=	variance of replications

The test of significance was carried out by referring to the 'F' table given by Snedecor and Cochran (1967).

3.4.2. Estimation of heterosis

The overall mean value for each parent and hybrid in all the three replications for each character was taken for doing estimation of heterosis.

i) Relative heterosis (d_i)

Heterosis expressed as per cent deviation of the cross from its mid parental value was estimated by adopting the following formula (Gowen, 1952).

$$\text{Relative heterosis (per cent)} = \frac{F_1 - \overline{MP}}{\overline{MP}} \times 100$$

Where,

$$\begin{aligned} F_1 &= \text{mean of } F_1 \text{ hybrid} \\ \overline{MP} &= \text{mean of mid parental value.} \end{aligned}$$

ii) Heterobeltiosis (d_{ii})

Heterosis expressed as per cent deviation of the cross from a better or higher parent involved in that particular cross combination was estimated by adopting the following formula (Gowen, 1952).

$$\text{Heterobeltiosis (per cent)} = \frac{F_1 - \overline{BP}}{\overline{BP}} \times 100$$

Where,

$$\begin{aligned} F_1 &= \text{mean of } F_1 \text{ hybrid} \\ \overline{BP} &= \text{mean of better parental value} \end{aligned}$$

iii) Standard heterosis (d_{iii})

Heterosis expressed as per cent deviation of the cross from best or highest parent in the experimental material in respect of a particular character was calculated by adopting the following formula (Gowen, 1952).

$$\text{Standard heterosis (per cent)} = \frac{F_1 - \overline{SV}}{\overline{SV}} \times 100$$

Where,

$$\begin{aligned} F_1 &= \text{mean of } F_1 \text{ hybrid} \\ \overline{SV} &= \text{mean of standard parental value.} \end{aligned}$$

Test of significance

The standard error pertaining to relative heterosis, heterobeltiosis and standard heterosis of hybrids was calculated as suggested by Turner (1953).

$$\text{S.E. of relative heterosis (d}_i\text{)} = \sqrt{3 \text{ EMS} / 2r}$$

$$\text{S.E of heterobeltiosis (d}_{ii}\text{) and Standard heterosis (d}_{iii}\text{)} = \sqrt{2 \text{ EMS} / r}$$

The significance of heterosis was estimated by 't' test using the formulae (Wynne *et al.*, 1970).

$$\text{'t' value of relative heterosis (d}_i\text{)} = \frac{(\overline{F_{ij}}) - (\overline{MP_{ij}})}{\sqrt{(3 - 2)(\sigma^2_e / r)}}$$

$$\text{'t' value of heterobeltiosis (d}_{ii}\text{)} = \frac{(\overline{F_{ij}}) - (\overline{BP_{ij}})}{\sqrt{2 \sigma^2_e / r}}$$

$$\text{'t' value of standard heterosis (d}_{iii}\text{)} = \frac{(\overline{F_{ij}}) - (\overline{SP})}{\sqrt{2 \sigma^2_e / r}}$$

Where,

$$\overline{F_{ij}} = \text{Mean of the } ij^{\text{th}} \text{ F}_1 \text{ cross}$$

$$\overline{MP_{ij}} = \text{Mean of mid parent value for } ij^{\text{th}} \text{ hybrid}$$

$$\overline{BP_{ij}} = \text{Mean of better parent value for } ij^{\text{th}} \text{ hybrid}$$

$$\overline{SP} = \text{Mean of standard parent}$$

$$\sigma_e^2 = \text{error variance}$$

3.4.3. Combining ability analysis

i) Analysis of variance for combining ability

The procedure outlined by Griffing (1956a) for model I, method 1 was considered as appropriate and was adopted.

Source	d.f.	Mean squares	Expectations of mean squares
<i>gca</i>	(p-1)	Mg	$\sigma^2 e + \frac{p+2}{p-1} \sum_i g_i^2$
<i>sca</i>	p(p-1)/ 2	Ms	$\sigma^2 e + \frac{2}{p(p-1)} \sum_i \leq \sum_j s_{ij}^2$
Reciprocals differences	P(p-1)/ 2	Mr	$\sigma^2 e + \frac{2}{p(p-1)} \sum_i \leq \sum_j s_{ij}^2$
Error	m	Me	$\sigma^2 e$

ii) Estimation of general combining ability effects (g_i) and specific combining ability effects (s_{ij})

These are estimated as follows

$$g_i = \frac{1}{p+2} \left[\sum (Y_i + Y_{ij}) - \frac{2}{p} Y_{..} \right]$$

$$s_{ij} = Y_{ij} - \frac{1}{(p+2)} (Y_i + Y_{..} + Y_j + Y_{jj}) + \frac{2}{(p+1)(p+2)} Y_{..}$$

$$\text{var}(g_i) = [(n-1) \sigma^2 e / p (p+2)]$$

$$\text{var}(s_{ij}) = [p(p-1) \sigma^2 e / (p+1)(p+2)]$$

The effects estimated in combining ability analysis were tested for their significance with the standard errors obtained by taking square root of the corresponding variances.

Testing the significance of *gca* and *sca* effects

The standard error of corresponding effect is multiplied with the table 't' value for error d.f., both at 5 per cent and 1 per cent levels. The resulting product is then compared with the corresponding effects for their significance.

3.4.4. Genetical and Graphical analysis

Hayman's Approach

The graphic and genetic component analysis of the diallel cross was analysed by following the methods that were suggested by Hayman (1954) and Aksel and Johnson (1962).

The diallel hypothesis assumptions were tested by "t²" test and uniformity of W_r and V_r (Hayman, 1954).

$$t^2 = \frac{n-2}{4} \times \frac{(\text{Var.}V_r - \text{Var.}W_r)^2}{(\text{Var}V_r.\text{Var.}W_r) - (\text{Cov}^2(V_r W_r))}$$

where, n is the number of parents under study.

t² values were compared with statistical tabular values for n, n-2 degrees of freedom, which is a 'F' test. The t² values when non-significant denote the uniformity of V_r - W_r and confirms the valuable application of Hayman (1954). Otherwise, significance of t² values indicates the failure of at least one of the assumptions postulated.

Deviation of Regression co-efficient (b) from zero and unity

The occurrence of non-allelic interactions was further tested and confirmed by calculating the regression co-efficient. The regression of covariance on variance and its standard error were calculated as follows:

$$b_{yx} = \frac{\text{Cov} (W_r, V_r)}{\text{Var} (V_r)}$$

$$\text{Standard Error } (b_{yx}) = \left[\frac{\text{Var } W_r - b \text{ Cov } (W_r, V_r)}{\text{Var } V_r (n-2)} \right]^{1/2}$$

The significance of b_{yx} from zero and unity was tested as follows :

$$\frac{b-0}{\text{SE}(b)} \quad \text{and} \quad \frac{1-b}{\text{SE}(b)} \quad \text{both following 't' distribution}$$

The significance of 'b' from zero and unity was tested against the table value of 't' for n-2 degrees of freedom. A non-significant value justifies the existence of regression of W_r and V_r.

i) Estimation of genetic components

The theory and method of Hayman (1954) were extended to estimate the genetic components or parameters viz., D, F, H₁, H₂, h² and E. Hayman (1954) derived the expectations for the statistics calculated for F₁ diallel table and also the expected values of the parameters of the variation using least square technique as follows:

$$(D) = V_{0L0} - E$$

$$(F) = 2 V_{0L0} - 4 W_{0L01} - 2 (n-2) E/n$$

$$\begin{aligned}
(H_1) &= V_{0L0} - 4 W_{0L01} + 4 V_{1L1} - (3n-2) E/n \\
(H_2) &= 4V_{1L1} - 4V_{0L1} - 2E \\
(h^2) &= 4 (M_{L1} - M_{L0})^2 - 4 (n-1) E/n^2 \\
(E) &= 2 (V_{0L0} - W_{0L01} + V_{1L1} - W_r - V_r) - 2 (n-1) E/n
\end{aligned}$$

where,

- D = Component of variation due to additive effects of the genes
- F = The mean of Fr over the arrays. For being the covariance of additive and non-additive effects in the r^{th} array. Additive x dominance variance.
- H₁ = Component of variation due to dominance effects of the genes
- H₂ = H₁ (1-(u-v)²) measures the dominance variance due to positive (u) and negative (v) effects of genes, where, u = proportion of positive alleles while, v = proportion of negative alleles since u + v = 1.
- h² = Net dominance effects (as the algebraic total over all loci in heterozygous state in all cross combinations)
- E = The expected environmental component of variation derived from the error variance divided by number of replications.

V_{0L1} is the variance of mean arrays.

M_{L1} - M_{L0} is the difference between the mean of the parents and the mean of their n² progenies. When F parameter is on positive direction, it explains higher proportion of dominant alleles, whereas the negative direction reveals more of recessive alleles.

All these genetic parameters were tested by 't' test for significance by the use of the respective standard errors of parameters.

These standard errors were estimated from

i) the formula $S^2 = \frac{1}{2} \text{Var} (W_r - V_r)$

ii) The main diagonal or covariance matrix (Hayman, 1954) as corresponding multipliers

$$\text{SE of D} = \left[\frac{(S^2 n^5 + n^4)}{n^5} \right]^{1/2}$$

$$\text{SE of } F = \left[\frac{4S^2 (4n^5 + 20n^4 - 16n^3 + 16n^2)}{n^5} \right]^{1/2}$$

$$\text{SE of } H_1 = \left[\frac{16S^2 (n^5 - 41n^4 - 12n^3 + 4n^2)}{n^5} \right]^{1/2}$$

$$\text{SE of } H_2 = \left[16 S^2 \frac{(36n^4)}{n^5} \right]^{1/2}$$

$$\text{SE of } h^2 = \left[16S^2 \frac{(16n^4 + 16n^2 - 32n + 16)}{n^5} \right]^{1/2}$$

$$\text{SE of } E = \left[\frac{S^2 n^4}{n^5} \right]^{1/2}$$

where, n = number of parents

Test for significance of components

The calculated 't' values of every parameter and error was derived by dividing the component value with its standard error and then the value was compared with the tabular value of 't' for n-2 d.f.

ii) Proportion of genetic components

The proportionate ratios of different components of variance were compared by using the equations given by Crumpacker and Allard (1962), as follows:

1. Mean degree of dominance over all loci

$$= (H_1 / D)^{1/2}$$

If it is > 1, reveals over dominance

< 1, partial or incomplete dominance

= 0, no dominance

= 1, complete dominance

2. Proportion of dominant and recessive genes in parents

$$\frac{KD}{KR} = \frac{4 (DH_1)^{1/2} + (F)}{4 (DH_1)^{1/2} - (F)}$$

If the proportion is equal to 1, it defines the equality of dominant and recessive genes greater than 1, predominance of dominant genes and less than 1, indicates predominance of recessive genes.

3. Proportion of genes with positive and negative effects in the parents

$$= \frac{(H_2)}{4(H_1)}$$

when u and v are symmetrically distributed

$$(u = v = 0.5) \text{ the ratio } H_2 / 4 (H_1) = 0.25$$

4. Number of groups of genes controlling the character and exhibiting dominance is

derived by (h^2 / H_2)

5. Narrow sense heritability estimates

$$\frac{1/2 (D) + 1/2 (H_1) - 1/2 (H_2) - 1/2 (F)}{1/2 (D) + 1/2 (H_1) - 1/4 (H_2) - 1/2 (F) + E} \text{ (or)}$$

(Crumpacker and Allard, 1962)

$$\frac{1/4 (D)}{1/2 (D) + 1/2 (H_1) - 1/4 (F) + E}$$

6. The correlation between parental order of dominance ($W_r + V_r$) and parental measures (Y_r) was computed. A significant positive correlation indicates that most of the dominant genes had negative effects for those characters, whereas a significant negative value indicates that most of the dominant genes had positive effects (Hayman, 1954).

iii) Graphical Analysis

Wr. Vr. Graph : The essential factors for the graph V_r and W_r were calculated from the diallel table and these values were used in constructing the W_r . V_r . Graph for each character.

Where,

V_r is the variance of offspring of the r^{th} parental array

W_r is the covariance of the offspring of the r^{th} array with respect to non recurrent parent.

Data from F_1 and parents were subjected to the analysis that was proposed by Jinks and Hayman (1953) as illustrated by Aksel and Johnson (1962). In this analysis the following statistical parameters are estimated from the data.

V_r - The variance of offspring of the r^{th} parental array

W_r - The covariance of offspring of the r^{th} array with respect to non recurring parent

V_{OLO} - The variance of all parental means

V_{OL1} - The variance of the means of arrays

W_{OLO1} - The mean covariance between parents and the arrays

V_{1L1} - The mean variance of arrays

$(M_{1L1} - M_{LO})^2$ - The square of difference between the mean of the parents and the mean of their n^2 progeny

By utilizing the regression values, the W_r , V_r graph was drawn for all the characters studied and the limiting parabola was constructed by using the formula

$$W_r^2 = V_r \times V_{OLO}$$

i.e., by plotting V_r . $(V_r \times V_{OLO})^{1/2}$ points starting with $V_r = V_{1L1}$. A few interpolations and extrapolations makes this possible to draw the parabola. The hypothesis was tested as indicated earlier.

3.5. Statistical analysis of F_3 generation of the KC 2 x MCU 5

Statistical analysis was carried out through TNAUSTAT package.

3.5.1. Variability studies

Phenotypic and genotypic variance and coefficient of variability

Phenotypic and genotypic variances, genotypic and phenotypic coefficient of variability, heritability and genetic advance as a percentage of mean were worked out for different characters by following the method suggested by Singh and Choudhary (1979).

i) Genotypic variance (σ^2_g)

$$\sigma^2_g = \sigma^2_p - \sigma^2_e$$

Where,

σ^2_p = Phenotypic variance and

σ^2_e = Error mean square

ii) Phenotypic variance (σ^2_p)

$$\sigma^2_p = \sigma^2_g + \sigma^2_e$$

Where,

σ^2_g = Genotypic variance and

σ^2_e = Error mean square

iii) Genotypic co-efficient of variation (GCV)

$$GCV = \frac{\sigma_g}{\bar{X}} \times 100$$

Where,

$\frac{\sigma_g}{\bar{X}}$ = Genotypic standard deviation and

$\bar{X}$ = Grand mean

iv) Phenotypic coefficient of variation (PCV)

$$PCV = \frac{\sigma_p}{\bar{X}} \times 100$$

Where,

σ_p = Phenotypic standard deviation and

$\bar{X}$ = Grand mean

The PCV and GCV were classified as per Sivasubramaniam and Madhava Menon (1973).

PCV and GCV	Category
Less than 10 %	Low
10 - 20%	Moderate
More than 20 %	High

v) Heritability (h^2)

Heritability in broad sense was calculated by following the method proposed by Lush (1940) and expressed in terms of percentage.

$$h^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

where,

σ_g^2 = Genotypic variance

σ_p^2 = Phenotypic variance

The heritability percent was categorized as suggested by Robinson *et al.* (1949).

Heritability in per cent	Category
0 - 30 per cent	Low
31 - 60 per cent	Moderate
Above 60 per cent	High

vi) Genetic advance as percentage of mean

Genetic advance was estimated by the method outlined by Johnson *et al.* (1955).

$$GA = h^2 \times \sigma_{ph} \times K$$

Where,

h^2 = Heritability

σ_{ph} = Phenotypic standard deviation

K = Selection differential at 5 per cent selection intensity (2.06 - Falconer, 1981)

Genetic advance (GA) was also expressed as mean

$$\text{GA as percentage of mean} = \frac{\text{GA}}{\text{Grand mean}} \times 100$$

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

GA per cent value	Category
Less than 10 %	Low
10 - 20%	Moderate
More than 20 %	High

3.5.2. Association analysis

i) Correlation co-efficient analysis

Simple correlation co-efficient was worked out between seed cotton yield and other component traits as well as among the component traits based on the method suggested by Goulden (1959) and Singh and Choudhary (1979) to find out the relationship between yield and its component in the genotypes. The variance and covariance values are utilized to calculate the correlation coefficients by applying the following formula:

$$r_{xy} = \frac{\text{Cov. (x,y)}}{\sqrt{V_{(x)} \cdot V_{(y)}}}$$

Where,

r_{xy} = Correlation co-efficient between character X and Y

Cov. (x,y) = Covariance between characters X and Y

$V_{(x)}$ = Variance of character X and

$V_{(y)}$ = Variance of character Y

The significance of correlation co-efficient was tested by using the 't' table given by Snedecor and Cochran (1967).

ii) Test of significance

Significance of correlation coefficients was tested by phenotypic correlation co-efficients with the correlation table values given by Fisher and Yates (1963) at (n-2) degrees of freedom where 'n' denotes the total number of entries under study.

3.5.3. QTL analysis

By using the genotypic data of 246 F₂ progenies and 13 phenotypic data of F₃ progenies the QTL analysis was carried out by SMA using ANOVA in Excel.

i) Single marker analysis (SMA) using ANOVA in Excel

Phenotypic and genotypic data were entered in excel sheet column wise and sorted according to ascending order. The individual RIL which has missing data in genotype or phenotype column were deleted. The phenotypic data was arranged in three columns in such a way that each column represents three marker allelic classes (*i.e.*, Parent A, Parent B and Heterozygous alleles - H). Under Data analysis, the option single factor ANOVA was selected and analysis was carried out for the data of each marker allele group. If calculated F-value was greater than the critical or tabulated F-value, the given marker was considered as linked to the trait of interest. The percentage of contribution to the expression of this trait was obtained from the P-value of the table.

Experimental Results

CHAPTER - IV

EXPERIMENTAL RESULTS

In the present investigation, nine parents were selected and crossed by the following diallel mating design, Model I and method I. The performance of nine parents and seventy two hybrids on fourteen characters were analysed statistically and their combining ability was also evaluated. The nine parents viz., Suraj, Surabhi, Khandwa 2, Anjali, KC 2, KC 3, MCU 5, MCU 7 and G.Cot 16 and the resultant seventy two hybrids obtained by crossing in a full diallel mating fashion were evaluated for their combining ability in order to have a effective selection of parents and hybrids to understand their breeding values.

Observations recorded for fourteen biometrical traits viz., days to first boll bursting (days), plant height at maturity (cm), number of sympodial branches per plant, number of bolls per plant, boll weight (g), single plant yield (g), ginning outturn (%), lint index, seed index, 2.5% span length (mm), bundle strength (g/tex), micronaire value ($\mu\text{g}/\text{inch}$), uniformity ratio (%) and elongation per cent (%) were used for estimating combining ability, gene action and extent of heterosis. In addition to this, an intraspecific F_2 population derived from *G. hirsutum* var. KC 2 and *G. hirsutum* var. MCU 5 was also developed and used for QTL analysis of fibre quality traits. The results were presented under the following sections.

4.1. Analysis of variance

Analysis of variance for genotypes, parents, hybrids, parents V_s hybrids, reciprocals, GCA and SCA were presented in Table 6 and Table 7. Analysis of variance showed significant variations among the genotypes for all the characters studied. Parents and hybrids showed significant differences between all the characters studied except number of bolls per plant, boll weight, single plant yield, lint index and seed index for parents. GCA and SCA variances showed significant for all the characters studied except the number of bolls per plant for GCA and number of sympodial branches per plant, boll weight and elongation per cent for SCA. Variances for GCA were larger than that of SCA for all the traits except number of bolls per plant (Figure 1). Reciprocals were significantly different for all traits.

Table 6. ANOVA for yield and fibre quality traits in *Gossypium hirsutum* L.

Source of Variation	Degrees of freedom	Days to first boll bursting	Plant height (cm)	Number of sympodial branches /plant	Number of bolls/plant	Boll weight (g)	Single plant yield (g)	Ginning outturn (%)	Lint index	Seed index	2.5% span length (mm)	Bundle strength (g/tex)	Micronaire value (µg/inch)	Uniformity ratio (%)	Elongation (%)
Genotypes	80	6.72**	358.86**	6.75**	14.82**	0.26**	277.86**	23.18**	0.64**	2.37**	12.69**	3.82**	0.39**	5.20**	0.52**
Parents	8	2.74**	156.16**	11.73**	6.48	0.19	47.23	3.71**	0.39	1.93	22.64**	5.38**	0.36**	4.95**	0.98**
Hybrids	71	7.174**	374.64**	6.02*	14.21**	0.27**	296.09**	25.690**	0.68**	2.41**	9.18**	3.32**	0.39**	5.27**	0.46**
Parents V_s Hybrids	1	6.44**	859.96**	18.26*	125.43**	0.02	828.76**	0.672	0.002	2.66	182.81**	27.02**	0.19**	1.80*	0.87*
F₁'s	35	2.880**	320.60**	6.31*	14.58**	0.33**	350.12**	23.748**	0.56**	2.13*	10.46**	2.61**	0.37**	5.09**	0.58**
Reciprocals	35	11.50**	405.37**	5.90*	14.04*	0.21	248.22**	28.337**	0.80**	2.71**	8.05**	3.85**	0.40**	5.28**	0.35*
F₁ V_s reciprocals	1	6.13**	1190.37**	0.70	6.86	0.09	80.66	1.015	0.85	2.05	3.95**	9.52**	0.99**	11.65**	0.14
Error	80	0.63	14.07	3.55	7.57	0.14	41.26	0.63	0.24	1.15	0.54	0.28	0.008	0.33	0.19
Total	161	3.655	185.401	5.147	11.207	0.197	158.652	11.830	0.442	1.761	6.616	2.050	0.197	2.771	0.35

****Significant at 1 per cent level**

***Significant at 5 per cent level**

Table 7. ANOVA for combining ability for yield and fibre quality traits in *Gossypium hirsutum* L.

Source of Variation	Degrees of freedom	Days to first boll bursting	Plant height (cm)	Number of sympodial branches /plant	Number of bolls/plant	Boll weight (g)	Single plant yield (g)	Ginning outturn (%)	Lint index	Seed index	2.5% span length (mm)	Bundle strength (g/tex)	Micronaire value (µg/inch)	Uniformity ratio (%)	Elongation (%)
GCA	8	6.18**	272.98**	7.88**	5.15	0.39**	243.81 **	13.93**	0.37**	1.79**	24.65**	7.004**	0.79**	3.59**	1.24**
SCA	36	2.01**	145.66**	2.07	6.02*	0.07	92.76**	7.23***	0.31**	1.04*	5.98**	1.49**	0.09**	2.33**	0.12
Reciprocal	36	4.09**	192.41**	3.68**	9.30**	0.13*	161.80**	15.42**	0.32**	1.20**	2.64**	1.20**	0.16**	2.65**	0.17*
Error	80	0.315	7.036	1.777	3.782	0.070	20.628	0.314	0.121	0.576	0.268	0.138	0.004	0.167	0.093

****Significant at 1 per cent level**

***Significant at 5 per cent level**

4.2. Mean performance

The mean performance of parents and hybrids for fourteen characters were furnished in Table 8 and 9.

4.2.1. Days to first boll bursting (days)

Days to first boll bursting ranges from 101.20 (MCU 5) to 105.20 (Anjali) in parents. The hybrids ranges from 100.50 (KC 2 x Khandwa 2) to 110.20 (G.Cot 16 x Anjali). Among the seventy two hybrids, sixty four hybrids recorded significantly as less duration for first boll bursting than the grand mean. The grand mean values of parents and hybrids were 102.49 and 103.03, respectively.

4.2.2. Plant height (cm)

Mean performance of the parents for plant height ranges from 86.07 (G.Cot 16) to 114.90 (MCU 5). The hybrid mean values ranges from 68.10 (Anjali x G.Cot 16) to 123.20 (KC 3 x Anjali). Among the parents, MCU 5 (114.90), Anjali (110.53) and Surabhi (103.80) recorded significantly more plant height than parental grand mean. Among the seventy two hybrids, twenty one hybrids showed significantly higher mean value than the grand mean of the plant height.

4.2.3. Number of sympodial branches per plant

Among the parents, MCU 5 recorded the maximum number of sympodial branches per plant (20.09), whereas Khandwa 2 recorded the minimum number of sympodial branches (12.10). The mean values of the hybrids ranges from 12.20 (G.Cot 16 x Surabi) to 20.00 (Surabi x KC 3). None of the hybrids recorded significantly greater mean value than the grand mean.

4.2.4. Number of bolls per plant

Number of bolls per plant ranges from 18.50 (Khandwa 2) to 24.50 (MCU 5) in parents. None of the parents recorded significantly greater mean value than the grand mean.

Among the hybrids, number of bolls per plant ranges from 19.50 (Suraj x KC 2) to 30.30 (Khandwa 2 x Suraj). Out of seventy two hybrids, only one hybrid showed significantly higher number of bolls when compared to the grand mean.

Table 8. Mean performance of parents for yield and fibre quality traits in *Gossypium hirsutum* L.

Parents	Days to first boll bursting	Plant height (cm)	Number of sympodial branches /plant	Number of bolls/plant	Boll weight (g)	Single plant yield (g)	Ginning outturn (%)	Lint index	Seed index	2.5% span length (mm)	Bundle strength (g/tex)	Micronaire value (µg/inch)	Uniformity ratio (%)	Elongation (%)
Suraj	102.63	95.03	12.50	20.00	4.51	76.60	34.50	5.35	10.14	27.28	22.93	3.90	47.13	4.45
Surabhi	102.33	103.80	15.50	20.10	4.29	80.06	33.85	4.87	9.46	32.06	24.59	3.58	50.74	4.40
Khandwa 2	101.90	96.10	12.10	18.50	3.91	75.14	30.76	4.14	9.32	24.25	22.42	4.56	48.50	4.75
Anjali	105.20	110.53	15.00	22.00	4.47	85.09	34.04	5.26	7.74	27.59	21.05	3.68	51.73	6.70
KC 2	103.00	93.70	15.63	19.50	4.34	78.70	33.03	5.17	10.47	25.36	19.08	4.44	49.86	5.00
KC 3	101.40	99.40	14.70	22.40	3.87	81.06	35.31	5.48	10.04	30.23	21.23	4.69	46.81	5.05
MCU 5	101.20	114.90	20.09	24.50	4.55	87.34	34.68	5.11	9.63	33.51	22.99	3.80	49.19	5.55
MCU 7	102.20	101.88	17.00	21.60	3.75	84.90	32.49	5.11	10.61	24.03	22.82	3.94	49.13	4.80
G.Cot 16	102.53	86.07	13.67	20.80	4.01	73.10	33.80	5.70	11.15	26.84	22.13	4.52	48.77	5.25
Grand mean	102.49	100.16	15.13	21.06	4.19	80.22	33.61	5.13	9.84	27.91	22.14	4.12	49.10	5.11
CD @ 5%	0.55	2.59	2.39	4.31	0.45	3.62	1.69	1.51	3.45	0.93	0.73	0.07	1.77	1.39
CD @ 1%	0.80	3.76	3.48	6.23	0.66	5.27	2.46	2.20	5.02	1.36	1.28	0.10	2.57	2.03

Table 9. Mean performance of hybrids for yield and fibre quality traits in *Gossypium hirsutum* L.

Hybrids	Days to first boll bursting	Plant height (cm)	Number of sympodial branches/plant	Number of bolls/plant	Boll weight (g)	Single plant yield (g)	Ginning outturn (%)
Suraj x Surabhi	102.50	100.27	17.90	22.00	4.75	101.28	31.38
Suraj x Khandwa 2	103.50	89.90	13.70	24.40	4.11	98.21	32.31
Suraj x Anjali	102.10	69.30	12.90	19.60	4.83	83.11	36.27
Suraj x KC 2	103.90	87.60	15.50	19.50	4.78	91.28	33.61
Suraj x KC 3	101.50	74.60	13.90	24.90	3.74	76.79	32.79
Suraj x MCU 5	103.20	120.00	18.50	25.50	4.15	100.16	34.83
Suraj x MCU 7	103.50	83.90	16.20	22.90	4.59	83.38	37.48
Suraj x G.Cot 16	102.20	107.35	14.10	23.80	4.91	96.17	34.23
Surabhi x Suraj	101.88	99.25	14.00	24.13	3.88	74.28	34.35
Surabhi x Khandwa 2	102.60	91.50	16.80	26.30	3.79	85.77	29.08
Surabhi x Anjali	107.10	103.67	18.50	27.77	4.22	102.15	31.52
Surabhi x KC 2	102.70	96.47	13.50	24.90	4.01	71.84	36.75
Surabhi x KC 3	104.00	101.20	20.00	25.50	4.35	93.83	32.68

Contd...

Table 9. Contd..

Hybrids	Days to first boll bursting	Plant height (cm)	Number of sympodial branches/plant	Number of bolls/plant	Boll weight (g)	Single plant yield (g)	Ginning outturn (%)
Surabhi x MCU 5	103.50	100.38	16.00	24.00	4.18	77.98	35.64
Surabhi x MCU 7	102.10	98.40	14.60	25.50	4.50	94.42	33.73
Surabhi x G.Cot 16	101.20	81.80	16.90	22.80	3.90	87.00	34.29
Khandwa 2 x Suraj	102.70	92.90	16.50	30.30	4.33	102.17	35.36
Khandwa 2 x Surabhi	102.00	101.50	18.50	25.50	4.11	93.31	34.45
Khandwa 2 x Anjali	102.13	89.27	17.60	27.37	3.93	85.05	36.23
Khandwa 2 x KC 2	104.50	93.70	15.50	20.40	4.05	79.11	26.95
Khandwa 2 x KC 3	101.96	79.88	16.71	21.08	3.78	67.34	35.09
Khandwa 2 x MCU 5	104.40	101.60	19.20	21.50	3.80	94.26	32.88
Khandwa 2 x MCU 7	102.58	80.23	16.08	21.43	4.37	76.88	32.35
Khandwa 2 x G.Cot 16	101.90	86.20	15.50	21.30	4.03	78.08	30.36
Anjali x Suraj	107.20	111.15	17.70	25.50	4.89	104.64	37.37
Anjali x Surabhi	102.10	77.25	15.55	24.95	4.17	77.47	31.10
Anjali x Khandwa 2	102.70	82.27	14.80	21.60	4.26	69.45	37.44

Contd...

Table 9. Contd..

Hybrids	Days to first boll bursting	Plant height (cm)	Number of sympodial branches/plant	Number of bolls/plant	Boll weight (g)	Single plant yield (g)	Ginning outturn (%)
Anjali x KC 2	101.50	71.70	17.20	21.80	4.92	81.00	30.32
Anjali x KC 3	102.17	105.24	16.50	24.50	3.63	70.89	30.80
Anjali x MCU 5	101.90	110.91	18.40	28.50	4.09	108.32	30.52
Anjali x MCU 7	103.70	74.70	17.10	23.00	3.97	100.17	37.18
Anjali x G.Cot 16	102.50	68.10	15.70	21.00	4.34	71.42	30.98
KC 2 x Suraj	101.20	112.16	17.10	26.70	4.78	95.36	33.05
KC 2 x Surabhi	105.20	105.53	17.50	25.00	4.79	98.54	25.00
KC 2 x Khandwa 2	100.50	85.70	15.70	27.40	4.27	86.31	34.82
KC 2 x Anjali	102.70	106.15	14.70	21.50	4.68	77.98	26.24
KC 2 x KC 3	102.70	90.90	17.10	24.30	4.22	85.58	37.46
KC 2 x MCU 5	102.20	101.84	18.60	27.00	3.69	109.63	31.13
KC 2 x MCU 7	102.50	87.40	16.50	21.90	4.97	95.30	35.43
KC 2 x G.Cot 16	101.55	72.68	13.83	20.50	4.27	72.16	32.70
KC 3 x Suraj	102.50	71.80	14.80	21.90	4.56	73.32	37.40

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Table 9. Contd..

Hybrids	Days to first boll bursting	Plant height (cm)	Number of sympodial branches/plant	Number of bolls/plant	Boll weight (g)	Single plant yield (g)	Ginning outturn (%)
KC 3 x Surabhi	103.50	97.30	14.10	23.40	3.55	68.83	33.26
KC 3 x Khandwa 2	102.70	93.90	15.00	23.50	3.90	94.71	28.06
KC 3 x Anjali	107.20	123.20	19.60	27.00	4.18	102.65	37.45
KC 3 x KC 2	102.70	120.90	19.10	25.50	3.63	96.09	33.03
KC 3 x MCU 5	105.20	77.10	15.20	26.20	3.94	77.61	36.93
KC 3 x MCU 7	102.60	98.40	18.20	27.50	4.58	97.72	36.31
KC 3 x G.Cot 16	102.20	75.30	15.10	24.30	3.67	71.63	23.98
MCU 5 x Suraj	102.50	90.70	15.50	27.10	4.57	95.12	34.94
MCU 5 x Surabhi	102.20	118.30	19.50	22.40	4.28	89.21	31.11
MCU 5 x Khandwa 2	101.95	94.98	14.60	24.57	4.22	88.20	36.07
MCU 5 x Anjali	110.10	83.57	16.97	20.77	4.55	94.75	32.62
MCU 5 x KC 2	102.71	92.30	14.54	19.88	4.10	86.42	29.43
MCU 5 x KC 3	102.20	88.10	17.30	20.40	4.06	77.08	36.79
MCU 5 x MCU 7	104.20	86.97	17.50	28.20	4.39	115.01	30.19

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Table 9. Contd..

Hybrids	Days to first boll bursting	Plant height (cm)	Number of sympodial branches/plant	Number of bolls/plant	Boll weight (g)	Single plant yield (g)	Ginning outturn (%)
MCU 5 x G.Cot 16	103.50	91.36	14.50	19.70	3.38	81.56	37.49
MCU 7 x Suraj	102.50	77.10	17.70	21.70	3.98	94.01	33.34
MCU 7 x Surabhi	102.20	94.90	16.20	23.80	4.33	76.14	27.45
MCU 7 x Khandwa 2	102.30	85.40	16.50	24.80	4.07	96.20	36.35
MCU 7 x Anjali	104.50	107.45	18.50	28.00	4.53	100.66	36.51
MCU 7 x KC 2	102.50	105.92	14.60	21.80	3.99	97.22	36.82
MCU 7 x KC 3	102.13	89.85	16.13	20.63	3.76	65.32	32.21
MCU 7 x MCU 5	101.90	117.25	15.50	26.50	4.43	99.25	37.42
MCU 7 x G.Cot 16	103.50	88.40	14.70	19.70	4.14	58.02	31.04
G.Cot 16 x Suraj	102.70	75.60	15.10	21.80	4.18	71.28	30.28
G.Cot 16 x Surabhi	102.20	84.77	12.20	19.70	4.11	79.60	28.65
G.Cot 16 x Khandwa 2	101.20	112.20	16.30	24.80	4.03	101.06	35.59
G.Cot 16 x Anjali	110.20	92.37	16.80	24.20	4.53	89.30	36.72
G.Cot 16 x KC 2	102.58	72.85	15.10	25.95	4.21	82.18	32.35

Contd...

Table 9. Contd..

Hybrids	Days to first boll bursting	Plant height (cm)	Number of sympodial branches/plant	Number of bolls/plant	Boll weight (g)	Single plant yield (g)	Ginning outturn (%)
G.Cot 16 x KC 3	101.90	99.83	13.80	20.50	4.70	86.97	35.83
G.Cot 16 x MCU 5	103.70	104.31	17.50	25.50	4.02	98.28	26.54
G.Cot 16 x MCU 7	108.90	76.50	15.70	27.60	4.15	90.67	37.10
MCU 13	103.15	115.70	14.18	21.26	4.00	89.73	34.44
Grand mean	103.03	92.82	16.20	23.83	4.22	87.42	33.27
CD @ 5%	1.78	7.90	3.91	5.41	0.77	13.53	1.60
CD @ 1%	2.37	10.48	5.20	7.18	1.02	17.96	2.13

Table 9. Contd..

Hybrids	Lint index	Seed index	2.5% span length (mm)	Bundle strength (g/tex)	Micronaire value (µg/inch)	Uniformity ratio (%)	Elongation per cent (%)
Suraj x Surabhi	5.09	11.13	34.73	25.53	3.95	49.55	4.70
Suraj x Khandwa 2	5.03	10.54	33.70	24.26	4.60	49.20	4.35
Suraj x Anjali	5.23	9.19	32.84	23.67	4.83	48.09	4.90
Suraj x KC 2	5.33	10.52	31.39	23.38	4.62	49.75	4.35
Suraj x KC 3	5.11	10.47	34.24	24.63	3.28	49.89	4.10
Suraj x MCU 5	5.21	9.77	34.65	23.15	4.25	48.80	4.80
Suraj x MCU 7	5.83	8.89	34.40	25.70	4.13	50.85	4.70
Suraj x G.Cot 16	5.41	10.43	33.15	24.85	4.55	49.50	4.20
Surabhi x Suraj	4.98	9.51	31.65	24.50	4.06	47.75	5.00
Surabhi x Khandwa 2	4.40	10.71	29.88	22.81	4.61	47.11	4.70
Surabhi x Anjali	4.60	10.09	31.90	24.75	4.07	49.05	4.60
Surabhi x KC 2	5.22	9.01	33.70	24.45	3.70	45.30	4.40
Surabhi x KC 3	5.24	10.76	32.53	24.38	4.33	47.42	4.10

Contd...

Table 9. Contd..

Hybrids	Lint index	Seed index	2.5% span length (mm)	Bundle strength (g/tex)	Micronaire value (µg/inch)	Uniformity ratio (%)	Elongation per cent (%)
Surabhi x MCU 5	5.86	10.61	33.07	26.48	3.70	46.20	4.25
Surabhi x MCU 7	5.17	10.15	32.30	23.38	4.03	48.95	4.40
Surabhi x G.Cot 16	4.99	9.57	32.94	23.42	4.88	47.94	4.25
Khandwa 2 x Suraj	5.29	9.68	31.35	19.70	4.47	50.70	4.45
Khandwa 2 x Surabhi	5.43	10.32	30.75	21.89	4.05	49.25	4.35
Khandwa 2 x Anjali	5.42	9.53	29.70	23.57	4.70	49.75	4.50
Khandwa 2 x KC 2	3.68	9.95	30.10	22.19	4.91	50.71	4.70
Khandwa 2 x KC 3	4.79	8.83	28.49	22.10	4.90	49.23	4.80
Khandwa 2 x MCU 5	5.03	10.26	31.85	24.70	4.23	48.73	4.50
Khandwa 2 x MCU 7	5.61	11.74	29.16	23.78	4.70	49.89	5.10
Khandwa 2 x G.Cot 16	4.61	10.56	29.10	23.83	4.35	48.89	5.00
Anjali x Suraj	6.20	10.38	29.70	23.40	4.20	49.70	5.25
Anjali x Surabhi	4.81	10.64	35.48	25.10	3.65	51.35	5.65
Anjali x Khandwa 2	5.55	9.35	30.55	21.75	4.86	50.65	5.50

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Table 9. Contd..

Hybrids	Lint index	Seed index	2.5% span length (mm)	Bundle strength (g/tex)	Micronaire value (µg/inch)	Uniformity ratio (%)	Elongation per cent (%)
Anjali x KC 2	4.92	11.30	31.39	23.48	4.04	51.25	5.70
Anjali x KC 3	4.53	10.18	29.80	22.01	3.60	49.13	6.05
Anjali x MCU 5	4.83	10.99	28.84	24.10	4.55	49.90	5.95
Anjali x MCU 7	5.41	8.89	29.91	23.55	4.15	50.28	5.55
Anjali x G.Cot 16	4.67	10.40	29.59	22.63	4.03	50.21	5.95
KC 2 x Suraj	5.21	10.55	30.29	23.38	4.17	50.46	4.60
KC 2 x Surabhi	4.31	12.90	32.70	24.18	4.44	51.80	4.55
KC 2 x Khandwa 2	4.91	9.28	29.15	23.20	4.47	49.90	4.90
KC 2 x Anjali	4.30	12.11	29.75	21.35	4.65	51.24	4.85
KC 2 x KC 3	5.50	8.59	28.90	22.20	4.85	47.15	5.15
KC 2 x MCU 5	4.37	9.66	36.90	25.60	3.45	51.25	5.20
KC 2 x MCU 7	4.68	8.52	29.84	21.86	4.37	49.55	5.05
KC 2 x G.Cot 16	5.75	11.83	28.41	23.18	4.38	49.85	4.90
KC 3 x Suraj	5.75	9.51	31.06	24.43	4.65	49.45	4.50

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Table 9. Contd..

Hybrids	Lint index	Seed index	2.5% span length (mm)	Bundle strength (g/tex)	Micronaire value (µg/inch)	Uniformity ratio (%)	Elongation per cent (%)
KC 3 x Surabhi	5.33	10.68	34.83	25.48	3.86	53.53	4.80
KC 3 x Khandwa 2	4.01	10.28	31.25	22.30	4.55	48.85	4.80
KC 3 x Anjali	6.18	9.81	29.20	22.80	4.70	51.10	5.45
KC 3 x KC 2	5.73	11.61	28.15	22.60	4.81	51.05	4.80
KC 3 x MCU 5	5.33	9.10	27.31	22.04	4.70	46.96	4.70
KC 3 x MCU 7	5.96	10.46	29.59	23.42	4.88	50.66	4.85
KC 3 x G.Cot 16	4.21	13.32	30.45	24.20	4.45	50.05	4.15
MCU 5 x Suraj	5.91	11.01	33.13	24.82	3.43	49.25	4.85
MCU 5 x Surabhi	5.68	12.58	35.91	26.32	3.74	51.95	4.30
MCU 5 x Khandwa 2	5.93	10.51	32.95	24.75	3.73	45.91	5.45
MCU 5 x Anjali	5.00	10.33	31.10	24.38	3.53	47.31	5.20
MCU 5 x KC 2	4.36	10.43	32.05	22.00	3.50	48.90	4.75
MCU 5 x KC 3	5.82	10.03	31.51	24.50	3.25	46.95	4.50
MCU 5 x MCU 7	4.55	10.55	33.95	24.99	3.98	52.97	5.50

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Table 9. Contd..

Hybrids	Lint index	Seed index	2.5% span length (mm)	Bundle strength (g/tex)	Micronaire value (µg/inch)	Uniformity ratio (%)	Elongation per cent (%)
MCU 5 x G.Cot 16	5.78	8.76	33.39	24.21	4.40	46.16	5.25
MCU 7 x Suraj	4.84	9.67	31.16	22.69	3.97	50.66	5.05
MCU 7 x Surabhi	3.91	10.33	32.93	24.55	3.64	49.45	4.55
MCU 7 x Khandwa 2	5.74	10.04	29.67	23.38	4.60	48.20	5.50
MCU 7 x Anjali	5.43	9.46	30.90	22.75	3.70	48.30	5.30
MCU 7 x KC 2	4.97	8.00	29.60	22.90	4.10	50.05	4.90
MCU 7 x KC 3	4.83	10.18	29.00	21.20	4.40	50.60	5.25
MCU 7 x MCU 5	4.42	7.40	35.26	25.22	3.40	51.35	4.25
MCU 7 x G.Cot 16	4.24	9.41	30.15	24.13	4.18	49.14	4.95
G.Cot 16 x Suraj	5.46	12.57	30.35	22.85	4.45	49.90	4.65
G.Cot 16 x Surabhi	4.61	11.49	30.51	22.98	4.35	49.25	4.10
G.Cot 16 x Khandwa 2	5.61	10.17	30.00	22.35	4.41	48.90	4.85
G.Cot 16 x Anjali	5.70	9.82	32.56	22.25	4.47	50.71	4.50
G.Cot 16 x KC 2	5.61	11.74	29.43	23.42	4.48	47.80	4.95

Contd...

Table 9. Contd..

Hybrids	Lint index	Seed index	2.5% span length (mm)	Bundle strength (g/tex)	Micronaire value (µg/inch)	Uniformity ratio (%)	Elongation per cent (%)
G.Cot 16 x KC 3	5.31	9.50	28.65	23.68	4.48	50.44	5.50
G.Cot 16 x MCU 5	4.14	11.46	28.90	21.78	3.80	46.84	5.55
G.Cot 16 x MCU 7	5.86	9.93	28.90	23.28	4.35	50.30	5.15
MCU 13	5.77	10.99	29.00	22.50	4.50	49.03	4.41
Grand mean	5.12	10.25	31.29	23.54	4.23	49.43	4.87
CD @ 5%	0.95	2.03	1.52	1.03	0.18	1.09	0.81
CD @ 1%	1.26	2.69	2.02	1.37	0.25	1.45	1.08

4.2.5. Boll weight (g)

Boll weight of the parents ranges from 3.75 (MCU 7) to 4.55 (MCU 5). None of the parents recorded significantly greater mean value than grand mean. Boll weight of the hybrids varied from 3.38 (MCU 5 x G.Cot 16) to 4.97 (KC 2 x MCU 7). Out of seventy two hybrids, none of the hybrids showed significantly higher boll weight when compared to the grand mean.

4.2.6. Single plant yield (g)

The maximum value for this trait was recorded by the parent MCU 5 (87.34) and minimum value was recorded by the parent G.Cot 16 (73.10) (Figure 2). The hybrid MCU 5 x MCU 7 (115.01) was found to have recorded significantly higher yield followed by KC 2 x MCU 5 (109.63), Anjali x MCU 5 (108.32), Anjali x Suraj (104.64), KC 3 x Anjali (102.65), Khandwa 2 x Suraj (102.17), Surabi x Anjali (102.15), Suraj x Surabi (101.28) and G.Cot 16 x Khandwa 2 (101.06). The grand mean value of parents and hybrids were 80.22 and 87.42, respectively.

4.2.7. Ginning outturn (%)

The mean value of ginning outturn ranges from 30.76 (Khandwa 2) to 35.31 (KC 3). Among the parents, KC 3 (35.31) recorded significantly higher mean value than grand mean. The mean values of hybrids ranges from 23.98 (KC 3 x G.Cot 16) to 37.49 (MCU 5 x G.Cot 16). Out of seventy two hybrids, twenty eight hybrids have recorded significantly higher mean value than the grand mean for this trait.

4.2.8. Lint index

Mean performance of the parents for lint index ranges from 4.14 (Khandwa 2) and 5.70 (G.Cot 16). The hybrid mean value ranges from 3.68 (Khandwa 2 x KC 2) to 6.20 (Anjali x Suraj). None of the parents recorded significantly greater mean value than grand mean. The hybrids, Anjali x Suraj and KC 3 x Anjali have recorded significantly higher mean value than grand mean value (5.12).

4.2.9. Seed index

In parents, seed index value ranges from 7.74 (Anjali) to 11.15 (G.Cot 16). None of the parents recorded significantly greater mean value when compared to the

Figure 1. Proportion of GCA and SCA variance for yield and fibre quality traits

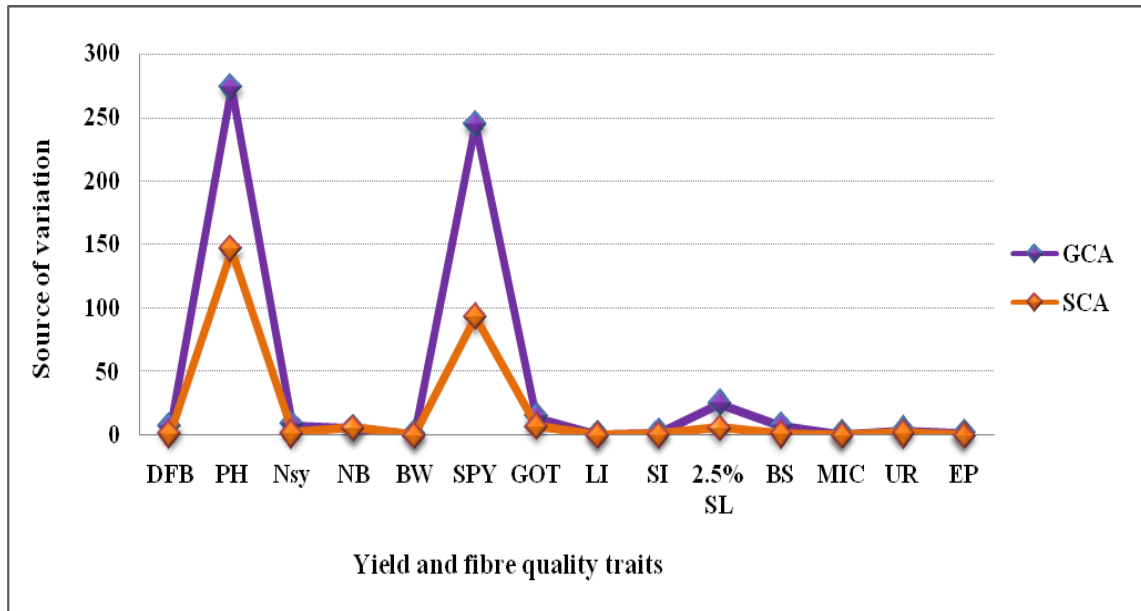
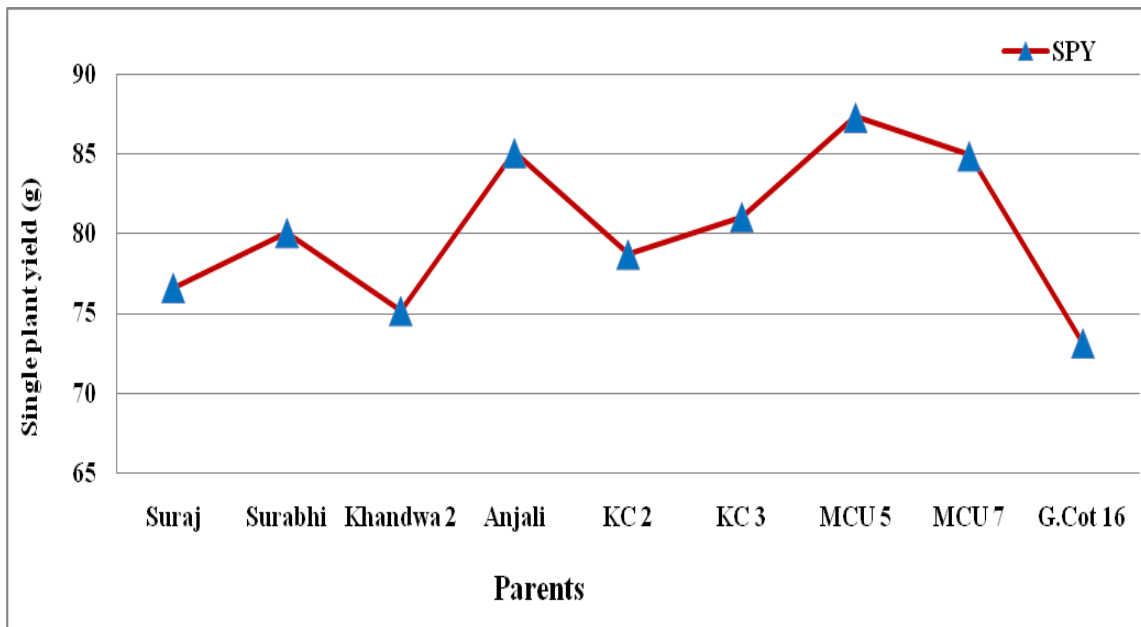


Figure 2. Mean performance of parents for single plant yield



grand mean. Among the hybrids, seed index value ranges varied from 7.40 (MCU 7 x MCU 5) to 13.32 (KC 3 x G.Cot 16). Out of seventy two hybrids, four hybrids recorded significantly higher mean value than the grand mean value for this trait.

4.2.10. 2.5% span length (mm)

Mean performance of the parents for 2.5% span length ranges from 24.03 (MCU 7) to 33.51 (MCU 5). The hybrid mean values ranges from 27.31 (KC 3 x MCU 5) to 36.90 (KC 2 x MCU 5). Among the parents, MCU 5 (33.51), Surabhi (32.06) and KC 3 (30.23) recorded significantly higher 2.5% span length than the parental grand mean. Out of seventy two hybrids, twenty hybrids recorded significantly higher mean value than the grand mean for its 2.5% span length.

4.2.11. Bundle strength (g/tex)

Among the parents, Surabhi recorded a maximum bundle strength (24.59) whereas, KC 2 recorded a minimum bundle strength (19.08). The mean values of the hybrids ranges from 19.70 (Khandwa 2 x Suraj) to 26.48 (Surabi x MCU 5). Among hybrids, fifteen hybrids showed significantly higher mean value than the grand mean value for its bundle strength.

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

Micronaire value ranges from 3.58 (Surabhi) to 4.69 (KC 3) parents. Among the hybrids, it ranges from 3.25 (MCU 5 x KC 3) to 4.91 (Khandwa 2 x KC 2). Out of seventy two hybrids, forty three hybrids recorded significantly lesser mean values for micronaire than the grand mean value. The grand mean values for parents and hybrids were 4.12 and 4.23, respectively.

4.2.13. Uniformity ratio (%)

In parents, uniformity ratio ranges from 46.81 (KC 3) to 51.73 (Anjali). The parent, Anjali recorded significantly greater mean value than the grand mean value. Uniformity ratio varied from 45.30 (Surabi x KC 2) to 53.53 (KC 3 x Surabi) among the hybrids. Out of seventy two hybrids, nineteen hybrids showed significantly higher uniformity ratio when compared to the grand mean value of uniformity ratio.

4.2.14. Elongation per cent (%)

The maximum value of this trait was recorded by the parent Anjali (6.70) whereas, the minimum value was recorded by the parent Surabhi (4.40). Among hybrids, it ranges from 4.10 (Suraj x KC 3, Surabi x KC 3 and G.cot 16 x Surabi) to 6.05 (Anjali x KC 3). Out of seventy two hybrids, four hybrids recorded significantly higher mean values when compared to the grand mean value. The grand mean values for parents and hybrids were 5.11 and 4.87, respectively.

4.3. Combining ability effects

The general combining ability effects of parents and specific combining ability effects of hybrids were presented in Tables 10 to 23. The results of these estimates with respect to individual traits were presented below.

4.3.1. Days to first boll bursting (days)

The *gca* effect of parents ranges from -0.640 (Khandwa 2) to 1.404 (Anjali). Among the parents, Khandwa 2 (-0.640), KC 2 (-0.406) and KC 3 (-0.277) recorded negative and also shown a significant *gca* effect for this character. In direct crosses, the *sca* effect ranges from -1.950 (Anjali x KC 2) to 2.975 (MCU 7 x G.Cot 16). Among the thirty six direct crosses, six hybrids recorded negative significant *sca* effect. Among the reciprocal crosses also, six hybrids exhibited negative significant *sca* effect for days to first boll bursting. MCU 5 x Anjali exhibited lowest negative significant *sca* effect with -4.100 followed by G.Cot 16 x Anjali with -3.850 (Table 10).

4.3.2. Plant height (cm)

Among the nine parents, parent G.Cot 16 exhibited lowest negative significant *gca* effect of -6.877 and parent MCU 5 recorded the highest positive significant *gca* effect of 6.886 for this character. Among thirty six direct crosses, ten hybrids showed a positive significant *sca* effect. The hybrid Suraj x KC 3 showed the lowest significant negative *sca* effect of -18.713 in direct crosses. Among the thirty six reciprocal crosses, eight crosses showed a positive significant *sca* effect and the highest value was recorded by the hybrid G.Cot 16 x Suraj (15.873). The hybrid Anjali x Suraj (-20.923) recorded the lowest significant negative *sca* effect for this trait (Table 11).

Table 10. General and specific combining ability effects for days to first boll bursting (days)

Genotypes	Suraj	Surabhi	Khandwa 2	Anjali	KC 2	KC 3	MCU 5	MCU 7	G.Cot 16
Suraj	-0.227	-0.453	0.915*	0.422	0.131	-0.548	-0.132	0.116	-0.489
Surabhi	0.313	-0.184	0.072	0.328	1.488**	1.159**	-0.175	-0.777*	-1.282**
Khandwa 2	0.400	0.300	-0.640**	-1.398**	0.493	0.195	0.606	-0.034	-0.977**
Anjali	-2.550**	2.500**	-0.283	1.404**	-1.950**	0.504	1.388**	-0.415	1.780**
KC 2	1.350**	-1.250**	2.000**	-0.600	-0.406**	0.331	-0.348	-0.205	-0.698
KC 3	-0.500	0.250	-0.370	-2.517**	0.000	-0.277*	0.768*	-0.472	-0.839*
MCU 5	0.350	0.650	1.225**	-4.100**	-0.255	1.500**	0.157	-0.218	0.277
MCU 7	0.500	-0.050	0.137	-0.400	0.000	0.238	1.150**	0.059	2.975**
G.Cot 16	-0.250	-0.500	0.350	-3.850**	-0.512	0.150	-0.100	-2.700**	0.114

Table 11. General and specific combining ability effects for plant height (cm)

Genotypes	Suraj	Surabhi	Khandwa 2	Anjali	KC 2	KC 3	MCU 5	MCU 7	G.Cot 16
Suraj	-1.770**	3.748*	1.319	-2.304	7.695**	-18.713**	6.596**	-9.758**	6.480**
Surabhi	0.510	4.143**	0.506	-7.979**	2.900	1.424	4.670**	0.479	-7.623**
Khandwa 2	-1.500	-5.000**	-1.788**	-6.740**	-2.466	-5.007**	-0.449	-7.428**	14.226**
Anjali	-20.923**	13.210**	3.497	0.657	-5.687**	19.880**	-3.944*	-1.611	-7.187**
KC 2	-12.280**	-4.533*	4.000*	-17.225**	0.316	11.901**	-3.773*	4.316*	-14.316**
KC 3	1.400	1.950	-7.012**	-8.980**	-15.000**	0.044	-17.968**	2.053	0.756
MCU 5	14.650**	-8.963**	3.313	13.673**	4.767*	-5.500**	6.886**	3.194	4.185*
MCU 7	3.400	1.750	-2.587	-16.375**	-9.260**	4.275*	-15.143**	-1.611**	-2.702
G.Cot 16	15.873**	-1.482	-13.000**	-12.132**	-0.087	-12.262**	-6.478**	5.950**	-6.877**

**Significant at 1 per cent level, *Significant at 5 per cent level; diagonal values indicate the *gca* effects

4.3.3. Number of sympodial branches per plant

The *gca* effect of parents ranges from -1.073 (G.Cot 16) to 1.112 (MCU 5). Among nine parents, MCU 5 showed a positive significant *gca* effects of 1.112 for this character. In direct crosses, among thirty six hybrids, KC 2 x KC 3 recorded the highest positive significant *sca* effect of 2.00 followed by Surabhi x Khandwa 2 with 1.735. Among thirty six reciprocal crosses, five hybrids showed a positive significant *sca* effect and the highest value (2.950) was recorded by the hybrid KC 3 x Surabhi (Table 12).

4.3.4. Number of bolls per plant

The lower *gca* effect among the parents was recorded in G.Cot 16 (-1.047) whereas, higher *gca* effect was registered in MCU 5 (0.728). Among the direct crosses, Suraj x Khandwa 2 (3.941) and MCU 5 x MCU 7 (2.836) registered positive and significant *sca* effect for number of bolls per plant. Among the thirty six reciprocal crosses, five hybrids registered as a positive significant *sca* and the hybrid MCU 5 x Anjali recorded highest positive significant *sca* effect with 3.868 (Table 13).

4.3.5. Boll weight (g)

Among nine parents, three parents viz., Suraj (0.231), Anjali (0.154) and KC 2 (0.119) recorded positive and significant *gca* effect. Among direct crosses, hybrid KC 2 x MCU 5 (-0.386) and MCU 5 x G.Cot 16 (-0.391) recorded negative significant *sca* effect for this trait. Among the thirty six reciprocal crosses, seven hybrids exhibited significant *sca* effect. The hybrids viz., MCU 7 x KC 2 (0.485), Surabhi x Suraj (0.440), MCU 7 x KC 3 (0.410) and KC 3 x Surabhi (0.400) showed positive significant *sca* effect (Table 14).

4.3.6. Single plant yield (g)

The *gca* effect of parents ranges from -5.419 (G.Cot 16) to 6.020 (MCU 5). Among the nine parents, MCU 5 and MCU 7 registered a positive and significant *gca* effect. Among the direct crosses, hybrid Suraj x Khandwa 2 exhibited highest positive significant *sca* effect with 12.357 followed by MCU 5 x MCU 7 (11.655) and among the reciprocal crosses, MCU 7 x KC 3 showed highest positive significant *sca* effect of 16.202 followed by Surabhi x Suraj (13.498). Seventeen hybrids registered a positive significant *sca* effect in both direct and reciprocal crosses for this trait (Table 15).

Table 12. General and specific combining ability effects for number of sympodial branches per plant

Genotypes	Suraj	Surabhi	Khandwa 2	Anjali	KC 2	KC 3	MCU 5	MCU 7	G.Cot 16
Suraj	-0.742*	0.428	0.110	-0.542	1.080	-1.126	0.549	1.265	0.334
Surabhi	1.950*	0.183	1.735*	0.258	-0.645	0.649	0.374	-1.210	-0.641
Khandwa 2	-1.400	-0.850	-0.349	-0.035	-0.014	-0.015	0.055	0.208	1.240
Anjali	-2.400*	1.475	1.400	0.503	-0.515	1.328	-0.014	0.869	0.738
KC 2	-0.800	-2.000	-0.100	1.250	-0.119	2.000*	-0.505	-0.759	-0.427
KC 3	-0.450	2.950**	0.855	-1.550	-1.000	0.137	-1.081	0.597	-0.696
MCU 5	1.500	-1.750	2.300*	0.717	2.030*	-1.050	1.112*	-1.040	-0.121
MCU 7	-0.750	-0.800	-0.212	-0.700	0.950	1.038	1.000	0.347	-0.155
G.Cot 16	-0.500	2.350*	-0.400	-0.550	-0.638	0.650	-1.500	-0.500	-1.073**

Table 13. General and specific combining ability effects for number of bolls per plant

Genotypes	Suraj	Surabhi	Khandwa 2	Anjali	KC 2	KC 3	MCU 5	MCU 7	G.Cot 16
Suraj	-0.104	-0.602	3.941**	-1.293	0.258	-0.158	2.143	-1.382	0.418
Surabhi	-1.063	0.236	2.151	2.175	1.769	0.553	-1.297	0.628	-1.472
Khandwa 2	-2.950*	0.400	-0.020	0.555	0.974	-1.349	-1.209	-0.654	0.584
Anjali	-2.950*	1.407	2.882*	0.414	-1.710	1.675	-0.043	1.300	-0.300
KC 2	-3.600*	-0.050	-3.500*	0.150	-0.587	1.826	-0.236	-1.349	1.326
KC 3	1.500	1.050	-1.208	-1.250	-0.600	0.128	-1.090	0.148	-0.215
MCU 5	-0.800	0.800	-1.532	3.868**	3.563*	2.900*	0.728	2.836*	-0.614
MCU 7	0.600	0.850	-1.688	-2.500	0.050	3.438*	0.850	0.253	0.911
G.Cot 16	1.000	1.550	-1.750	-1.600	-2.725	1.900	-2.900*	-3.950**	-1.047*

**Significant at 1 per cent level, *Significant at 5 per cent level; diagonal values indicate the *gca* effects

Table 14. General and specific combining ability effects for boll weight (g)

Genotypes	Suraj	Surabhi	Khandwa 2	Anjali	KC 2	KC 3	MCU 5	MCU 7	G.Cot 16
Suraj	0.231**	-0.109	-0.056	0.258	0.210	-0.082	-0.039	-0.183	0.172
Surabhi	0.440*	-0.021	-0.077	-0.151	0.082	-0.030	0.087	0.197	-0.116
Khandwa 2	-0.108	-0.165	-0.166**	-0.108	-0.008	0.005	0.015	0.152	0.054
Anjali	-0.033	0.023	-0.170	0.154*	0.309	-0.246	0.002	-0.141	0.136
KC 2	0.000	-0.390*	-0.110	0.117	0.119*	-0.193	-0.386*	0.126	-0.027
KC 3	-0.410*	0.400*	-0.055	-0.275	0.297	-0.214**	0.050	0.149	0.259
MCU 5	-0.210	-0.050	-0.208	-0.230	-0.207	-0.055	-0.051	0.224	-0.391*
MCU 7	0.308	0.085	0.150	-0.278	0.485*	0.410*	-0.023	0.020	-0.020
G.Cot 16	0.365	-0.105	-0.005	-0.092	0.030	-0.517**	-0.320	-0.007	-0.072

Table 15. General and specific combining ability effects for single plant yield (g)

Genotypes	Suraj	Surabhi	Khandwa 2	Anjali	KC 2	KC 3	MCU 5	MCU 7	G.Cot 16
Suraj	1.924	0.757	12.357**	3.662	4.541	-8.446**	3.076	-2.684	0.605
Surabhi	13.498**	-1.521	5.147	3.042	-0.141	1.265	-7.523*	-2.654	3.621
Khandwa 2	-1.980	-3.770	-0.709	-10.328**	-3.439	0.149	-0.701	-2.206	9.080**
Anjali	-10.768**	12.343**	7.800*	1.669	-9.034**	3.519	7.224*	9.291**	-2.512
KC 2	-2.035	-13.347**	-3.603	1.510	0.237	9.013**	5.148	6.568*	-4.266
KC 3	1.735	12.500**	-13.683**	-15.880**	-5.252	-5.036**	-10.259**	-2.894	3.137
MCU 5	2.523	-5.613	3.032	6.785*	11.608**	0.262	6.020**	11.655**	2.702
MCU 7	-5.313	9.138**	-9.662**	-0.243	-0.957	16.202**	7.877*	2.835**	-9.688**
G.Cot 16	12.442**	3.697	-11.490**	-8.940**	-5.010	-7.670*	-8.360*	-16.320**	-5.419**

**Significant at 1 per cent level, *Significant at 5 per cent level; diagonal values indicate the *gca* effects

4.3.7. Ginning outturn (%)

The *gca* effects of parents ranges from -1.307 (Surabhi) to 1.041 (Suraj). Among the nine parents, Suraj (1.041), MCU 7 (1.027), KC 3 (0.673), Anjali (0.418) and MCU 5 (0.250) registered positive significant *gca* effect. Among the direct crosses, a total of eleven hybrids registered positive significant *sca* effect for this character. The hybrid KC 2 x MCU 7 recorded the highest significant positive *sca* effect with 3.397. Among the reciprocal crosses, total of twelve hybrids has registered positive significant *sca* effects and the hybrid G.Cot 16 x MCU 5 recorded the highest positive significant *sca* effect of 6.610 of this character. In this trait, twenty three hybrids registered positive significant *sca* effect in both direct and reciprocal crosses (Table 16).

4.3.8. Lint index

In nine parents, Suraj exhibited positive significant *gca* effect with 0.243 and three parents viz., Surabhi (-0.158), Khandwa 2 (-0.161) and KC 2 (-0.167) recorded negative significant *gca* effect. In the direct crosses, Surabhi x MCU 5 (0.793) recorded the highest positive significant *sca* effect and in the reciprocal crosses, four hybrids viz., G.Cot 16 x MCU 5 (0.822), MCU 7 x Surabhi (0.630), MCU 7 x KC 3 (0.565) and MCU 7 x Suraj (0.495) exhibited the positive significant *sca* effects (Table 17).

4.3.9. Seed index

The *gca* effect of parents ranges from -0.490 (MCU 7) to 0.533 (G.Cot 16). For this character, among the nine parents, G.Cot 16 showed the positive significant *gca* effects of 0.533. In the direct crosses, among thirty six hybrids, Anjali x KC 2 (1.635), Khandwa 2 x MCU 7 (1.357) and Surabhi x MCU 5 (1.125) recorded a positive significant *sca* effect. In reciprocal crosses, G.Cot 16 x KC 3 (1.910) and MCU 7 x MCU 5 (1.575) showed the positive significant *sca* effect (Table 18).

4.3.10. 2.5% span length (mm)

The *gca* effect of parents ranges from -1.124 (Khandwa 2) to 1.863 (Surabhi). In parents, Surabhi (1.863), MCU 5 (1.745) and Suraj (0.886) recorded a positive significant *gca* effect. In direct crosses, total of fifteen hybrids registered a positive significant *sca* effect and the hybrid MCU 5 x MCU 7 recorded the highest positive significant *sca* effect with value of 2.595. In reciprocal crosses, a total of twelve hybrids

Table 16. General and specific combining ability effects for ginning outturn (%)

Genotypes	Suraj	Surabhi	Khandwa 2	Anjali	KC 2	KC 3	MCU 5	MCU 7	G.Cot 16
Suraj	1.041**	-0.296	-0.256	1.937**	-0.170	0.104	0.165	0.976**	-1.456**
Surabhi	-1.485**	-1.307**	0.020	-1.225**	-0.277	0.177	1.010**	-2.559**	0.112
Khandwa 2	-1.525**	-2.682**	-0.377**	3.365**	-1.197**	-2.153**	1.175**	0.274	0.685
Anjali	-0.547	0.208	-0.608	0.418**	-4.599**	0.217	-2.522**	2.291**	0.760*
KC 2	0.280	5.875**	-3.935**	2.038**	-0.968**	2.908**	-2.427**	3.397**	0.826*
KC 3	-2.455**	-0.290	3.515**	-3.930**	3.010**	0.673**	2.508**	-0.866*	-3.438**
MCU 5	-0.052	2.265**	-1.600**	-1.052**	0.847*	0.073	0.250*	-0.899*	0.238
MCU 7	3.135**	3.137**	-2.005**	0.647	-1.452**	2.045**	-3.620**	1.027**	0.376
G.Cot 16	1.977**	2.818**	-2.615**	-2.870**	0.180	-5.928**	6.610**	-3.030**	-0.759**

Table 17. General and specific combining ability effects for lint index

Genotypes	Suraj	Surabhi	Khandwa 2	Anjali	KC 2	KC 3	MCU 5	MCU 7	G.Cot 16
Suraj	0.243**	-0.174	-0.043	0.288	0.071	-0.070	0.183	0.001	0.007
Surabhi	0.058	-0.158*	0.108	-0.319	-0.033	0.189	0.793**	-0.393	-0.230
Khandwa 2	-0.130	-0.515*	-0.161*	0.459*	-0.500*	-0.696**	0.502*	0.742**	0.086
Anjali	-0.482	-0.105	-0.065	0.061	-0.407	0.040	-0.282	0.266	-0.063
KC 2	0.057	0.457	-0.617*	0.307	-0.167*	0.528*	-0.604**	-0.101	0.663**
KC 3	-0.322	-0.045	0.392	-0.825**	-0.115	0.133	0.307	0.171	-0.563*
MCU 5	-0.350	0.090	-0.450	-0.082	0.007	-0.245	0.014	-0.619**	-0.241
MCU 7	0.495*	0.630*	-0.062	-0.013	-0.148	0.565*	0.065	-0.030	-0.110
G.Cot 16	-0.025	0.187	-0.500*	-0.517*	0.070	-0.550*	0.822**	-0.810**	0.064

**Significant at 1 per cent level, *Significant at 5 per cent level; diagonal values indicate the *gca* effects

Table 18. General and specific combining ability effects for seed index

Genotypes	Suraj	Surabhi	Khandwa 2	Anjali	KC 2	KC 3	MCU 5	MCU 7	G.Cot 16
Suraj	0.026	-0.225	0.064	-0.124	0.125	-0.224	0.215	-0.457	0.740
Surabhi	0.810	0.318	0.172	0.163	0.252	0.213	1.125*	0.210	-0.528
Khandwa 2	0.430	0.195	-0.181	-0.262	-0.591	-0.452	0.419	1.357**	-0.188
Anjali	-0.595	-0.275	0.090	-0.318	1.635**	0.122	0.825	-0.224	-0.309
KC 2	-0.017	-1.947**	0.335	-0.405	0.181	-0.270	-0.288	-1.635**	0.865
KC 3	0.483	0.043	-0.722	0.185	-1.513**	-0.015	-0.570	0.621	0.691
MCU 5	-0.623	-0.985	-0.125	0.330	-0.385	-0.462	-0.054	-0.683	-0.575
MCU 7	-0.390	-0.090	0.848	-0.285	0.263	0.143	1.575**	-0.490**	-0.577
G.Cot 16	-1.070*	-0.960	0.195	0.288	0.045	1.910**	-1.350*	-0.262	0.533**

Table 19. General and specific combining ability effects for 2.5% span length (mm)

Genotypes	Suraj	Surabhi	Khandwa 2	Anjali	KC 2	KC 3	MCU 5	MCU 7	G.Cot 16
Suraj	0.886**	-0.469	1.851**	-0.084	-0.181	1.458**	0.352	1.626**	0.855*
Surabhi	1.540**	1.863**	-1.336**	1.359**	1.200**	1.517**	-0.030	0.484	-0.150
Khandwa 2	1.172**	-0.432	-1.124**	0.784*	0.610	0.694*	0.867**	0.277	0.665*
Anjali	1.567**	-1.787**	-0.425	-0.444**	0.877**	-0.357	-2.241**	0.581	1.512**
KC 2	0.547	0.500	0.472	0.820*	-0.772**	-1.003**	2.590**	0.230	-0.317
KC 3	1.590**	-1.150**	-1.380**	0.300	0.375	-0.609**	-2.636**	-0.361	0.150
MCU 5	0.757*	-1.422**	-0.547	-1.130**	2.423**	-2.095**	1.745**	2.595**	-0.607
MCU 7	1.623**	-0.313	-0.257	-0.493	0.123	0.295	-0.655	-0.644**	0.160
G.Cot 16	1.400**	1.218**	-0.450	-1.488**	-0.510	0.900*	2.247**	0.625	-0.900**

**Significant at 1 per cent level, *Significant at 5 per cent level; diagonal values indicate the *gca* effects

registered a positive significant *sca* effect and the hybrid G.Cot 16 x MCU 5 recorded the highest positive significant *sca* effect with value of 2.247. Twenty seven hybrids registered a positive significant *sca* effect among both direct and reciprocal crosses (Table 19).

4.3.11. Bundle strength (g/tex)

The *gca* effect of parents ranges from -0.753 (KC 2) to 1.018 (Surabhi). In parents, Suraj (0.317), Surabhi (1.018) and MCU 5 (0.874) recorded a positive significant *gca* effect. In direct crosses, twelve hybrids exhibited positive significant *sca* effect and the hybrid KC 2 x MCU 5 recorded the highest positive significant *sca* effect with 1.797. In the reciprocal crosses, eight hybrids exhibited positive significant *sca* effect and the hybrid Khandwa 2 x Suraj recorded the highest positive significant *sca* effect with 2.280 (Table 20).

4.3.12. Micronaire value (µg/inch)

The *gca* effect of parents ranges from -0.373 (MCU 5) to 0.295 (Khandwa 2). Among the parents, MCU 5 (-0.373), Surabhi (-0.207), MCU 7 (-0.084), Anjali (-0.049) and Suraj (-0.031) recorded a negative significant *gca* effect. In direct crosses, the *sca* effect ranges from -0.474 (KC 2 x MCU 5) to 0.431 (Surabhi x G.Cot 16). Among the thirty six direct crosses, twelve hybrids recorded a negative significant *sca* effect. In the reciprocal crosses, the *sca* effect ranges from -0.683 (KC 3 x Suraj) to 0.727 (MCU 5 x KC 3). Six hybrids viz., KC 3 x Suraj (-0.683), KC 3 x Anjali (-0.547), KC 2 x Surabhi (-0.370), KC 2 x Anjali (-0.303), G.Cot 16 x Anjali (-0.220) and G.Cot 16 x MCU 7 (-0.088) exhibited negative significant *sca* effect (Table 21).

4.3.13. Uniformity ratio (%)

The *gca* effect of a parents ranges from -0.628 (MCU 5) to 0.688 (Anjali). In the nine parents, Anjali (0.688), MCU 7 (0.575) and KC 2 (0.368) registered positive significant *gca* effect. In the direct crosses, twelve hybrids registered positively significant *sca* effect and the hybrid MCU 5 x MCU 7 recorded the highest positive significant *sca* effect with 2.819. In the reciprocal crosses, eight hybrids registered a positive significant *sca* effects and the hybrid MCU 5 x Khandwa 2 recorded the highest

Table 20. General and specific combining ability effects for bundle strength (g/tex)

Genotypes	Suraj	Surabhi	Khandwa 2	Anjali	KC 2	KC 3	MCU 5	MCU 7	G.Cot 16
Suraj	0.317**	0.285	-1.192**	0.234	0.424	1.185**	-0.601*	0.410	0.350
Surabhi	0.517	1.018**	-1.520**	0.928**	0.658**	0.887**	1.116**	-0.518	-1.000**
Khandwa 2	2.280**	0.463	-0.537**	0.218	0.591*	-0.285	0.994**	0.650**	0.442
Anjali	0.135	-0.175	0.910**	-0.413**	0.189	-0.204	0.387	0.093	-0.332
KC 2	0.000	0.135	-0.503	1.065**	-0.753**	0.128	1.797**	-0.334	0.871**
KC 3	0.100	-0.547*	-0.100	-0.395	-0.203	-0.370**	-0.629**	-0.790**	1.125**
MCU 5	-0.833**	0.080	-0.023	-0.140	0.285	-1.227**	0.874**	0.764**	-1.061**
MCU 7	1.505**	-0.583*	0.200	0.398	-0.520	1.108**	-0.110	0.075	0.447
G.Cot 16	1.000**	0.215	0.738**	0.188	-0.120	0.263	1.215**	0.425	-0.210*

Table 21. General and specific combining ability effects for micronaire value (µg/inch)

Genotypes	Suraj	Surabhi	Khandwa 2	Anjali	KC 2	KC 3	MCU 5	MCU 7	G.Cot 16
Suraj	-0.031*	0.022	0.050	0.373**	0.107**	-0.393**	0.023	-0.059	0.140**
Surabhi	-0.057	-0.207**	0.026	-0.105*	-0.045	-0.089*	0.079*	-0.093*	0.431**
Khandwa 2	0.067	0.282**	0.295**	0.313**	0.071	0.039	-0.160**	0.218**	-0.308**
Anjali	0.313**	0.207**	-0.078	-0.049**	0.070	-0.195**	0.243**	-0.161**	-0.092*
KC 2	0.222**	-0.370**	0.222**	-0.303**	0.103**	0.331**	-0.474**	-0.003	-0.067
KC 3	-0.683**	0.230**	0.175**	-0.547**	0.020	0.172**	-0.045	0.328**	-0.098*
MCU 5	0.408**	-0.018	0.250**	0.510**	-0.025	0.727**	-0.373**	-0.074	0.082*
MCU 7	0.080	0.195**	0.052	0.225**	0.135**	0.240**	0.287**	-0.084**	-0.045*
G.Cot 16	0.050	0.265**	-0.027	-0.220**	-0.053	-0.015	0.300**	-0.088*	0.172**

**Significant at 1 per cent level, *Significant at 5 per cent level; diagonal values indicate the *gca* effects

Table 22. General and specific combining ability effects for uniformity ratio (%)

Genotypes	Suraj	Surabhi	Khandwa 2	Anjali	KC 2	KC 3	MCU 5	MCU 7	G.Cot 16
Suraj	-0.074	-0.571*	0.976**	-1.113**	0.412	0.520*	0.333	0.860**	0.696**
Surabhi	0.900**	-0.099	-0.772**	0.217	-1.113**	1.345**	0.408	-0.675*	-0.382
Khandwa 2	-0.750*	-1.068**	-0.346**	0.464	0.892**	0.160	-1.103**	-0.578*	0.158
Anjali	-0.805**	-1.150**	-0.450	0.688**	0.795**	0.201	-0.851**	-1.370**	0.692**
KC 2	-0.355	-3.250**	0.407	0.005	0.368**	-0.494	0.941**	-0.537*	-0.621*
KC 3	0.223	-3.057**	0.190	-0.985**	-1.950**	-0.168	-1.646**	0.829**	1.335**
MCU 5	-0.225	-2.875**	1.407**	1.298**	1.175**	0.003	-0.628**	2.819**	-1.953**
MCU 7	0.095	-0.250	0.845**	0.993**	-0.250	0.030	0.810**	0.575**	0.067
G.Cot 16	-0.200	-0.653*	-0.005	-0.252	1.025**	-0.195	-0.337	-0.580*	-0.316**

Table 23. General and specific combining ability effects for elongation per cent (%)

Genotypes	Suraj	Surabhi	Khandwa 2	Anjali	KC 2	KC 3	MCU 5	MCU 7	G.Cot 16
Suraj	-0.268**	0.590**	-0.162	-0.118	-0.132	-0.298	0.088	0.163	-0.218
Surabhi	-0.150	-0.371**	0.065	0.035	-0.029	-0.046	-0.360	-0.135	-0.365
Khandwa 2	-0.050	0.175	-0.068	-0.393*	-0.007	0.002	0.038	0.388*	0.082
Anjali	-0.175	-0.525*	-0.500*	0.562**	-0.162	0.321	0.007	-0.118	-0.248
KC 2	-0.125	-0.075	-0.100	0.425	-0.024	0.132	-0.007	0.018	0.038
KC 3	-0.200	-0.350	0.000	0.300	0.175	-0.032	-0.373	0.102	-0.054
MCU 5	-0.025	-0.025	-0.475*	0.375	0.225	0.100	0.107	-0.212	0.382*
MCU 7	-0.175	-0.075	-0.200	0.125	0.075	-0.200	0.625**	0.082	0.057
G.Cot 16	-0.225	0.075	0.075	0.725**	-0.025	-0.675**	-0.150	-0.100	0.012

**Significant at 1 per cent level, *Significant at 5 per cent level; diagonal values indicate the *gca* effects

positive significant *sca* effect with the value of 1.407. Twenty hybrids registered positive significant *sca* effect in both direct and reciprocal crosses (Table 22).

4.3.14. Elongation per cent (%)

The *gca* effect of nine parents ranges from -0.371 (Surabhi) to 0.562 (Anjali). In parents, Suraj (-0.268) and Surabhi (-0.371) registered a negative significant *gca* effect. In the direct crosses, the *sca* effect ranges from -0.393 (Khandwa 2 x Anjali) to 0.590 (Suraj x Surabhi). Among the thirty six direct crosses, three hybrids recorded a positive significant *sca* effect. In reciprocal crosses, the *sca* effect ranges from -0.675 (G.Cot 16 x KC 3) to 0.725 (G.Cot 16 x Anjali) and a total of two hybrids exhibited positive significant *sca* effect (Table 23).

4.4. Heterosis

The expression of heterosis in seventy two hybrids involving nine parents was measured in terms of relative heterosis (di) in relation to mid parental values, heterobeltiosis (dii) in relation to better parental values and standard heterosis (diii) in comparison with MCU 13 as the standard check variety. The results on heterosis in respect of individual yield and fibre contributing characters were furnished below (Figure 3 to 5).

4.4.1. Days to first boll bursting (days)

The mid parental heterosis ranges from -2.40% (Anjali x KC 2) to 6.79% (MCU 5 x Anjali). Seven hybrids recorded a negative significant heterosis over mid parent. The range of heterobeltiosis was -3.33% (Anjali x KC 2) to 5.73% (G.Cot 16 x MCU 7). Twelve hybrids recorded a negative significant heterosis over better parent. The standard heterosis ranged from -2.60% (KC 2 x Khandwa 2) to 6.92% (G.Cot 16 x Anjali). Out of seventy two, only six hybrids showed negative significant heterosis over the check MCU 13 (Table 24).

4.4.2. Plant height (cm)

The magnitude of heterosis over mid parent ranges from -32.56% (Suraj x Anjali) to 25.48% (KC 3 x KC 2). Out of seventy two hybrids, only twelve hybrids recorded a positive significant heterosis, however thirty six hybrids showed a negative significant heterosis. Heterobeltiosis ranges from -38.65% (Anjali x G.Cot 16) to 22.12% (KC 3 x

Table 24. Expression of heterosis for days to first boll bursting

SI. No.	Hybrids	Days to first boll bursting		
		d _i	d _{ii}	d _{iii}
1	Suraj x Surabhi	-0.16	-0.49	-0.64
2	Suraj x Khandwa 2	1.02	0.49	0.34
3	Suraj x Anjali	-1.92**	-2.95**	-1.03
4	Suraj x KC 2	0.87	0.87	0.74
5	Suraj x KC 3	-0.68	-1.46	-1.62*
6	Suraj x MCU 5	1.08	0.19	0.05
7	Suraj x MCU 7	0.88	0.49	0.34
8	Suraj x G.Cot 16	-0.55	-0.78	-0.93
9	Surabhi x Suraj	-0.43	-0.74	-1.25
10	Surabhi x Khandwa 2	0.64	0.59	-0.54
11	Surabhi x Anjali	3.38**	1.81*	3.88**
12	Surabhi x KC 2	0.20	-0.29	-0.44
13	Surabhi x KC 3	2.26**	1.96*	0.83
14	Surabhi x MCU 5	1.87**	1.47	0.34
15	Surabhi x MCU 7	0.00	-0.10	-1.03
16	Surabhi x G.Cot 16	-1.04	-1.30	-1.91*
17	Khandwa 2 x Suraj	0.37	0.06	-0.44
18	Khandwa 2 x Surabhi	-0.16	-0.32	-1.13
19	Khandwa 2 x Anjali	-1.41*	-2.91**	-1.00
20	Khandwa 2 x KC 2	1.95**	1.46	1.32
21	Khandwa 2 x KC 3	0.26	-0.04	-1.17

Contd...

Table 24. Contd..

SI. No.	Hybrids	Days to first boll bursting		
		d _i	d _{ii}	d _{iii}
22	Khandwa 2 x MCU 5	2.76**	2.35**	1.23
23	Khandwa 2 x MCU 7	0.47	0.37	-0.57
24	Khandwa 2 x G.Cot 16	-0.36	-0.62	-1.23
25	Anjali x Suraj	3.26**	2.10**	3.97**
26	Anjali x Surabhi	-1.51*	-2.76**	-1.03
27	Anjali x Khandwa 2	-0.72	-2.19**	-0.44
28	Anjali x KC 2	-2.40**	-3.33**	-1.62*
29	Anjali x KC 3	-1.00	-2.70**	-0.96
30	Anjali x MCU 5	-1.16	-2.95**	-1.23
31	Anjali x MCU 7	0.10	-1.24	0.54
32	Anjali x G.Cot 16	-1.22	-2.38**	-0.64
33	KC 2 x Suraj	-1.57*	-1.75*	-1.91*
34	KC 2 x Surabhi	2.47**	2.14**	2.01*
35	KC 2 x Khandwa 2	-1.90**	-2.43**	-2.60**
36	KC 2 x Anjali	-1.34*	-2.38**	-0.44
37	KC 2 x KC 3	0.49	-0.29	-0.44
38	KC 2 x MCU 5	0.10	-0.78	-0.93
39	KC 2 x MCU 7	-0.10	-0.49	-0.64
40	KC 2 x G.Cot 16	-1.18	-1.41	-1.57
41	KC 3 x Suraj	0.67	-0.13	-0.64
42	KC 3 x Surabhi	1.81**	1.15	0.34
43	KC 3 x Khandwa 2	1.23	0.79	-0.44
44	KC 3 x Anjali	3.98 **	1.90*	3.97**

Contd...

Table 24. Contd..

SI. No.	Hybrids	Days to first boll bursting		
		d _i	d _{ii}	d _{iii}
45	KC 3 x KC 2	0.69	-0.29	-0.44
46	KC 3 x MCU 5	4.06**	3.95**	2.01*
47	KC 3 x MCU 7	0.98	0.39	-0.54
48	KC 3 x G.Cot 16	0.42	-0.33	-0.93
49	MCU 5 x Suraj	0.67	-0.13	-0.64
50	MCU 5 x Surabhi	0.53	-0.12	-0.93
51	MCU 5 x Khandwa 2	0.49	0.05	-1.18
52	MCU 5 x Anjali	6.79**	4.66**	6.82**
53	MCU 5 x KC 2	0.70	-0.28	-0.43
54	MCU 5 x KC 3	0.99	0.79	-0.93
55	MCU 5 x MCU 7	2.56**	1.96*	1.03
56	MCU 5 x G.Cot 16	1.70*	0.94	0.34
57	MCU 7 x Suraj	0.18	-0.13	-0.64
58	MCU 7 x Surabhi	0.04	-0.12	-0.93
59	MCU 7 x Khandwa 2	0.34	0.29	-0.83
60	MCU 7 x Anjali	0.87	-0.67	1.32
61	MCU 7 x KC 2	0.00	-0.49	-0.64
62	MCU 7 x KC 3	0.42	0.12	-1.00
63	MCU 7 x MCU 5	0.30	-0.10	-1.23
64	MCU 7 x G.Cot 16	1.21	0.94	0.34
65	G.Cot 16 x Suraj	-0.11	-0.29	-0.44
66	G.Cot 16 x Surabhi	-0.45	-0.78	-0.93
67	G.Cot 16 x Khandwa 2	-1.22	-1.75*	-1.91*

Contd...

Table 24. Contd..

SI. No.	Hybrids	Days to first boll bursting		
		d_i	d_{ii}	d_{iii}
68	G.Cot 16 x Anjali	5.86**	4.75**	6.92**
69	G.Cot 16 x KC 2	-0.41	-0.41	-0.57
70	G.Cot 16 x KC 3	-0.29	-1.07	-1.23
71	G.Cot 16 x MCU 5	1.57*	0.68	0.54
72	G.Cot 16 x MCU 7	6.14**	5.73**	5.64**

*significant at 5 per cent level, ** significant at 1 per cent level

d_i = Relative heterosis

d_{ii} = Heterobeltiosis

d_{iii} = Standard heterosis

Table 25. Expression of heterosis for plant height (cm)

SI. No.	Hybrids	Plant height		
		d _i	d _{ii}	d _{iii}
1	Suraj x Surabhi	0.88	-3.40	-13.34**
2	Suraj x Khandwa 2	-5.91	-6.45	-22.30**
3	Suraj x Anjali	-32.56**	-37.30**	-40.10**
4	Suraj x KC 2	-7.15*	-7.79	-24.29**
5	Suraj x KC 3	-23.25**	-24.95**	-35.52**
6	Suraj x MCU 5	14.34**	4.44	3.72
7	Suraj x MCU 7	-14.77**	-17.64**	-27.48**
8	Suraj x G.Cot 16	18.57**	12.99**	-7.22*
9	Surabhi x Suraj	-0.27	-4.57	-14.22**
10	Surabhi x Khandwa 2	-8.55*	-12.02**	-20.92**
11	Surabhi x Anjali	-3.35	-6.20	-10.40**
12	Surabhi x KC 2	-2.41	-7.25*	-16.63**
13	Surabhi x KC 3	-0.49	-2.69	-12.53**
14	Surabhi x MCU 5	-8.29**	-12.64**	-13.24**
15	Surabhi x MCU 7	-4.41	-5.38	-14.95**
16	Surabhi x G.Cot 16	-13.92**	-21.35**	-29.30**
17	Khandwa 2 x Suraj	-2.74	-3.23	-19.71**
18	Khandwa 2 x Surabhi	1.60	-2.22	-12.27**
19	Khandwa 2 x Anjali	-13.56**	-19.24**	-22.85**
20	Khandwa 2 x KC 2	-1.21	-2.40	-19.01**
21	Khandwa 2 x KC 3	-18.24**	-19.64**	-30.96**
22	Khandwa 2 x MCU 5	-3.65	-11.58**	-12.19**

Contd...

Table 25. Contd..

SI. No.	Hybrids	Plant height		
		d _i	d _{ii}	d _{iii}
23	Khandwa 2 x MCU 7	-18.91**	-21.25**	-30.67**
24	Khandwa 2 x G.Cot 16	-5.31	-10.21*	-25.50**
25	Anjali x Suraj	7.89*	0.13	-3.93
26	Anjali x Surabhi	-28.07**	-30.41**	-33.23**
27	Anjali x Khandwa 2	-20.55**	-25.88**	-28.89**
28	Anjali x KC 2	-29.95**	-35.41**	-38.03**
29	Anjali x KC 3	0.04	-5.19	-9.04**
30	Anjali x MCU 5	-1.81	-3.47	-4.14
31	Anjali x MCU 7	-29.82**	-32.70**	-35.44**
32	Anjali x G.Cot 16	-30.89**	-38.65**	-41.14**
33	KC 2 x Suraj	18.67**	18.02**	-3.06
34	KC 2 x Surabhi	6.70*	1.67	-8.79*
35	KC 2 x Khandwa 2	-9.84**	-10.82**	-25.93**
36	KC 2 x Anjali	3.80	-3.96	-8.25*
37	KC 2 x KC 3	-6.00	-8.55*	-21.43**
38	KC 2 x MCU 5	-2.50	-11.37**	-11.99**
39	KC 2 x MCU 7	-10.76**	-14.21**	-24.46**
40	KC 2 x G.Cot 16	-19.28**	-22.69**	-37.18**
41	KC 3 x Suraj	-25.99**	-27.47**	-37.94**
42	KC 3 x Surabhi	-4.04	-6.26	-15.90**
43	KC 3 x Khandwa 2	-3.74	-5.15	-18.84**
44	KC 3 x Anjali	17.60**	11.47**	6.48
45	KC 3 x KC 2	25.48**	22.12**	4.49

Contd...

Table 25. Contd..

SI. No.	Hybrids	Plant height		
		d _i	d _{ii}	d _{iii}
46	KC 3 x MCU 5	-27.91**	-32.90**	-33.36**
47	KC 3 x MCU 7	-2.03	-3.41	-14.95**
48	KC 3 x G.Cot 16	-18.62**	-23.94**	-34.92**
49	MCU 5 x Suraj	-13.63**	-21.13**	-21.61**
50	MCU 5 x Surabhi	8.14**	2.87	2.25
51	MCU 5 x Khandwa 2	-10.02**	-17.41**	-17.92**
52	MCU 5 x Anjali	-25.89**	-27.33**	-27.77**
53	MCU 5 x KC 2	-11.55**	-19.74**	-20.22**
54	MCU 5 x KC 3	-17.82**	-23.39**	-23.85**
55	MCU 5 x MCU 7	-19.80**	-24.38**	-24.84**
56	MCU 5 x G.Cot 16	-9.13**	-20.56**	-21.05**
57	MCU 7 x Suraj	-21.74**	-24.41**	-33.36**
58	MCU 7 x Surabhi	-7.77*	-8.57*	-17.98**
59	MCU 7 x Khandwa 2	-13.78**	-16.27**	-26.19**
60	MCU 7 x Anjali	1.12	-2.78	-7.13**
61	MCU 7 x KC 2	8.25*	3.84	-8.45**
62	MCU 7 x KC 3	-10.77**	-11.91**	-22.34**
63	MCU 7 x MCU 5	8.11**	2.05	1.34
64	MCU 7 x G.Cot 16	-5.99	-13.33**	-23.60**
65	G.Cot 16 x Suraj	-16.48**	-20.45**	-34.66**
66	G.Cot 16 x Surabhi	-10.68**	-18.34**	-26.74**
67	G.Cot 16 x Khandwa 2	23.23**	16.75**	-3.03
68	G.Cot 16 x Anjali	-6.00	-16.43**	-20.17**

Contd...

Table 25. Contd..

SI. No.	Hybrids	Plant height		
		d_i	d_{ii}	d_{iii}
69	G.Cot 16 x KC 2	-18.92**	-22.25**	-37.04**
70	G.Cot 16 x KC 3	7.69*	0.43	-13.73**
71	G.Cot 16 x MCU 5	3.84	-9.22**	-9.84**
72	G.Cot 16 x MCU 7	-18.56**	-24.91**	-33.88**

*significant at 5 per cent level, ** significant at 1 per cent level

d_i = Relative heterosis

d_{ii} = Heterobeltiosis

d_{iii} = Standard heterosis

KC 2) and it was found to be positively significant for only five hybrids. The range of standard heterosis over the check MCU 13 was from -40.10% (Suraj x Anjali) to 6.48% (KC 3 x Anjali). None of the hybrids recorded positively significant standard heterosis (Table 25).

4.4.3. Number of sympodial branches per plant

The hybrids, MCU 5 x KC 2 and Khandwa 2 x Surabhi showed minimum (-18.38%) and maximum (34.55%) relative heterosis, respectively. Positive significant relative heterosis was exhibited in ten hybrids. The range of heterobeltiosis ranges from -27.50% in MCU 5 x G.Cot 16 to 32.00% in Khandwa 2 x Suraj and a total of three hybrids recorded positive significant heterosis over the better parent. The range of standard heterosis ranges from -13.96% in G.Cot 16 x Surabhi to 41.04% in Surabhi x KC 3. Out of seventy two hybrids, twelve hybrids recorded a positive significant standard heterosis and none of the hybrids exhibited a negative significant standard heterosis over the check of MCU 13 (Table 26).

4.4.4. Number of bolls per plant

The hybrid Khandwa 2 x Suraj recorded the highest positive significant relative heterosis (59.47%), heterobeltiosis (51.50%) and standard heterosis (42.52%) followed by the hybrids Anjali x MCU 5 (34.05%), MCU 5 x MCU 7 (32.64%) and KC 2 x MCU 5 (27.00%) which exhibited a positive significant values of standard heterosis. Out of seventy two hybrids, twenty one hybrids recorded a positive significant relative heterosis, eight hybrids were found to have positive significant heterobeltiosis and thirteen hybrids registered positive significant standard heterosis over the check MCU 13. None of the hybrids exhibited negative significant heterosis (Table 27).

4.4.5. Boll weight (g)

The hybrid KC 2 x MCU 7 recorded both highest relative heterosis (28.13%) and heterobeltiosis (24.13%), while the hybrids Suraj x G.Cot 16 and Anjali x KC 2 recorded the highest value of standard heterosis (22.75%), whereas, MCU 5 x G.Cot 16 recorded lowest negative significant relative heterosis (-24.93%), heterobeltiosis (-32.40%) and standard heterosis (-15.50%). None of the hybrids exhibited negative significant standard

Table 26. Expression of heterosis for number of sympodial branches/plant

SI. No.	Hybrids	Number of sympodial branches/plant		
		d_i	d_{ii}	d_{iii}
1	Suraj x Surabhi	30.18*	15.48	26.23
2	Suraj x Khandwa 2	13.69	13.22	-3.39
3	Suraj x Anjali	-4.44	-14.00	-9.03
4	Suraj x KC 2	12.20	-0.83	9.31
5	Suraj x KC 3	4.12	-5.44	-1.97
6	Suraj x MCU 5	15.30	-7.91	30.47*
7	Suraj x MCU 7	11.72	-4.71	14.25
8	Suraj x G.Cot 16	9.88	3.18	-0.56
9	Surabhi x Suraj	-1.75	-12.50	-1.27
10	Surabhi x Khandwa 2	19.57	5.00	18.48
11	Surabhi x Anjali	19.35	15.63	30.47*
12	Surabhi x KC 2	-14.64	-15.63	-4.80
13	Surabhi x KC 3	30.29**	25.00*	41.04**
14	Surabhi x MCU 5	-11.33	-20.36*	12.83
15	Surabhi x MCU 7	-11.52	-14.12	2.96
16	Surabhi x G.Cot 16	13.94	5.62	19.18
17	Khandwa 2 x Suraj	34.69*	32.00*	16.36
18	Khandwa 2 x Surabhi	34.55**	19.35	30.47*
19	Khandwa 2 x Anjali	30.37*	17.33	24.12
20	Khandwa 2 x KC 2	12.20	-0.83	9.31
21	Khandwa 2 x KC 3	25.17*	13.67	17.84
22	Khandwa 2 x MCU 5	19.66	-4.43	35.40*

Contd...

Table 26. Contd..

SI. No.	Hybrids	Number of sympodial branches/plant		
		d_i	d_{ii}	d_{iii}
23	Khandwa 2 x MCU 7	10.86	-5.44	13.40
24	Khandwa 2 x G.Cot 16	20.79	13.43	9.31
25	Anjali x Suraj	28.73*	18.00	24.82
26	Anjali x Surabhi	1.97	0.32	9.66
27	Anjali x Khandwa 2	9.23	-1.33	4.37
28	Anjali x KC 2	12.31	10.04	21.30
29	Anjali x KC 3	11.11	10.00	16.36
30	Anjali x MCU 5	4.87	-8.41	29.76*
31	Anjali x MCU 7	6.87	0.59	20.59
32	Anjali x G.Cot 16	9.54	4.67	10.72
33	KC 2 x Suraj	20.00	6.88	20.59
34	KC 2 x Surabhi	11.11	9.38	23.41
35	KC 2 x Khandwa 2	11.74	-1.88	10.72
36	KC 2 x Anjali	-5.16	-8.12	3.67
37	KC 2 x KC 3	11.40	6.87	20.59
38	KC 2 x MCU 5	3.08	-7.42	31.17*
39	KC 2 x MCU 7	0.00	-2.94	16.36
40	KC 2 x G.Cot 16	-6.79	-13.59	-2.54
41	KC 3 x Suraj	7.64	-1.33	4.37
42	KC 3 x Surabhi	-7.54	-9.03	-0.56
43	KC 3 x Khandwa 2	10.70	0.00	5.78
44	KC 3 x Anjali	30.67**	30.67*	38.22**
45	KC 3 x KC 2	24.71*	22.20	34.70*

Contd...

Table 26. Contd..

SI. No.	Hybrids	Number of sympodial branches/plant		
		d_i	d_{ii}	d_{iii}
46	KC 3 x MCU 5	-13.37	-24.34*	7.19
47	KC 3 x MCU 7	13.75	7.06	28.35*
48	KC 3 x G.Cot 16	5.35	0.67	6.49
49	MCU 5 x Suraj	-4.62	-22.50*	9.31
50	MCU 5 x Surabhi	9.86	-2.50	37.52**
51	MCU 5 x Khandwa 2	-9.03	-27.00**	2.96
52	MCU 5 x Anjali	-3.06	-15.18	19.68
53	MCU 5 x KC 2	-18.38*	-27.30**	2.54
54	MCU 5 x KC 3	-0.29	-13.50	22.00
55	MCU 5 x MCU 7	-5.41	-12.50	23.41
56	MCU 5 x G.Cot 16	-13.86	-27.50**	2.26
57	MCU 7 x Suraj	20.00	4.12	24.82
58	MCU 7 x Surabhi	-0.31	-4.71	14.25
59	MCU 7 x Khandwa 2	13.40	-2.94	16.36
60	MCU 7 x Anjali	15.63	8.82	30.47*
61	MCU 7 x KC 2	-10.51	-14.12	2.96
62	MCU 7 x KC 3	1.74	-5.15	13.75
63	MCU 7 x MCU 5	-16.42	-22.85*	9.31
64	MCU 7 x G.Cot 16	-4.13	-13.53	3.67
65	G.Cot 16 x Suraj	13.96	7.86	6.49
66	G.Cot 16 x Surabhi	-17.29	-21.29	-13.96
67	G.Cot 16 x Khandwa 2	24.90*	16.43	14.95
68	G.Cot 16 x Anjali	15.86	12.00	18.48

Contd...

Table 26. Contd..

SI. No.	Hybrids	Number of sympodial branches/plant		
		d_i	d_{ii}	d_{iii}
69	G.Cot 16 x KC 2	1.92	-3.39	6.49
70	G.Cot 16 x KC 3	-3.83	-6.12	-2.68
71	G.Cot 16 x MCU 5	2.67	-12.89	23.41
72	G.Cot 16 x MCU 7	1.29	-7.65	10.72

*significant at 5 per cent level, ** significant at 1 per cent level

d_i = Relative heterosis

d_{ii} = Heterobeltiosis

d_{iii} = Standard heterosis

Table 27. Expression of heterosis for number of bolls per plant

SI. No.	Hybrids	Number of bolls per plant		
		d _i	d _{ii}	d _{iii}
1	Suraj x Surabhi	9.73	9.45	3.48
2	Suraj x Khandwa 2	26.75*	22.00	14.77
3	Suraj x Anjali	-6.67	-10.91	-7.81
4	Suraj x KC 2	-1.27	-2.50	-8.28
5	Suraj x KC 3	17.45	11.16	17.12
6	Suraj x MCU 5	14.61	4.08	19.94
7	Suraj x MCU 7	10.10	6.02	7.71
8	Suraj x G.Cot 16	16.67	14.42	11.95
9	Surabhi x Suraj	20.63	20.63	13.50
10	Surabhi x Khandwa 2	36.62**	31.50*	23.71
11	Surabhi x Anjali	32.21**	26.20*	30.57*
12	Surabhi x KC 2	26.08*	24.50	17.12
13	Surabhi x KC 3	20.28	13.84	19.94
14	Surabhi x MCU 5	7.87	-2.04	12.89
15	Surabhi x MCU 7	22.60	18.06	19.94
16	Surabhi x G.Cot 16	11.76	9.62	7.24
17	Khandwa 2 x Suraj	59.47**	51.50**	42.52**
18	Khandwa 2 x Surabhi	33.86**	26.87	19.94
19	Khandwa 2 x Anjali	36.82**	24.39	28.69*
20	Khandwa 2 x KC 2	8.80	4.62	-4.05
21	Khandwa 2 x KC 3	4.38	-5.87	-0.85
22	Khandwa 2 x MCU 5	1.18	-12.24	1.13

Contd...

Table 27. Contd..

SI. No.	Hybrids	Number of bolls per plant		
		d_i	d_{ii}	d_{iii}
23	Khandwa 2 x MCU 7	8.21	-0.81	0.75
24	Khandwa 2 x G.Cot 16	9.79	2.40	0.19
25	Anjali x Suraj	21.43	15.91	19.94
26	Anjali x Surabhi	18.53	13.41	17.36
27	Anjali x Khandwa 2	6.67	-1.82	1.60
28	Anjali x KC 2	5.06	-0.91	2.54
29	Anjali x KC 3	10.36	9.37	15.24
30	Anjali x MCU 5	22.58*	16.33	34.05**
31	Anjali x MCU 7	5.50	4.55	8.18
32	Anjali x G.Cot 16	-1.87	-4.55	-1.22
33	KC 2 x Suraj	33.50**	33.50*	25.59*
34	KC 2 x Surabhi	24.69*	24.38	17.59
35	KC 2 x Khandwa 2	42.34**	37.00**	28.88*
36	KC 2 x Anjali	2.38	-2.27	1.13
37	KC 2 x KC 3	14.62	8.48	14.30
38	KC 2 x MCU 5	21.35*	10.20	27.00*
39	KC 2 x MCU 7	5.29	1.39	3.01
40	KC 2 x G.Cot 16	0.49	-1.44	-3.57
41	KC 3 x Suraj	4.29	-0.45	3.01
42	KC 3 x Surabhi	11.16	6.36	10.07
43	KC 3 x Khandwa 2	16.05	6.82	10.54
44	KC 3 x Anjali	22.73*	22.73	27.00*
45	KC 3 x KC 2	22.89*	15.91	19.94

Contd...

Table 27. Contd..

SI. No.	Hybrids	Number of bolls per plant		
		d_i	d_{ii}	d_{iii}
46	KC 3 x MCU 5	12.69	6.94	23.24
47	KC 3 x MCU 7	26.15*	25.00*	29.35*
48	KC 3 x G.Cot 16	13.55	10.45	14.30
49	MCU 5 x Suraj	23.18*	12.92	27.47*
50	MCU 5 x Surabhi	1.59	-6.67	5.36
51	MCU 5 x Khandwa 2	15.60	2.35	15.52
52	MCU 5 x Anjali	-9.72	-13.48	-2.35
53	MCU 5 x KC 2	-8.62	-17.19	-6.49
54	MCU 5 x KC 3	-12.07	-15.00	-4.05
55	MCU 5 x MCU 7	23.68*	17.50	32.64*
56	MCU 5 x G.Cot 16	-12.05	-17.92	-7.34
57	MCU 7 x Suraj	3.33	-1.36	2.07
58	MCU 7 x Surabhi	13.06	8.18	11.95
59	MCU 7 x Khandwa 2	22.47	12.73	16.65
60	MCU 7 x Anjali	27.27*	27.27*	31.70*
61	MCU 7 x KC 2	5.06	-0.91	2.54
62	MCU 7 x KC 3	-7.09	-7.92	-2.96
63	MCU 7 x MCU 5	13.98	8.16	24.65
64	MCU 7 x G.Cot 16	-7.94	-10.45	-7.34
65	G.Cot 16 x Suraj	6.34	3.81	2.54
66	G.Cot 16 x Surabhi	-4.14	-6.19	-7.34
67	G.Cot 16 x Khandwa 2	25.57*	18.10	16.65
68	G.Cot 16 x Anjali	12.56	10.00	13.83

Contd...

Table 27. Contd..

SI. No.	Hybrids	Number of bolls per plant		
		d_i	d_{ii}	d_{iii}
69	G.Cot 16 x KC 2	28.15*	23.57	22.06
70	G.Cot 16 x KC 3	-5.53	-8.48	-3.57
71	G.Cot 16 x MCU 5	12.09	4.08	19.94
72	G.Cot 16 x MCU 7	29.58**	27.78*	29.82*

*significant at 5 per cent level, ** significant at 1 per cent level

d_i = Relative heterosis

d_{ii} = Heterobeltiosis

d_{iii} = Standard heterosis

Table 28. Expression of heterosis for boll weight (g)

SI. No.	Hybrids	Boll weight		
		d _i	d _{ii}	d _{iii}
1	Suraj x Surabhi	2.37	-4.90	19.00*
2	Suraj x Khandwa 2	-7.58	-17.70*	2.75
3	Suraj x Anjali	1.95	-3.50	20.50*
4	Suraj x KC 2	2.25	-4.50	19.25*
5	Suraj x KC 3	-15.72*	-25.20**	-6.50
6	Suraj x MCU 5	-13.19	-17.10*	3.50
7	Suraj x MCU 7	4.91	-8.20	14.75
8	Suraj x G.Cot 16	9.05	-1.80	22.75*
9	Surabhi x Suraj	-8.88	-13.98	-3.00
10	Surabhi x Khandwa 2	-4.24	-5.38	-5.50
11	Surabhi x Anjali	-0.30	-5.49	5.50
12	Surabhi x KC 2	-3.96	-7.72	0.25
13	Surabhi x KC 3	10.48	8.75	8.75
14	Surabhi x MCU 5	-2.22	-8.13	4.50
15	Surabhi x MCU 7	16.00	12.37	12.25
16	Surabhi x G.Cot 16	-2.56	-2.62	-2.50
17	Khandwa 2 x Suraj	1.82	-3.88	8.25
18	Khandwa 2 x Surabhi	-0.72	-4.08	3.00
19	Khandwa 2 x Anjali	-7.27	-12.09	-1.75
20	Khandwa 2 x KC 2	-2.88	-6.68	1.25
21	Khandwa 2 x KC 3	-3.87	-5.37	-5.25
22	Khandwa 2 x MCU 5	-10.99	-16.37*	-5.00

Contd...

Table 28. Contd..

SI. No.	Hybrids	Boll weight		
		d _i	d _{ii}	d _{iii}
23	Khandwa 2 x MCU 7	12.77	9.25	9.25
24	Khandwa 2 x G.Cot 16	0.56	0.50	0.75
25	Anjali x Suraj	14.99	8.55	22.25*
26	Anjali x Surabhi	0.72	-2.68	4.50
27	Anjali x Khandwa 2	7.91	6.62	6.50
28	Anjali x KC 2	17.87*	13.25	22.75*
29	Anjali x KC 3	-7.68	-9.13	-9.25
30	Anjali x MCU 5	-4.33	-10.11	2.25
31	Anjali x MCU 7	2.45	-0.75	-0.75
32	Anjali x G.Cot 16	8.43	8.36	8.50
33	KC 2 x Suraj	12.29	5.99	19.50*
34	KC 2 x Surabhi	15.44	11.54	19.50*
35	KC 2 x Khandwa 2	8.03	6.75	6.75
36	KC 2 x Anjali	10.57	4.82	17.00
37	KC 2 x KC 3	7.30	5.62	5.50
38	KC 2 x MCU 5	-13.68	-18.90*	-7.75
39	KC 2 x MCU 7	28.13**	24.13*	24.25*
40	KC 2 x G.Cot 16	6.56	6.49	6.50
41	KC 3 x Suraj	7.23	1.22	14.00
42	KC 3 x Surabhi	-14.35	-17.25	-11.25
43	KC 3 x Khandwa 2	-1.45	-2.63	-2.75
44	KC 3 x Anjali	-1.12	-6.27	4.50
45	KC 3 x KC 2	-12.95	-16.36	-9.25

Contd...

Table 28. Contd..

SI. No.	Hybrids	Boll weight		
		d_i	d_{ii}	d_{iii}
46	KC 3 x MCU 5	-7.72	-13.30	-1.25
47	KC 3 x MCU 7	18.19*	14.50	14.50
48	KC 3 x G.Cot 16	-8.31	-8.36	-8.25
49	MCU 5 x Suraj	-3.95	-8.70	14.25
50	MCU 5 x Surabhi	-7.86	-14.40	7.00
51	MCU 5 x Khandwa 2	-5.22	-15.60*	5.50
52	MCU 5 x Anjali	-3.86	-9.00	13.75
53	MCU 5 x KC 2	-12.10	-17.90*	2.75
54	MCU 5 x KC 3	-8.62	-18.90*	1.50
55	MCU 5 x MCU 7	0.23	-12.30	9.75
56	MCU 5 x G.Cot 16	-24.93**	-32.40**	-15.50
57	MCU 7 x Suraj	-6.53	-11.76	-0.75
58	MCU 7 x Surabhi	4.34	0.82	8.00
59	MCU 7 x Khandwa 2	2.97	1.75	1.75
60	MCU 7 x Anjali	6.91	1.34	13.25
61	MCU 7 x KC 2	-4.20	-7.95	-0.25
62	MCU 7 x KC 3	-4.51	-6.00	-6.00
63	MCU 7 x MCU 5	3.63	-2.64	10.75
64	MCU 7 x G.Cot 16	3.31	3.25	3.50
65	G.Cot 16 x Suraj	-1.70	-7.21	4.50
66	G.Cot 16 x Surabhi	-0.84	-4.20	2.75
67	G.Cot 16 x Khandwa 2	2.09	0.87	0.75
68	G.Cot 16 x Anjali	6.91	1.34	13.00

Contd...

Table 28. Contd..

SI. No.	Hybrids	Boll weight		
		d_i	d_{ii}	d_{iii}
69	G.Cot 16 x KC 2	0.84	-3.11	5.00
70	G.Cot 16 x KC 3	19.49*	17.62	17.50
71	G.Cot 16 x MCU 5	-5.96	-11.65	0.50
72	G.Cot 16 x MCU 7	7.10	3.75	3.75

*significant at 5 per cent level, ** significant at 1 per cent level

d_i = Relative heterosis

d_{ii} = Heterobeltiosis

d_{iii} = Standard heterosis

heterosis over the check MCU 13. Among the seventy two hybrids, four hybrids recorded a positive significant relative heterosis, one hybrid showed positive significant heterobeltiosis and nine hybrids showed positive significant standard heterosis (Table 28).

4.4.6. Single plant yield (g)

Out of seventy two hybrids, thirty two hybrids recorded a positive significant relative heterosis, twenty hybrids showed a positive significant heterobeltiosis and four hybrids showed a positive significant standard heterosis (Table 29). The hybrid MCU 5 x MCU 7 recorded positive significant relative heterosis (33.80%), heterobeltiosis (32.19%) and standard heterosis (27.40%) followed by KC 2 x MCU 5 with positive significant values of relative heterosis (31.82%), heterobeltiosis (25.53%) and standard heterosis (22.18%) and also hybrid Anjali x MCU 5 recorded positive significant relative heterosis (25.70%), heterobeltiosis (24.02%) and standard heterosis (20.72%).

4.4.7. Ginning outturn (%)

The hybrid MCU 7 x KC 2 recorded the maximum positive significant relative heterosis (17.90%) and heterobeltiosis (16.06%) followed by MCU 5 x G.Cot 16 with positive significant values of relative heterosis (15.59%), heterobeltiosis (13.61%) and standard heterosis (15.45%). The hybrid KC 3 x G.Cot 16 recorded the lowest negative significant relative heterosis (-30.31%), heterobeltiosis (-31.50%) and standard heterosis (-30.37%). Among seventy two hybrids, twenty seven hybrids recorded a positive significant relative heterosis, twenty hybrids showed a positive significant heterobeltiosis and twenty one hybrids showed a positive significant standard heterosis (Table 30).

4.3.8. Lint index

The magnitude of relative heterosis ranges from -25.56% (G.Cot 16 x MCU 5) to 29.65% (MCU 5 x Khandwa 2) whereas, eight hybrids exhibited positive significant heterosis. The range of heterobeltiosis was -31.08% (G.Cot 16 x MCU 5) to 18.50% (MCU 5 x Khandwa 2). None of the hybrids exhibited positive significant heterosis over the better parent. But nine hybrids exhibited negative significant heterosis for heterobeltiosis. The standard heterosis ranges from -36.22% (Khandwa 2 x KC 2) to

Table 29. Expression of heterosis for single plant yield (g)

SI. No.	Hybrids	Single plant yield		
		d_i	d_{ii}	d_{iii}
1	Suraj x Surabhi	28.96**	26.50**	12.52
2	Suraj x Khandwa 2	29.10**	27.55**	9.45
3	Suraj x Anjali	2.54	-2.33	-7.19
4	Suraj x KC 2	17.26*	15.99	1.74
5	Suraj x KC 3	-2.83	-5.26	-14.03
6	Suraj x MCU 5	21.90**	14.68*	11.62
7	Suraj x MCU 7	3.00	-1.79	-6.88
8	Suraj x G.Cot 16	28.14**	24.90**	7.18
9	Surabhi x Suraj	-5.13	-7.15	-16.75*
10	Surabhi x Khandwa 2	10.56	7.21	-4.42
11	Surabhi x Anjali	23.75**	20.05**	13.47
12	Surabhi x KC 2	-9.46	-10.19	-19.93**
13	Surabhi x KC 3	16.51*	15.75	4.43
14	Surabhi x MCU 5	-6.80	-10.71	-13.09
15	Surabhi x MCU 7	14.51*	11.21	5.09
16	Surabhi x G.Cot 16	13.64	8.74	-3.05
17	Khandwa 2 x Suraj	34.79**	33.39**	13.49
18	Khandwa 2 x Surabhi	20.35**	16.54*	3.99
19	Khandwa 2 x Anjali	6.25	-0.05	-5.07
20	Khandwa 2 x KC 2	2.93	0.51	-11.85
21	Khandwa 2 x KC 3	-13.70	-16.93*	-24.28**
22	Khandwa 2 x MCU 5	16.13*	7.93	5.05

Contd...

Table 29. Contd..

SI. No.	Hybrids	Single plant yield		
		d_i	d_{ii}	d_{iii}
23	Khandwa 2 x MCU 7	-3.85	-9.45	-13.93
24	Khandwa 2 x G.Cot 16	5.44	4.11	-12.98
25	Anjali x Suraj	29.51**	23.11**	16.17*
26	Anjali x Surabhi	-6.14	-8.86	-13.67
27	Anjali x Khandwa 2	-13.26	-18.29*	-21.99**
28	Anjali x KC 2	-1.04	-4.71	-9.73
29	Anjali x KC 3	-14.62*	-16.60*	-20.43**
30	Anjali x MCU 5	25.70**	24.02**	20.72**
31	Anjali x MCU 7	17.92**	17.85*	11.32
32	Anjali x G.Cot 16	-9.66	-15.98*	-20.41**
33	KC 2 x Suraj	22.57**	20.70*	6.09
34	KC 2 x Surabhi	23.90**	23.08**	9.82
35	KC 2 x Khandwa 2	11.99	9.25	-3.71
36	KC 2 x Anjali	-4.95	-8.36	-13.09
37	KC 2 x KC 3	6.93	5.58	-4.50
38	KC 2 x MCU 5	31.82**	25.53**	22.18**
39	KC 2 x MCU 7	16.29*	12.25	6.04
40	KC 2 x G.Cot 16	-5.12	-8.66	-19.58*
41	KC 3 x Suraj	-6.95	-9.48	-17.79*
42	KC 3 x Surabhi	-14.53*	-15.03	-23.30**
43	KC 3 x Khandwa 2	21.31**	16.92*	5.40
44	KC 3 x Anjali	23.61**	20.64**	14.40
45	KC 3 x KC 2	20.33**	18.62*	6.88

Contd...

Table 29. Contd..

SI. No.	Hybrids	Single plant yield		
		d _i	d _{ii}	d _{iii}
46	KC 3 x MCU 5	-7.80	-11.14	-13.52
47	KC 3 x MCU 7	17.81**	15.11*	8.66
48	KC 3 x G.Cot 16	-7.03	-11.57	-20.17**
49	MCU 5 x Suraj	16.28*	9.33	5.83
50	MCU 5 x Surabhi	6.79	2.53	-0.58
51	MCU 5 x Khandwa 2	8.79	1.37	-1.67
52	MCU 5 x Anjali	10.11	8.90	5.58
53	MCU 5 x KC 2	4.30	-0.67	-3.59
54	MCU 5 x KC 3	-8.27	-11.40	-14.10
55	MCU 5 x MCU 7	33.80**	32.19**	27.40**
56	MCU 5 x G.Cot 16	1.89	-6.25	-9.11
57	MCU 7 x Suraj	16.35 *	10.59	4.63
58	MCU 7 x Surabhi	-7.74	-10.42	-15.15*
59	MCU 7 x Khandwa 2	20.14**	13.18	7.02
60	MCU 7 x Anjali	18.35**	18.29*	12.17
61	MCU 7 x KC 2	18.77**	14.37	8.11
62	MCU 7 x KC 3	-21.33**	-23.15**	-27.20**
63	MCU 7 x MCU 5	15.18*	13.64	10.32
64	MCU 7 x G.Cot 16	-26.60**	-31.74**	-35.33**
65	G.Cot 16 x Suraj	-4.70	-6.93	-19.99**
66	G.Cot 16 x Surabhi	4.01	-0.57	-11.29
67	G.Cot 16 x Khandwa 2	36.44**	34.50**	12.28
68	G.Cot 16 x Anjali	12.97	4.94	-0.49

Contd...

Table 29. Contd..

SI. No.	Hybrids	Single plant yield		
		d_i	d_{ii}	d_{iii}
69	G.Cot 16 x KC 2	8.34	4.42	-8.19
70	G.Cot 16 x KC 3	12.90	7.29	-3.08
71	G.Cot 16 x MCU 5	22.59**	12.53	9.27
72	G.Cot 16 x MCU 7	14.84*	6.79	1.05

*significant at 5 per cent level, ** significant at 1 per cent level

d_i = Relative heterosis

d_{ii} = Heterobeltiosis

d_{iii} = Standard heterosis

Table 30. Expression of heterosis for ginning outturn (%)

SI. No.	Hybrids	Ginning outturn		
		d_i	d_{ii}	d_{iii}
1	Suraj x Surabhi	-8.85**	-10.34**	-8.89**
2	Suraj x Khandwa 2	-1.73	-7.69**	-6.18**
3	Suraj x Anjali	5.08*	3.64	5.34*
4	Suraj x KC 2	-1.19	-3.97	-2.41
5	Suraj x KC 3	-6.73**	-7.15**	-4.79*
6	Suraj x MCU 5	-0.03	-0.49	1.13
7	Suraj x MCU 7	17.37**	13.16**	14.98**
8	Suraj x G.Cot 16	-0.50	-2.20	-0.61
9	Surabhi x Suraj	0.28	-0.45	-0.26
10	Surabhi x Khandwa 2	-10.19**	-14.47**	-15.56**
11	Surabhi x Anjali	-7.35**	-7.40**	-8.48**
12	Surabhi x KC 2	9.65**	8.09**	6.71**
13	Surabhi x KC 3	-5.71**	-7.46**	-5.11*
14	Surabhi x MCU 5	3.80	2.78	3.51
15	Surabhi x MCU 7	1.44	-0.81	-2.09
16	Surabhi x G.Cot 16	1.14	0.85	-0.44
17	Khandwa 2 x Suraj	7.96**	2.48	2.67
18	Khandwa 2 x Surabhi	6.23**	1.76	0.00
19	Khandwa 2 x Anjali	11.39**	6.42**	5.17*
20	Khandwa 2 x KC 2	-15.82**	-18.41**	-21.75**
21	Khandwa 2 x KC 3	5.81**	-0.65	1.86
22	Khandwa 2 x MCU 5	0.11	-5.20*	-4.53

Contd...

Table 30. Contd..

SI. No.	Hybrids	Ginning outturn		
		d _i	d _{ii}	d _{iii}
23	Khandwa 2 x MCU 7	1.89	-0.45	-6.07*
24	Khandwa 2 x G.Cot 16	-6.30**	-10.19**	-11.85**
25	Anjali x Suraj	9.10**	8.30**	8.51**
26	Anjali x Surabhi	-8.31**	-8.51**	-9.70**
27	Anjali x Khandwa 2	15.63**	10.12**	8.71**
28	Anjali x KC 2	-9.55**	-10.84**	-11.96**
29	Anjali x KC 3	-11.12**	-12.77**	-10.54**
30	Anjali x MCU 5	-11.12**	-12.00**	-11.38**
31	Anjali x MCU 7	13.73**	11.21**	9.79**
32	Anjali x G.Cot 16	-8.64**	-8.90**	-10.05**
33	KC 2 x Suraj	-2.08	-4.22	-4.04
34	KC 2 x Surabhi	-25.21**	-26.14**	-27.41**
35	KC 2 x Khandwa 2	9.22**	5.52*	1.10
36	KC 2 x Anjali	-21.72**	-22.91**	-23.81**
37	KC 2 x KC 3	14.32**	10.58**	13.39**
38	KC 2 x MCU 5	-8.01**	-10.24**	-9.61**
39	KC 2 x MCU 7	8.20**	7.36**	2.87
40	KC 2 x G.Cot 16	-2.09	-3.25	-5.02*
41	KC 3 x Suraj	8.48**	7.71**	9.47**
42	KC 3 x Surabhi	-3.38	-4.97*	-3.43
43	KC 3 x Khandwa 2	-14.67**	-19.84**	-18.52**
44	KC 3 x Anjali	12.01**	10.47**	12.28**
45	KC 3 x KC 2	-2.90	-5.63*	-4.09

Contd...

Table 30. Contd..

SI. No.	Hybrids	Ginning outturn		
		d _i	d _{ii}	d _{iii}
46	KC 3 x MCU 5	6.00**	5.51*	7.23**
47	KC 3 x MCU 7	7.59**	3.73	5.43*
48	KC 3 x G.Cot 16	-30.31**	-31.50**	-30.37**
49	MCU 5 x Suraj	0.53	-0.19	1.42
50	MCU 5 x Surabhi	-9.62**	-11.10**	-9.67**
51	MCU 5 x Khandwa 2	9.72**	3.07	4.76*
52	MCU 5 x Anjali	-5.49**	-6.79**	-5.26*
53	MCU 5 x KC 2	-13.46**	-15.90**	-14.52**
54	MCU 5 x KC 3	4.63*	4.16	6.79**
55	MCU 5 x MCU 7	-10.55**	-13.76**	-12.37**
56	MCU 5 x G.Cot 16	15.59**	13.61**	15.45**
57	MCU 7 x Suraj	0.25	-3.39	-3.22
58	MCU 7 x Surabhi	-16.63**	-18.91**	-20.30**
59	MCU 7 x Khandwa 2	15.85**	13.61**	5.55*
60	MCU 7 x Anjali	10.58**	7.27**	6.01*
61	MCU 7 x KC 2	17.90**	16.06**	11.30**
62	MCU 7 x KC 3	-4.29*	-8.78**	-6.45**
63	MCU 7 x MCU 5	12.25**	7.92**	8.65**
64	MCU 7 x G.Cot 16	-5.66**	-8.18**	-9.87**
65	G.Cot 16 x Suraj	-11.61**	-12.26**	-12.08**
66	G.Cot 16 x Surabhi	-15.53**	-15.72**	-16.81**
67	G.Cot 16 x Khandwa 2	9.91**	4.68*	3.34
68	G.Cot 16 x Anjali	7.92**	7.86**	6.62**

Contd...

Table 30. Contd..

SI. No.	Hybrids	Ginning outturn		
		d_i	d_{ii}	d_{iii}
69	G.Cot 16 x KC 2	-3.49	-4.87*	-6.07*
70	G.Cot 16 x KC 3	3.38	1.46	4.04
71	G.Cot 16 x MCU 5	-22.70**	-23.46**	-22.91**
72	G.Cot 16 x MCU 7	11.60**	9.12**	7.72**

*significant at 5 per cent level, ** significant at 1 per cent level

d_i = Relative heterosis

d_{ii} = Heterobeltiosis

d_{iii} = Standard heterosis

Table 31. Expression of heterosis for lint index

SI. No.	Hybrids	Lint index		
		d _i	d _{ii}	d _{iii}
1	Suraj x Surabhi	3.19	1.80	-11.79
2	Suraj x Khandwa 2	10.07	0.60	-12.82
3	Suraj x Anjali	1.95	-0.57	-9.36
4	Suraj x KC 2	4.72	3.00	-7.80
5	Suraj x KC 3	-2.58	-6.84	-11.44
6	Suraj x MCU 5	3.07	1.96	-9.71
7	Suraj x MCU 7	15.39	14.20	1.04
8	Suraj x G.Cot 16	1.12	-5.09	-6.24
9	Surabhi x Suraj	-3.82	-6.92	-13.86
10	Surabhi x Khandwa 2	-3.83	-12.10	-23.92**
11	Surabhi x Anjali	-10.33	-12.55	-20.28*
12	Surabhi x KC 2	2.65	0.97	-9.53
13	Surabhi x KC 3	0.00	-4.38	-9.19
14	Surabhi x MCU 5	15.92	14.68	1.56
15	Surabhi x MCU 7	2.33	1.27	-10.40
16	Surabhi x G.Cot 16	-6.82	-12.54	-13.69
17	Khandwa 2 x Suraj	13.22	-1.03	-8.32
18	Khandwa 2 x Surabhi	22.39*	11.51	-5.89
19	Khandwa 2 x Anjali	16.95	2.95	-6.24
20	Khandwa 2 x KC 2	-19.85*	-28.92**	-36.22**
21	Khandwa 2 x KC 3	1.05	-12.59	-16.98*
22	Khandwa 2 x MCU 5	10.32	-1.66	-13.00

Contd...

Table 31. Contd..

SI. No.	Hybrids	Lint index		
		d_i	d_{ii}	d_{iii}
23	Khandwa 2 x MCU 7	23.23*	9.89	-2.77
24	Khandwa 2 x G.Cot 16	-4.95	-19.12*	-20.10*
25	Anjali x Suraj	19.77*	15.90	7.28
26	Anjali x Surabhi	-2.48	-3.80	-16.64*
27	Anjali x Khandwa 2	21.33*	10.90	-3.81
28	Anjali x KC 2	-3.34	-4.93	-14.90
29	Anjali x KC 3	-13.55	-17.34	-21.49**
30	Anjali x MCU 5	-4.45	-5.48	-16.29*
31	Anjali x MCU 7	6.98	5.88	-6.41
32	Anjali x G.Cot 16	-12.80	-18.16*	-19.24*
33	KC 2 x Suraj	0.72	-2.53	-9.71
34	KC 2 x Surabhi	-12.72	-13.90	-25.30**
35	KC 2 x Khandwa 2	7.44	-1.80	-14.90
36	KC 2 x Anjali	-16.18	-18.25	-25.48**
37	KC 2 x KC 3	4.96	0.36	-4.68
38	KC 2 x MCU 5	-13.55	-14.48	-24.26**
39	KC 2 x MCU 7	-7.47	-8.42	-18.89*
40	KC 2 x G.Cot 16	7.48	0.88	-0.35
41	KC 3 x Suraj	11.16	7.58	-0.35
42	KC 3 x Surabhi	8.06	6.60	-7.63
43	KC 3 x Khandwa 2	-12.36	-19.90*	-30.50**
44	KC 3 x Anjali	20.47*	17.49	7.11
45	KC 3 x KC 2	12.68	10.83	-0.69

Contd...

Table 31. Contd..

SI. No.	Hybrids	Lint index		
		d_i	d_{ii}	d_{iii}
46	KC 3 x MCU 5	5.44	4.31	-7.63
47	KC 3 x MCU 7	17.96*	16.75	3.29
48	KC 3 x G.Cot 16	-21.40**	-26.23**	-27.21**
49	MCU 5 x Suraj	14.26	10.57	2.43
50	MCU 5 x Surabhi	15.15	13.60	-1.56
51	MCU 5 x Khandwa 2	29.65**	18.50	2.77
52	MCU 5 x Anjali	-2.63	-5.04	-13.52
53	MCU 5 x KC 2	-14.36	-15.76	-24.44**
54	MCU 5 x KC 3	11.07	6.20	0.87
55	MCU 5 x MCU 7	-9.95	-10.87	-21.14*
56	MCU 5 x G.Cot 16	8.04	1.40	0.17
57	MCU 7 x Suraj	-6.43	-9.45	-16.12
58	MCU 7 x Surabhi	-20.73*	-21.80*	-32.24**
59	MCU 7 x Khandwa 2	25.49**	14.70	-0.69
60	MCU 7 x Anjali	5.85	3.23	-5.89
61	MCU 7 x KC 2	-2.26	-3.87	-13.86
62	MCU 7 x KC 3	-7.82	-11.86	-16.29*
63	MCU 7 x MCU 5	-12.56	-13.50	-23.40**
64	MCU 7 x G.Cot 16	-20.84*	-25.70**	-26.69**
65	G.Cot 16 x Suraj	-3.75	-9.00	-5.37
66	G.Cot 16 x Surabhi	-15.14	-23.17**	-20.10*
67	G.Cot 16 x Khandwa 2	10.65	-6.50	-2.77
68	G.Cot 16 x Anjali	1.24	-5.00	-1.21

Contd...

Table 31. Contd..

SI. No.	Hybrids	Lint index		
		d_i	d_{ii}	d_{iii}
69	G.Cot 16 x KC 2	0.45	-6.50	-2.77
70	G.Cot 16 x KC 3	-7.58	-11.58	-7.97
71	G.Cot 16 x MCU 5	-25.56**	-31.08**	-28.25**
72	G.Cot 16 x MCU 7	5.45	-2.42	1.56

*significant at 5 per cent level, ** significant at 1 per cent level

d_i = Relative heterosis

d_{ii} = Heterobeltiosis

d_{iii} = Standard heterosis

7.28% (Anjali x Suraj). None of the hybrids exhibited positive significant standard heterosis, but twenty three hybrids exhibited negative significant for this trait (Table 31).

4.4.9. Seed index

The mid parent heterosis ranges from -28.24% (MCU 7 x MCU 5) to 36.47% (KC 2 x Anjali). Out of seventy two hybrids, nine hybrids exhibited a positive significant relative heterosis whereas negative significant expression over mid parent was observed in two hybrids namely, MCU 7 x KC 2 (-25.52) and MCU 7 x MCU 5 (-28.24). Both positive significant and negative significant expression of heterobeltiosis were exhibited in three hybrids over the better parent. The lowest (-32.73%) and highest (29.00%) values of heterobeltiosis was recorded in MCU 7 x MCU 5 and KC 2 x Surabhi, respectively. The range of standard heterosis varies from -32.67% (MCU 7 x MCU 5) to 21.20% (KC 3 x G.Cot 16) for this trait. Only one hybrid recorded a positive significant heterosis and eight hybrids exhibited a negative significant heterosis over the check MCU 13 (Table 32).

4.4.10. 2.5% span length (mm)

The hybrid Suraj x MCU 7 recorded the maximum positive significant relative heterosis (34.82%) and heterobeltiosis (27.41%) followed by Suraj x Khandwa 2 with positive significant values of relative heterosis (31.49%) and heterobeltiosis (24.80%). The hybrid KC 3 x MCU 5 recorded the minimum negative significant relative heterosis (-13.98%), heterobeltiosis (-18.49%) and standard heterosis (-5.82%). Out of seventy two hybrids, sixty one, thirty eight and thirty nine hybrids showed a positive significant heterosis over the mid parent, better parent and standard check, respectively (Table 33).

4.4.11. Bundle strength (g/tex)

The hybrid Anjali x KC 2 recorded both highest positive significant relative heterosis (17.18%) and heterobeltiosis (11.81%) whereas, hybrid Khandwa 2 x Suraj recorded lowest negative significant relative heterosis (-12.31%), heterobeltiosis (-14.09%) and also standard heterosis (-12.44%). Out of seventy two hybrids, forty eight, nineteen and thirty four hybrids recorded a positive significant heterosis over the mid

Table 32. Expression of heterosis for seed index

SI. No.	Hybrids	Seed index		
		d_i	d_{ii}	d_{iii}
1	Suraj x Surabhi	14.42	11.30	1.27
2	Suraj x Khandwa 2	9.11	5.40	-4.09
3	Suraj x Anjali	3.61	-8.10	-16.38
4	Suraj x KC 2	2.74	0.43	-4.28
5	Suraj x KC 3	4.49	4.28	-4.73
6	Suraj x MCU 5	-0.48	-2.35	-11.19
7	Suraj x MCU 7	-13.73	-16.21	-19.11*
8	Suraj x G.Cot 16	-1.37	-6.46	-5.10
9	Surabhi x Suraj	-0.63	-6.21	-13.47
10	Surabhi x Khandwa 2	16.87	14.86	-2.64
11	Surabhi x Anjali	20.55	12.11	-8.19
12	Surabhi x KC 2	-7.50	-13.99	-18.02
13	Surabhi x KC 3	13.03	7.17	-2.09
14	Surabhi x MCU 5	13.88	10.18	-3.55
15	Surabhi x MCU 7	3.52	-4.34	-7.64
16	Surabhi x G.Cot 16	-5.06	-14.22	-12.92
17	Khandwa 2 x Suraj	1.15	-4.54	-11.92
18	Khandwa 2 x Surabhi	11.79	9.10	-6.10
19	Khandwa 2 x Anjali	13.86	5.89	-13.28
20	Khandwa 2 x KC 2	2.16	-5.01	-9.55
21	Khandwa 2 x KC 3	-7.25	-12.05	-19.65*
22	Khandwa 2 x MCU 5	10.17	6.60	-6.64

Contd...

Table 32. Contd..

SI. No.	Hybrids	Seed index		
		d_i	d_{ii}	d_{iii}
23	Khandwa 2 x MCU 7	19.68*	10.60	6.82
24	Khandwa 2 x G.Cot 16	4.81	-5.29	-3.91
25	Anjali x Suraj	14.44	2.37	-5.55
26	Anjali x Surabhi	21.91*	12.53	-3.18
27	Anjali x Khandwa 2	7.97	0.32	-14.92
28	Anjali x KC 2	22.31*	7.88	2.82
29	Anjali x KC 3	12.80	1.34	-7.37
30	Anjali x MCU 5	24.65*	14.13	-0.09
31	Anjali x MCU 7	-4.51	-16.26	-19.11*
32	Anjali x G.Cot 16	8.56	-6.77	-5.37
33	KC 2 x Suraj	4.77	4.04	-4.00
34	KC 2 x Surabhi	32.61**	29.00**	17.38
35	KC 2 x Khandwa 2	-3.99	-7.25	-15.65
36	KC 2 x Anjali	36.47**	21.05	10.10
37	KC 2 x KC 3	-14.32	-14.49	-21.84*
38	KC 2 x MCU 5	-1.61	-3.45	-12.19
39	KC 2 x MCU 7	-17.32	-19.70	-22.47*
40	KC 2 x G.Cot 16	11.82	6.05	7.64
41	KC 3 x Suraj	-5.61	-6.26	-13.47
42	KC 3 x Surabhi	9.74	6.75	-2.91
43	KC 3 x Khandwa 2	6.37	2.75	-6.55
44	KC 3 x Anjali	10.54	-1.95	-10.74
45	KC 3 x KC 2	13.43	10.89	5.64

Contd...

Table 32. Contd..

SI. No.	Hybrids	Seed index		
		d_i	d_{ii}	d_{iii}
46	KC 3 x MCU 5	-7.26	-9.00	-17.20
47	KC 3 x MCU 7	1.50	-1.41	-4.82
48	KC 3 x G.Cot 16	25.96**	19.46*	21.20*
49	MCU 5 x Suraj	9.33	8.58	0.18
50	MCU 5 x Surabhi	29.27**	25.75*	14.47
51	MCU 5 x Khandwa 2	8.80	5.10	-4.37
52	MCU 5 x Anjali	16.40	3.25	-6.10
53	MCU 5 x KC 2	1.86	-0.43	-5.19
54	MCU 5 x KC 3	0.05	-0.15	-8.83
55	MCU 5 x MCU 7	2.38	-0.57	-4.00
56	MCU 5 x G.Cot 16	-17.21	-21.48*	-20.29*
57	MCU 7 x Suraj	-8.51	-12.09	-12.01
58	MCU 7 x Surabhi	1.00	-6.09	-6.01
59	MCU 7 x Khandwa 2	-1.18	-8.73	-8.64
60	MCU 7 x Anjali	0.91	-14.05	-14.01
61	MCU 7 x KC 2	-25.52**	-27.32**	-27.30**
62	MCU 7 x KC 3	-3.28	-7.50	-7.46
63	MCU 7 x MCU 5	-28.24**	-32.73**	-32.67**
64	MCU 7 x G.Cot 16	-15.08	-15.65	-14.38
65	G.Cot 16 x Suraj	18.92*	14.27	14.38
66	G.Cot 16 x Surabhi	12.30	4.41	4.46
67	G.Cot 16 x Khandwa 2	0.10	-7.55	-7.46
68	G.Cot 16 x Anjali	4.80	-10.73	-10.65

Contd...

Table 32. Contd..

SI. No.	Hybrids	Seed index		
		d_i	d_{ii}	d_{iii}
69	G.Cot 16 x KC 2	9.32	6.68	6.82
70	G.Cot 16 x KC 3	-9.70	-13.64	-13.56
71	G.Cot 16 x MCU 5	11.08	4.14	4.19
72	G.Cot 16 x MCU 7	-8.10	-9.73	-9.65

*significant at 5 per cent level, ** significant at 1 per cent level

d_i = Relative heterosis

d_{ii} = Heterobeltiosis

d_{iii} = Standard heterosis

Table 33. Expression of heterosis for 2.5% span length (mm)

SI. No.	Hybrids	2.5% span length		
		d _i	d _{ii}	d _{iii}
1	Suraj x Surabhi	17.61**	8.33**	19.76**
2	Suraj x Khandwa 2	31.49**	24.80**	16.20**
3	Suraj x Anjali	20.30**	19.01**	13.23**
4	Suraj x KC 2	19.90**	16.26**	8.24**
5	Suraj x KC 3	19.64**	13.25**	18.05**
6	Suraj x MCU 5	14.53**	3.40	19.48**
7	Suraj x MCU 7	34.82**	27.41**	18.62**
8	Suraj x G.Cot 16	23.14**	22.78**	14.31**
9	Surabhi x Suraj	6.79**	-1.09	9.14**
10	Surabhi x Khandwa 2	6.24**	-6.62**	3.03
11	Surabhi x Anjali	7.06**	-0.31	10.00**
12	Surabhi x KC 2	17.50**	5.31*	16.21**
13	Surabhi x KC 3	4.55*	1.66	12.18**
14	Surabhi x MCU 5	0.95	-1.33	14.02**
15	Surabhi x MCU 7	15.30**	0.94	11.38**
16	Surabhi x G.Cot 16	11.96**	2.94	13.58**
17	Khandwa 2 x Suraj	22.28**	14.94**	8.10**
18	Khandwa 2 x Surabhi	9.69**	-4.10	6.02*
19	Khandwa 2 x Anjali	15.14**	7.65**	2.41
20	Khandwa 2 x KC 2	21.94**	18.67**	3.78
21	Khandwa 2 x KC 3	5.07*	-5.76*	-1.76
22	Khandwa 2 x MCU 5	10.76**	-4.95*	9.83**

Contd...

Table 33. Contd..

SI. No.	Hybrids	2.5% span length		
		d_i	d_{ii}	d_{iii}
23	Khandwa 2 x MCU 7	21.42**	21.35**	0.56
24	Khandwa 2 x G.Cot 16	14.48**	8.42**	0.34
25	Anjali x Suraj	7.46**	6.07*	2.41
26	Anjali x Surabhi	18.13**	10.65**	22.33**
27	Anjali x Khandwa 2	16.94**	9.11**	5.34*
28	Anjali x KC 2	17.65**	12.11**	8.24**
29	Anjali x KC 3	2.35	-1.42	2.76
30	Anjali x MCU 5	-6.23**	-13.94**	-0.55
31	Anjali x MCU 7	14.97**	6.82*	3.14
32	Anjali x G.Cot 16	7.91**	5.68*	2.03
33	KC 2 x Suraj	15.91**	11.07**	4.46
34	KC 2 x Surabhi	14.62**	2.00	12.75**
35	KC 2 x Khandwa 2	18.38**	16.60**	0.52
36	KC 2 x Anjali	13.14**	7.83**	2.59
37	KC 2 x KC 3	4.65*	-4.40	-0.34
38	KC 2 x MCU 5	26.12**	10.10**	27.23**
39	KC 2 x MCU 7	21.74**	19.38**	2.9
40	KC 2 x G.Cot 16	9.61**	5.85*	-2.03
41	KC 3 x Suraj	8.44**	3.52	7.09**
42	KC 3 x Surabhi	12.25**	8.64**	20.11**
43	KC 3 x Khandwa 2	15.21**	4.17	7.76**
44	KC 3 x Anjali	1.41	-2.67	0.69
45	KC 3 x KC 2	1.70	-6.17*	-2.93

Contd...

Table 33. Contd..

SI. No.	Hybrids	2.5% span length		
		d_i	d_{ii}	d_{iii}
46	KC 3 x MCU 5	-13.98**	-18.49**	-5.82*
47	KC 3 x MCU 7	9.53**	-1.37	2.03
48	KC 3 x G.Cot 16	7.14**	1.50	5.00
49	MCU 5 x Suraj	8.15**	-2.54	14.25**
50	MCU 5 x Surabhi	8.72**	5.62*	23.83**
51	MCU 5 x Khandwa 2	13.12**	-3.10	13.61**
52	MCU 5 x Anjali	0.99	-8.53**	7.24**
53	MCU 5 x KC 2	7.99**	-5.74**	10.52**
54	MCU 5 x KC 3	-1.90	-7.34**	8.64**
55	MCU 5 x MCU 7	17.01**	-0.15	17.07**
56	MCU 5 x G.Cot 16	9.78**	-1.78	15.15**
57	MCU 7 x Suraj	21.52**	14.23**	7.43**
58	MCU 7 x Surabhi	17.46**	2.70	13.53**
59	MCU 7 x Khandwa 2	23.01**	22.37**	2.32
60	MCU 7 x Anjali	19.77**	11.98**	6.53*
61	MCU 7 x KC 2	19.94**	16.72**	2.07
62	MCU 7 x KC 3	6.95**	-4.07	0.00
63	MCU 7 x MCU 5	22.62**	5.22*	21.59**
64	MCU 7 x G.Cot 16	18.61**	12.33**	3.96
65	G.Cot 16 x Suraj	11.84**	11.27**	4.66
66	G.Cot 16 x Surabhi	3.30	-4.85*	5.19
67	G.Cot 16 x Khandwa 2	17.07**	11.11**	3.45
68	G.Cot 16 x Anjali	19.31**	18.03**	12.28**

Contd...

Table 33. Contd..

SI. No.	Hybrids	2.5% span length		
		d_i	d_{ii}	d_{iii}
69	G.Cot 16 x KC 2	12.41**	9.00**	1.47
70	G.Cot 16 x KC 3	0.12	-5.23*	-1.21
71	G.Cot 16 x MCU 5	-4.48*	-13.76**	-0.34
72	G.Cot 16 x MCU 7	13.27**	7.04*	-0.34

*significant at 5 per cent level, ** significant at 1 per cent level

d_i = Relative heterosis

d_{ii} = Heterobeltiosis

d_{iii} = Standard heterosis

Table 34. Expression of heterosis for bundle strength (g/tex)

SI. No.	Hybrids	Bundle strength		
		d _i	d _{ii}	d _{iii}
1	Suraj x Surabhi	7.29**	3.82	13.47**
2	Suraj x Khandwa 2	6.83**	5.48*	7.82**
3	Suraj x Anjali	7.45**	2.89	5.18*
4	Suraj x KC 2	11.13**	1.65	3.91
5	Suraj x KC 3	11.34**	7.07**	9.44**
6	Suraj x MCU 5	-1.25	-3.08	2.89
7	Suraj x MCU 7	12.18**	11.74**	14.22**
8	Suraj x G.Cot 16	10.13**	8.04**	10.44**
9	Surabhi x Suraj	2.21	-2.02	8.87**
10	Surabhi x Khandwa 2	-3.77	-8.74**	1.39
11	Surabhi x Anjali	7.49**	-1.00	10.00**
12	Surabhi x KC 2	10.95**	-2.20	8.67**
13	Surabhi x KC 3	5.46**	-2.48	8.36**
14	Surabhi x MCU 5	8.34**	5.92**	17.69**
15	Surabhi x MCU 7	-2.20	-6.46**	3.92
16	Surabhi x G.Cot 16	-0.64	-6.34**	4.07
17	Khandwa 2 x Suraj	-12.31**	-14.09**	-12.44**
18	Khandwa 2 x Surabhi	-6.03**	-10.98**	-2.71
19	Khandwa 2 x Anjali	9.50**	7.14**	4.75*
20	Khandwa 2 x KC 2	8.05**	0.86	-1.38
21	Khandwa 2 x KC 3	2.23	0.45	-1.78
22	Khandwa 2 x MCU 5	7.66**	3.41	9.78**

Contd...

Table 34. Contd..

SI. No.	Hybrids	Bundle strength		
		d_i	d_{ii}	d_{iii}
23	Khandwa 2 x MCU 7	6.11**	4.21	5.69*
24	Khandwa 2 x G.Cot 16	7.98**	7.66**	5.89*
25	Anjali x Suraj	6.51**	2.03	3.98
26	Anjali x Surabhi	10.11**	2.07	11.56**
27	Anjali x Khandwa 2	0.18	-2.99	-3.33
28	Anjali x KC 2	17.18**	11.81**	4.36
29	Anjali x KC 3	4.23	3.65	-2.18
30	Anjali x MCU 5	7.39**	0.90	7.11**
31	Anjali x MCU 7	7.46**	3.18	4.66*
32	Anjali x G.Cot 16	4.92*	2.24	0.56
33	KC 2 x Suraj	11.52**	1.96	3.91
34	KC 2 x Surabhi	10.94**	-1.67	7.47**
35	KC 2 x Khandwa 2	12.00**	3.46	3.09
36	KC 2 x Anjali	6.62**	1.43	-5.11*
37	KC 2 x KC 3	10.33**	4.52	-1.36
38	KC 2 x MCU 5	19.37**	7.16**	13.76**
39	KC 2 x MCU 7	4.54*	-4.21	-2.84
40	KC 2 x G.Cot 16	12.72**	4.74*	3.02
41	KC 3 x Suraj	11.20**	6.52**	8.56**
42	KC 3 x Surabhi	11.76**	3.60	13.23**
43	KC 3 x Khandwa 2	2.72	-0.54	-0.89
44	KC 3 x Anjali	8.44**	8.31**	1.33
45	KC 3 x KC 2	12.79**	7.62**	0.44

Contd...

Table 34. Contd..

SI. No.	Hybrids	Bundle strength		
		d_i	d_{ii}	d_{iii}
46	KC 3 x MCU 5	-1.79	-7.72**	-2.05
47	KC 3 x MCU 7	6.87**	2.61	4.07
48	KC 3 x G.Cot 16	12.22**	9.35**	7.56**
49	MCU 5 x Suraj	5.75**	3.4	10.30**
50	MCU 5 x Surabhi	8.34**	7.04**	16.98**
51	MCU 5 x Khandwa 2	6.61**	3.10	9.98**
52	MCU 5 x Anjali	8.24**	1.58	8.36**
53	MCU 5 x KC 2	2.15	-8.33**	-2.22
54	MCU 5 x KC 3	8.30**	2.06	8.87**
55	MCU 5 x MCU 7	6.77**	4.15	11.07**
56	MCU 5 x G.Cot 16	4.96*	0.87	7.59**
57	MCU 7 x Suraj	-1.20	-1.35	0.83
58	MCU 7 x Surabhi	3.17	-0.16	9.11**
59	MCU 7 x Khandwa 2	2.95	1.65	3.91
60	MCU 7 x Anjali	3.29	-1.09	1.11
61	MCU 7 x KC 2	8.85**	-0.43	1.78
62	MCU 7 x KC 3	-4.15*	-7.83**	-5.78*
63	MCU 7 x MCU 5	7.56**	5.57*	12.07**
64	MCU 7 x G.Cot 16	6.94**	4.91*	7.24**
65	G.Cot 16 x Suraj	1.71	-0.35	1.56
66	G.Cot 16 x Surabhi	-1.33	-6.53**	2.15
67	G.Cot 16 x Khandwa 2	0.63	-0.31	-0.67
68	G.Cot 16 x Anjali	3.37	1.14	-1.11

Contd...

Table 34. Contd..

SI. No.	Hybrids	Bundle strength		
		d_i	d_{ii}	d_{iii}
69	G.Cot 16 x KC 2	14.04**	6.45**	4.09
70	G.Cot 16 x KC 3	9.52**	7.61**	5.22*
71	G.Cot 16 x MCU 5	-5.07*	-8.81**	-3.19
72	G.Cot 16 x MCU 7	3.88	2.02	3.47

*significant at 5 per cent level, ** significant at 1 per cent level

d_i = Relative heterosis

d_{ii} = Heterobeltiosis

d_{iii} = Standard heterosis

parent, better parent and standard check, respectively. The hybrid MCU 5 x Surabhi exhibited highest positive significant standard heterosis with 16.98% (Table 34).

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

The mid parent heterosis ranges from -25.27% (MCU 5 x KC 3) to 25.73% (Suraj x Anjali). Out of seventy two hybrids, twenty three hybrids exhibited a negative significant relative heterosis whereas positive expression over mid parent was observed in twenty eight hybrids. The lowest (-30.74%) and highest (20.62%) values of heterobeltiosis was recorded in MCU 5 x KC 3 and Suraj x Anjali, respectively. Among the hybrids, forty three hybrids exhibited negative significant expression of heterobeltiosis. The range of standard heterosis varies from -27.89% (MCU 5 x KC 3) to 9.11% (Khandwa 2 x KC 2) for this trait. Twelve hybrids were found to record positively significant heterosis and thirty four hybrids exhibited negatively significant heterosis over the check MCU 13 (Table 35).

4.4.13. Uniformity ratio (%)

In this character, the range of heterosis over mid parent varies from -10.17% (Surabhi x KC 2) to 9.54% (KC 3 x Surabhi), however twenty seven hybrids exhibited a positive significant heterosis. Heterobeltiosis ranges from -11.18% (Surabhi x KC 2) to 7.82% (MCU 5 x MCU 7). Seventeen hybrids recorded a positive significant heterobeltiosis. The standard heterosis varies from -7.61% (Surabhi x KC 2) to 9.18% (KC 3 x Surabhi). Among the seventy two hybrids, twenty four hybrids showed a positive significant heterosis over the standard check (Table 36).

4.4.14. Elongation per cent (%)

The mid parental heterosis ranges from -23.08% (Khandwa 2 x Anjali and G.Cot 16 x Anjali) to 18.34% (Surabhi x Suraj). Out of seventy two hybrids, only one exhibited a positive significant relative heterosis whereas negative expression over mid parent was observed in eleven hybrids. The range of heterobeltiosis was -32.84% (Khandwa 2 x Anjali and G.Cot 16 x Anjali) to 12.36% (Surabhi x Suraj). None of the hybrids recorded a positive significant heterobeltiosis. The standard heterosis ranges from -7.03% (Surabi x KC 3 and Suraj x KC 3) to 37.19% (Anjali x KC 3). Among the seventy

Table 35. Expression of heterosis for micronaire value ($\mu\text{g}/\text{inch}$)

SI. No.	Hybrids	Micronaire value		
		d_i	d_{ii}	d_{iii}
1	Suraj x Surabhi	4.09*	-1.37	-12.33**
2	Suraj x Khandwa 2	7.48**	0.88	2.22
3	Suraj x Anjali	25.73**	20.62**	7.22**
4	Suraj x KC 2	9.54**	4.17*	2.67
5	Suraj x KC 3	-24.35**	-29.88**	-27.03**
6	Suraj x MCU 5	8.85**	6.12**	-5.67**
7	Suraj x MCU 7	3.90*	3.13	-8.33**
8	Suraj x G.Cot 16	6.81**	0.66	1.11
9	Surabhi x Suraj	2.85	1.50	-9.78**
10	Surabhi x Khandwa 2	7.83**	1.21	2.52
11	Surabhi x Anjali	5.93**	1.63	-9.67**
12	Surabhi x KC 2	-12.27**	-16.57**	-17.78**
13	Surabhi x KC 3	-0.40	-7.68**	-3.88
14	Surabhi x MCU 5	-5.13*	-7.50**	-17.78**
15	Surabhi x MCU 7	1.51	0.75	-10.44**
16	Surabhi x G.Cot 16	14.55**	7.96**	8.44**
17	Khandwa 2 x Suraj	0.39	-10.70**	-0.78
18	Khandwa 2 x Surabhi	-5.59**	-19.00**	-10.00**
19	Khandwa 2 x Anjali	8.36**	-6.00**	4.44*
20	Khandwa 2 x KC 2	4.08*	-1.80	9.11**
21	Khandwa 2 x KC 3	1.19	-2.00	8.89**
22	Khandwa 2 x MCU 5	-3.86*	-15.40**	-6.00**

Contd...

Table 35. Contd..

SI. No.	Hybrids	Micronaire value		
		d _i	d _{ii}	d _{iii}
23	Khandwa 2 x MCU 7	5.15**	-6.00**	4.41*
24	Khandwa 2 x G.Cot 16	-8.61**	-13.00**	-3.33
25	Anjali x Suraj	6.40**	5.00*	-6.67**
26	Anjali x Surabhi	-3.69	-8.75**	-18.89**
27	Anjali x Khandwa 2	13.43**	6.47**	7.90**
28	Anjali x KC 2	-4.21*	-8.91**	-10.22**
29	Anjali x KC 3	-17.10**	-23.16**	-20.00**
30	Anjali x MCU 5	16.67**	13.75**	1.11
31	Anjali x MCU 7	4.53*	3.75	-7.78**
32	Anjali x G.Cot 16	-5.40**	-10.84**	-10.46**
33	KC 2 x Suraj	5.76**	4.38	-7.30**
34	KC 2 x Surabhi	17.15**	11.00**	-1.33
35	KC 2 x Khandwa 2	4.32*	-2.08	-0.78
36	KC 2 x Anjali	21.04**	16.13**	3.22
37	KC 2 x KC 3	11.57**	3.42	7.67**
38	KC 2 x MCU 5	-11.54**	-13.75**	-23.33**
39	KC 2 x MCU 7	10.08**	9.25**	-2.89
40	KC 2 x G.Cot 16	2.70	-3.21	-2.78
41	KC 3 x Suraj	4.55**	-7.00**	3.33
42	KC 3 x Surabhi	-9.91**	-22.70**	-14.13**
43	KC 3 x Khandwa 2	-4.81**	-9.00**	1.11
44	KC 3 x Anjali	8.24**	-6.10**	4.33*
45	KC 3 x KC 2	1.85	-3.90*	6.78**

Contd...

Table 35. Contd..

SI. No.	Hybrids	Micronaire value		
		d_i	d_{ii}	d_{iii}
46	KC 3 x MCU 5	6.82**	-6.00**	4.44*
47	KC 3 x MCU 7	9.06**	-2.50	8.33**
48	KC 3 x G.Cot 16	-6.51**	-11.00**	-1.11
49	MCU 5 x Suraj	-13.11**	-14.25**	-23.78**
50	MCU 5 x Surabhi	-1.45	-6.62**	-16.96**
51	MCU 5 x Khandwa 2	-12.85**	-18.20**	-17.11**
52	MCU 5 x Anjali	-8.01**	-11.75**	-21.56**
53	MCU 5 x KC 2	-17.01**	-21.08**	-22.22**
54	MCU 5 x KC 3	-25.27**	-30.74**	-27.89**
55	MCU 5 x MCU 7	0.13	-0.63	-11.67**
56	MCU 5 x G.Cot 16	3.29	-2.65	-2.22
57	MCU 7 x Suraj	0.44	-0.87	-11.89**
58	MCU 7 x Surabhi	-3.96	-9.00**	-19.16**
59	MCU 7 x Khandwa 2	7.36**	0.77	2.18
60	MCU 7 x Anjali	-3.58	-7.50**	-17.78**
61	MCU 7 x KC 2	-2.79	-7.55**	-8.89**
62	MCU 7 x KC 3	1.21	-6.19**	-2.33
63	MCU 7 x MCU 5	-12.82**	-15.00**	-24.44**
64	MCU 7 x G.Cot 16	-2.00	-7.63**	-7.22**
65	G.Cot 16 x Suraj	0.06	-11.00**	-1.16
66	G.Cot 16 x Surabhi	1.40	-13.00**	-3.33
67	G.Cot 16 x Khandwa 2	-7.85**	-11.90**	-2.11
68	G.Cot 16 x Anjali	3.05	-10.60**	-0.67

Contd...

Table 35. Contd..

SI. No.	Hybrids	Micronaire value		
		d_i	d_{ii}	d_{iii}
69	G.Cot 16 x KC 2	-5.03**	-10.40**	-0.44
70	G.Cot 16 x KC 3	-7.49**	-10.40**	-0.44
71	G.Cot 16 x MCU 5	-13.64**	-24.00**	-15.56**
72	G.Cot 16 x MCU 7	-2.68	-13.00**	-3.33

*significant at 5 per cent level, ** significant at 1 per cent level

d_i = Relative heterosis

d_{ii} = Heterobeltiosis

d_{iii} = Standard heterosis

Table 36. Expression of heterosis for uniformity ratio (%)

SI. No.	Hybrids	Uniformity ratio		
		d_i	d_{ii}	d_{iii}
1	Suraj x Surabhi	1.39	-2.35*	1.06
2	Suraj x Khandwa 2	3.03**	1.43	0.35
3	Suraj x Anjali	-2.59*	-7.05**	-1.92
4	Suraj x KC 2	2.72*	-0.22	1.46
5	Suraj x KC 3	6.37**	6.16**	1.76
6	Suraj x MCU 5	1.47	-0.79	-0.47
7	Suraj x MCU 7	5.79**	3.50**	3.71**
8	Suraj x G.Cot 16	3.37**	1.50	0.95
9	Surabhi x Suraj	-2.68*	-6.37**	-2.61*
10	Surabhi x Khandwa 2	-5.31**	-7.63**	-3.92**
11	Surabhi x Anjali	-4.51**	-5.19**	0.04
12	Surabhi x KC 2	-10.17**	-11.18**	-7.61**
13	Surabhi x KC 3	-3.05**	-7.03**	-3.29**
14	Surabhi x MCU 5	-7.78**	-9.41**	-5.77**
15	Surabhi x MCU 7	-2.24*	-4.03**	-0.17
16	Surabhi x G.Cot 16	-3.89**	-5.99**	-2.22
17	Khandwa 2 x Suraj	5.48**	3.47**	3.41**
18	Khandwa 2 x Surabhi	-1.25	-2.95*	0.44
19	Khandwa 2 x Anjali	-1.23	-3.84**	1.47
20	Khandwa 2 x KC 2	2.60*	1.73	3.44**
21	Khandwa 2 x KC 3	2.77**	0.47	0.41
22	Khandwa 2 x MCU 5	-0.75	-0.95	-0.62

Contd...

Table 36. Contd..

SI. No.	Hybrids	Uniformity ratio		
		d_i	d_{ii}	d_{iii}
23	Khandwa 2 x MCU 7	1.68	1.55	1.75
24	Khandwa 2 x G.Cot 16	0.00	-0.23	-0.29
25	Anjali x Suraj	0.27	-4.42**	1.37
26	Anjali x Surabhi	-0.04	-1.25	4.73**
27	Anjali x Khandwa 2	0.79	-2.60*	3.30**
28	Anjali x KC 2	0.63	-1.44	4.53**
29	Anjali x KC 3	-0.56	-5.52**	0.20
30	Anjali x MCU 5	-1.37	-4.04**	1.77
31	Anjali x MCU 7	-0.56	-3.31**	2.55*
32	Anjali x G.Cot 16	-0.36	-3.45**	2.40*
33	KC 2 x Suraj	3.89**	0.91	2.91*
34	KC 2 x Surabhi	2.84**	2.09	5.65**
35	KC 2 x Khandwa 2	1.31	-0.20	1.77
36	KC 2 x Anjali	0.73	-0.96	4.51**
37	KC 2 x KC 3	-2.59*	-5.70**	-3.83**
38	KC 2 x MCU 5	3.34**	2.50*	4.53**
39	KC 2 x MCU 7	-0.03	-0.90	1.06
40	KC 2 x G.Cot 16	0.94	-0.30	1.67
41	KC 3 x Suraj	5.07**	4.92**	0.86
42	KC 3 x Surabhi	9.54**	5.50**	9.18**
43	KC 3 x Khandwa 2	2.30*	0.71	-0.37
44	KC 3 x Anjali	3.51**	-1.23	4.22**
45	KC 3 x KC 2	5.42**	2.40*	4.12**

Contd...

Table 36. Contd..

SI. No.	Hybrids	Uniformity ratio		
		d_i	d_{ii}	d_{iii}
46	KC 3 x MCU 5	-2.37*	-4.54**	-4.23**
47	KC 3 x MCU 7	5.40**	3.11**	3.32**
48	KC 3 x G.Cot 16	4.52**	2.62*	2.08
49	MCU 5 x Suraj	2.47*	0.51	0.45
50	MCU 5 x Surabhi	4.17**	2.38*	5.96**
51	MCU 5 x Khandwa 2	-5.83**	-6.31**	-6.36**
52	MCU 5 x Anjali	-6.08**	-8.56**	-3.52**
53	MCU 5 x KC 2	-1.07	-1.92	-0.27
54	MCU 5 x KC 3	-1.99	-4.18**	-4.24**
55	MCU 5 x MCU 7	7.96**	7.82**	8.04**
56	MCU 5 x G.Cot 16	-5.57**	-5.80**	-5.85**
57	MCU 7 x Suraj	5.40**	3.39**	3.32**
58	MCU 7 x Surabhi	-0.85	-2.55*	0.85
59	MCU 7 x Khandwa 2	-1.13	-1.63	-1.69
60	MCU 7 x Anjali	-4.11**	-6.65**	-1.50
61	MCU 7 x KC 2	1.26	0.39	2.08
62	MCU 7 x KC 3	5.63**	3.27**	3.20**
63	MCU 7 x MCU 5	4.59**	4.39**	4.73**
64	MCU 7 x G.Cot 16	0.52	0.29	0.22
65	G.Cot 16 x Suraj	3.82**	1.84	1.77
66	G.Cot 16 x Surabhi	-1.24	-2.94*	0.45
67	G.Cot 16 x Khandwa 2	0.29	-0.21	-0.28
68	G.Cot 16 x Anjali	0.68	-1.98	3.43**

Contd...

Table 36. Contd..

SI. No.	Hybrids	Uniformity ratio		
		d_i	d_{ii}	d_{iii}
69	G.Cot 16 x KC 2	-3.29**	412**	-2.51*
70	G.Cot 16 x KC 3	5.29**	2.94*	2.88*
71	G.Cot 16 x MCU 5	-4.60**	-4.79**	-4.48**
72	G.Cot 16 x MCU 7	2.52*	2.38*	2.59*

*significant at 5 per cent level, ** significant at 1 per cent level

d_i = Relative heterosis

d_{ii} = Heterobeltiosis

d_{iii} = Standard heterosis

Table 37. Expression of heterosis for elongation per cent (%)

SI. No.	Hybrids	Elongation per cent		
		d_i	d_{ii}	d_{iii}
1	Suraj x Surabhi	11.90	6.82	6.58
2	Suraj x Khandwa 2	-0.57	-8.42	-1.36
3	Suraj x Anjali	-8.41	-26.87**	11.11
4	Suraj x KC 2	-3.33	-13.00	-1.36
5	Suraj x KC 3	-9.39	-18.81*	-7.03
6	Suraj x MCU 5	0.52	-13.51	8.84
7	Suraj x MCU 7	6.82	-2.08	6.58
8	Suraj x G.Cot 16	-9.19	-20.00*	-4.76
9	Surabhi x Suraj	18.34*	12.36	13.38
10	Surabhi x Khandwa 2	7.43	-1.05	6.58
11	Surabhi x Anjali	-14.02*	-31.34**	4.31
12	Surabhi x KC 2	-2.22	-12.00	-0.23
13	Surabhi x KC 3	-9.39	-18.81*	-7.03
14	Surabhi x MCU 5	-10.99	-23.42**	-3.63
15	Surabhi x MCU 7	0.00	-8.33	-0.23
16	Surabhi x G.Cot 16	-8.11	-19.05*	-3.63
17	Khandwa 2 x Suraj	-5.82	-11.00	0.91
18	Khandwa 2 x Surabhi	-7.45	-13.00	-1.36
19	Khandwa 2 x Anjali	-23.08**	-32.84**	2.04
20	Khandwa 2 x KC 2	-6.00	-6.00	6.58
21	Khandwa 2 x KC 3	-4.48	-4.95	8.84
22	Khandwa 2 x MCU 5	-14.69*	-18.92*	2.04

Contd...

Table 37. Contd..

SI. No.	Hybrids	Elongation per cent		
		d _i	d _{ii}	d _{iii}
23	Khandwa 2 x MCU 7	4.08	2.00	15.65
24	Khandwa 2 x G.Cot 16	-2.44	-4.76	13.38
25	Anjali x Suraj	-8.30	-25.00**	19.05*
26	Anjali x Surabhi	-0.88	-19.29**	28.12**
27	Anjali x Khandwa 2	-6.38	-21.43**	24.72**
28	Anjali x KC 2	-5.00	-18.57**	29.25**
29	Anjali x KC 3	0.41	-13.57*	37.19**
30	Anjali x MCU 5	-5.18	-15.00*	34.92**
31	Anjali x MCU 7	-5.93	-20.71**	25.85**
32	Anjali x G.Cot 16	-2.86	-15.00*	34.92**
33	KC 2 x Suraj	-2.65	-8.00	4.31
34	KC 2 x Surabhi	-3.19	-9.00	3.17
35	KC 2 x Khandwa 2	0.51	-2.00	11.11
36	KC 2 x Anjali	-17.09**	-27.61**	9.98
37	KC 2 x KC 3	2.49	1.98	16.78
38	KC 2 x MCU 5	-1.42	-6.31	17.91*
39	KC 2 x MCU 7	3.06	1.00	14.51
40	KC 2 x G.Cot 16	-4.39	-6.67	11.11
41	KC 3 x Suraj	-4.76	-10.00	2.04
42	KC 3 x Surabhi	2.13	-4.00	8.84
43	KC 3 x Khandwa 2	-1.54	-4.00	8.84
44	KC 3 x Anjali	-6.84	-18.66**	23.58*
45	KC 3 x KC 2	-4.00	-4.00	8.84

Contd...

Table 37. Contd..

SI. No.	Hybrids	Elongation per cent		
		d _i	d _{ii}	d _{iii}
46	KC 3 x MCU 5	-10.90	-15.32	6.58
47	KC 3 x MCU 7	-1.02	-3.00	9.98
48	KC 3 x G.Cot 16	-19.02*	-20.95*	-5.9
49	MCU 5 x Suraj	-7.18	-19.17 **	9.98
50	MCU 5 x Surabhi	-17.31*	-28.33**	-2.49
51	MCU 5 x Khandwa 2	1.40	-9.17	23.58*
52	MCU 5 x Anjali	-18.11**	-22.39**	17.91
53	MCU 5 x KC 2	-13.64*	-20.83**	7.71
54	MCU 5 x KC 3	-18.55**	-25.00**	2.04
55	MCU 5 x MCU 7	1.85	-8.33	24.72**
56	MCU 5 x G.Cot 16	-6.67	-12.50	19.05*
57	MCU 7 x Suraj	6.88	1.00	14.51
58	MCU 7 x Surabhi	-3.19	-9.00	3.17
59	MCU 7 x Khandwa 2	12.82	10.00	24.72**
60	MCU 7 x Anjali	-9.40	-20.90**	20.18*
61	MCU 7 x KC 2	-2.00	-2.00	11.11
62	MCU 7 x KC 3	4.48	3.96	19.05*
63	MCU 7 x MCU 5	-19.43**	-23.42**	-3.63
64	MCU 7 x G.Cot 16	-3.41	-5.71	12.24
65	G.Cot 16 x Suraj	-1.59	-7.00	5.44
66	G.Cot 16 x Surabhi	-12.77	-18.00*	-7.03
67	G.Cot 16 x Khandwa 2	-0.51	-3.00	9.98
68	G.Cot 16 x Anjali	-23.08**	-32.84**	2.04

Contd...

Table 37. Contd..

SI. No.	Hybrids	Elongation per cent		
		d_i	d_{ii}	d_{iii}
69	G.Cot 16 x KC 2	-1.00	-1.00	12.24
70	G.Cot 16 x KC 3	9.45	8.91	24.72**
71	G.Cot 16 x MCU 5	5.21	0.00	25.85**
72	G.Cot 16 x MCU 7	5.10	3.00	16.78

*significant at 5 per cent level, ** significant at 1 per cent level

d_i = Relative heterosis

d_{ii} = Heterobeltiosis

d_{iii} = Standard heterosis

Figure 3. Range of relative heterosis (di) for different traits

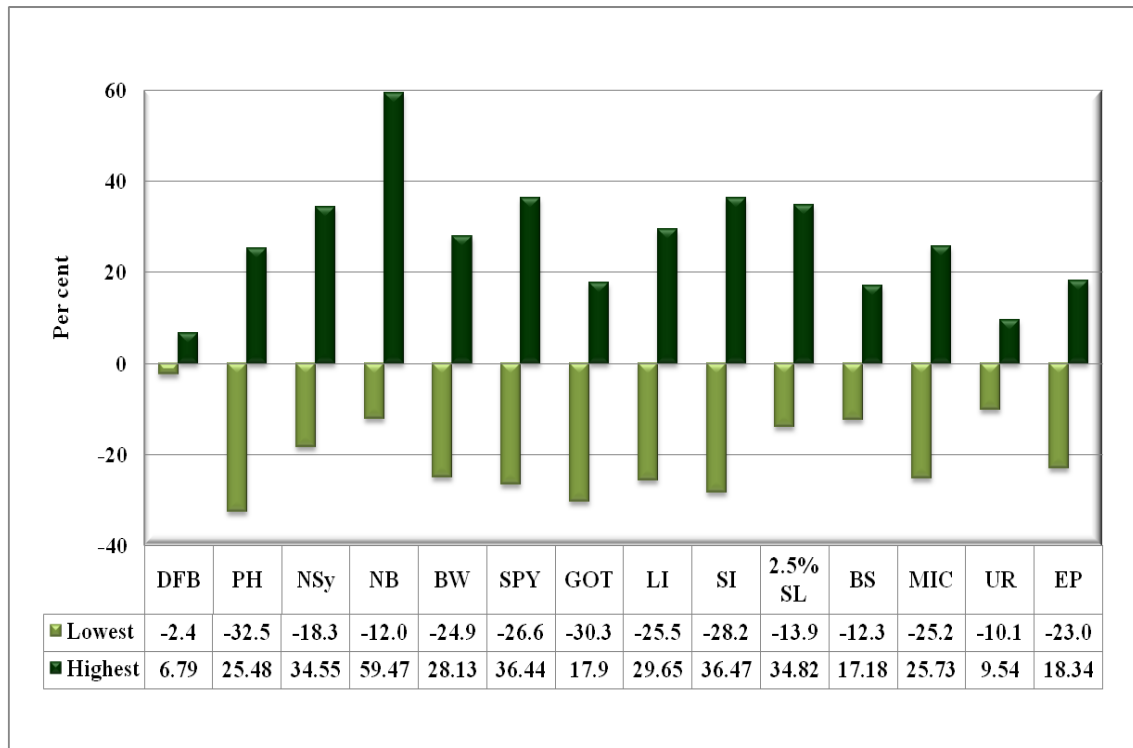


Figure 4. Range of heterobeltiosis (dii) for different traits

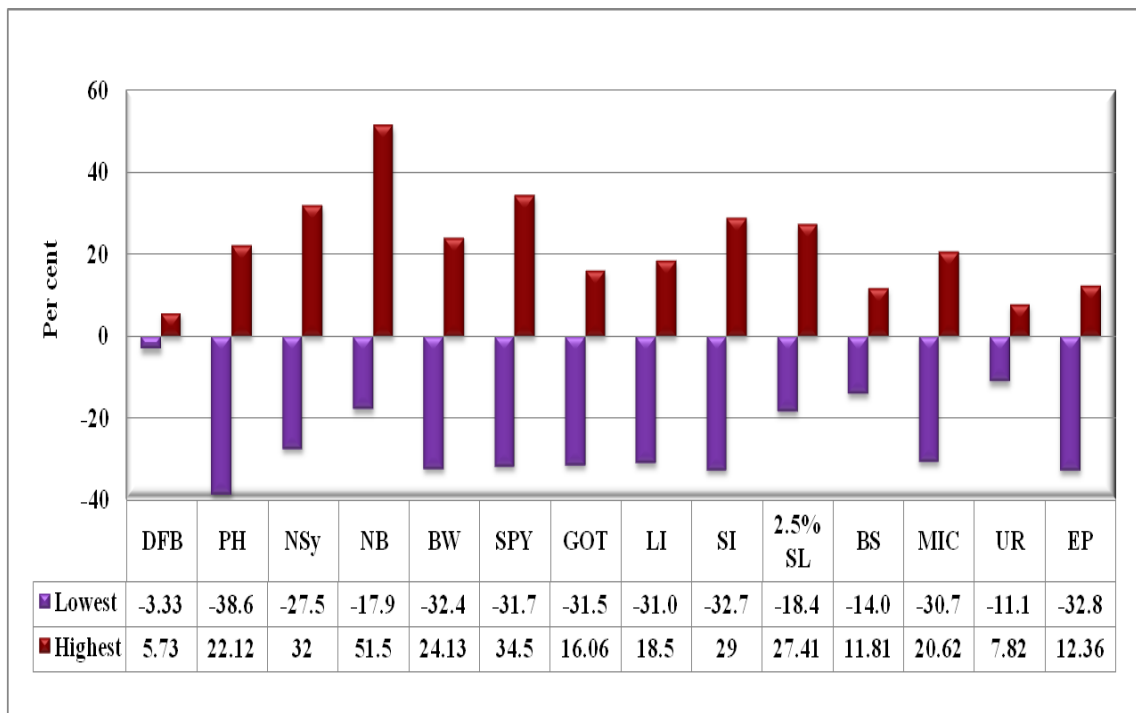
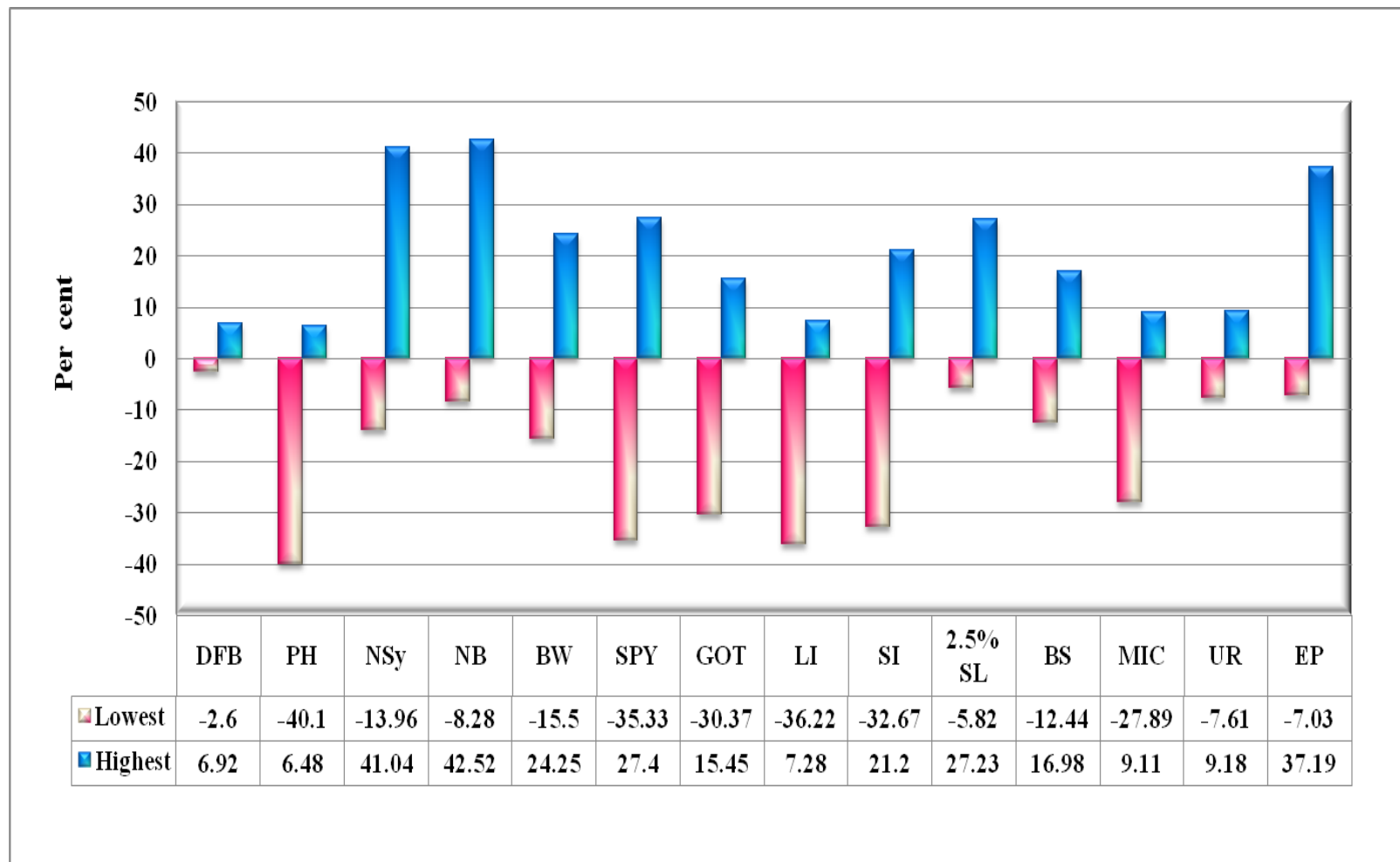


Figure 5. Range of standard heterosis (dii) for different traits



two hybrids, eighteen hybrids showed a positive significant heterosis over the standard check for elongation per cent (Table 37).

4.5. Genetical and Graphical analysis

i. Testing Validity of the hypothesis

Two broad tests were followed in order to test whether the diallel data conformed to the hypothesis postulated by Hayman (1954) viz., t^2 test and estimation of regression co-efficient.

The calculated values of t^2 for each character are given in Table 38. The t^2 statistic, test the constancy of Vr-Wr over the arrays, a significant t^2 indicates heterogeneity of Vr-Wr, when one or more of the hypothesis are not satisfied for that particular character. The value of t^2 was not significant for boll weight, lint index, seed index, 2.5% span length, bundle strength, micronaire value, uniformity ratio and elongation per cent. This test therefore indicates that for these eight characters, the assumptions of the diallel were fulfilled.

In the second test, if all the assumptions of diallel hold true, the (Vr-Wr) regression co-efficient b, for each character is expected to be significantly different from zero, but not different from unity (Jinks and Hayman, 1953). The results of this test were also given in Table 38. The values of regression co-efficient were not significantly different from unity for the following five characters namely number of sympodial branches per plant, 2.5% span length, bundle strength, micronaire value and elongation per cent. The characters such as number of sympodial branches per plant, single plant yield, 2.5% span length, bundle strength, micronaire value and elongation per cent were significantly different from zero. The characters 2.5% span length, bundle strength, micronaire value and elongation per cent satisfied both the assumptions.

ii. Estimates of genetic parameters and genetic ratios

In genetic analysis, various genetic parameters viz., D, H_1 , H_2 , F, h^2 and E were estimated and furnished in the Table 39. Above six components helps in the estimation of various genetic ratios viz., $(H_1/D)^{1/2}$, $H_2/4H_1$, K_D/K_r and h^2/H_2 (Table 40). The salient features of analysis for fourteen characters are discussed below.

Table 38. Values of t^2 for Wr-Vr regression, estimates of b, standard error of b and deviation of b from zero and unity in the Wr-Vr regression graph

SI. No.	Characters	t^2 value	b	SE	b $\pm$ SE	b-0/SE	1-b/SE
1.	Days to first boll bursting	6.45*	0.27	0.15	0.27 $\pm$ 0.15	1.80	4.87**
2.	Plant height (cm)	3.77*	0.23	0.18	0.23 $\pm$ 0.18	1.28	4.28**
3.	Number of sympodial branches per plant	4.77*	1.30	0.33	1.30 $\pm$ 0.33	3.94**	-0.91
4.	Number of bolls per plant	5.71*	0.06	0.17	0.06 $\pm$ 0.17	0.35	5.53**
5.	Boll weight (g)	2.52	0.41	0.19	0.41 $\pm$ 0.19	2.16	3.11*
6.	Single plant yield (g)	11.95**	0.31	0.12	0.31 $\pm$ 0.12	2.58*	5.75**
7.	Ginning outturn (%)	16.70**	-0.09	0.11	-0.09 $\pm$ 0.11	-0.82	9.91**
8.	Lint index	0.24	0.24	0.30	0.24 $\pm$ 0.30	0.80	2.53*
9.	Seed index	0.10	-0.02	0.34	-0.02 $\pm$ 0.34	-0.06	3.00*
10.	2.5% span length (mm)	0.03	0.85	0.23	0.85 $\pm$ 0.23	3.70**	0.65
11.	Bundle strength (g/tex)	1.28	1.06	0.26	1.06 $\pm$ 0.26	4.08**	-0.23
12.	Micronaire value (μ g/inch)	0.59	1.03	0.18	1.03 $\pm$ 0.18	5.72**	-0.17
13.	Uniformity ratio (%)	0.72	0.34	0.26	0.34 $\pm$ 0.26	1.31	2.54*
14.	Elongation per cent (%)	1.68	1.10	0.12	1.10 $\pm$ 0.12	9.17**	-0.83

*significant at 5 per cent level, ** significant at 1 per cent level

4.5.1. Days to first boll bursting (days)

Only H_1 and H_2 were found to be significant. The value of dominance effect (H_1) was greater than additive effect (D).

The mean degree of dominance $(H_1/D)^{1/2}$ was more than unity (1.91) since H_1 was greater than D. The ratio of $H_2/4H_1$ was less than 0.25 (0.22). The ratio of K_D/K_r was found to be more than unity (1.11). The ratio of h^2/H_2 was 0.34. The narrow sense heritability was moderate (35.91 per cent).

4.5.2. Plant height (cm)

All the genetic parameters except F and E were significant. The value of dominance effect (H_1) was greater than additive effect (D).

The mean degree of dominance $(H_1/D)^{1/2}$ was more than unity (2.04). The ratio of $H_2/4H_1$ was less than 0.25 (0.24). The ratio of K_D/K_r was found to be more than unity (1.23). The ratio of h^2/H_2 was 0.60. The narrow sense heritability was moderate (38.41 per cent).

4.5.3. Number of sympodial branches per plant

All the genetic components except H_1 and H_2 were significant. The value of additive effect (D) was greater than dominance effect (H_1).

The mean degree of dominance $(H_1/D)^{1/2}$ was less than unity (0.60). The ratio of $H_2/4H_1$ was less than 0.25 (0.10). The ratio of K_D/K_r was found to be more than unity (6.73). The ratio of h^2/H_2 was 5.13. The narrow sense heritability was low (26.15 per cent).

4.5.4. Number of bolls per plant

For this trait the genetic parameters D, F, H_1 and H_2 were non-significant. The components h^2 and E were significant. The mean degree of dominance $(H_1/D)^{1/2}$ was more than unity (2.51). The ratio of $H_2/4H_1$ was 0.30. The ratio of K_D/K_r was found to be less than unity (0.28). The ratio of h^2/H_2 was 5.28. The narrow sense heritability was low (2.96 per cent).

Table 39. Estimation of genetic parameters for yield and fibre quality traits in *Gossypium hirsutum* L.

Characters	D	F	H ₁	H ₂	h ²	E
Days to first boll bursting	1.05±0.63	0.22±1.46	3.86±1.39*	3.39±1.19*	1.15±0.80	0.31±0.20
Plant height (cm)	71.03±25.09*	29.29±58.52	294.60±55.37*	277.24±47.60*	167.09±31.89*	7.04±7.93
Number of sympodial branches	4.08±0.42*	3.64±0.98*	1.48±0.93	0.57±0.80	2.90±0.53*	1.78±0.13*
Number of bolls per plant	-0.58±1.25	-1.63±2.92	3.66±2.76	4.41±2.37	23.27±1.59*	3.82±0.40*
Boll weight (g)	0.02±0.02	-0.04±0.04	0.01±0.04	0.003±0.03	-0.02±0.02	0.07±0.006*
Single plant yield (g)	3.16±17.32	-32.14±40.41	158.94±38.23*	144.60±32.86*	155.62±22.02*	20.46±5.48*
Ginning outturn (%)	1.55±2.16	1.95±5.03	17.28±4.76*	13.85±4.10*	0.01±2.74	0.31±0.68
Lint index	0.07±0.07	0.03±0.16	0.40±0.15*	0.38±0.13*	-0.05±0.09	0.12±0.02*
Seed index	0.38±0.35	0.48±0.82	1.27±0.78	0.91±0.67	0.30±0.45	0.58±0.11*
2.5% span length (mm)	11.01±1.12*	9.56±2.61*	15.30±2.46*	11.35±2.12*	35.99±1.42*	0.31±0.35
Bundle strength (g/tex)	2.54±0.28*	1.51±0.65*	3.17±0.62*	2.67±0.53*	5.28±0.36*	0.15±0.09
Micronaire value (µg/inch)	0.17±0.01*	0.05±0.03	0.23±0.03*	0.18±0.02*	0.04±0.02*	0.004±0.005
Uniformity ratio (%)	2.29±0.52*	3.29±1.21*	6.04±1.14*	4.28±0.98*	0.28±0.66	0.19±0.16
Elongation per cent (%)	0.40±0.02*	0.14±0.04*	0.06±0.04	0.06±0.03	0.13±0.02*	0.09±0.01*

D - Additive effect

h² - Heritability

F - Mean of Fr over the arrays

E - Environmental component of variance

H₁ - Dominance effect

H₂ - $H_1 [1 - (u-v)^2]$, where u and v are the proportions of positive and negative genes, respectively in parents

*significant at 5 per cent level

Table 40. Estimation of genetic ratios for yield and fibre quality traits in *Gossypium hirsutum* L.

Characters	Genetic ratios				
	$(H_1/D)^{1/2}$	$H_2/4H_1$	K_D/K_r	h^2/H_2	Heritability (%) (Narrow sense)
Days to first boll bursting	1.91	0.22	1.11	0.34	35.91
Plant height (cm)	2.04	0.24	1.23	0.60	38.41
Number of sympodial branches per plant	0.60	0.10	6.73	5.13	26.15
Number of bolls per plant	2.51	0.30	0.28	5.28	2.96
Boll weight (g)	0.75	0.06	-0.04	-7.28	31.65
Single plant yield (g)	7.09	0.23	0.17	1.08	30.48
Ginning outturn (%)	3.34	0.20	1.47	0.001	28.75
Lint index	2.32	0.24	1.21	-0.12	12.24
Seed index	1.82	0.18	2.04	0.33	13.86
2.5% span length (mm)	1.18	0.19	2.17	3.17	46.15
Bundle strength (g/tex)	1.12	0.21	1.73	1.98	48.34
Micronaire value ($\mu\text{g}/\text{inch}$)	1.14	0.20	1.31	0.20	64.75
Uniformity ratio (%)	1.63	0.18	2.60	0.07	23.17
Elongation per cent (%)	0.40	0.25	2.64	2.12	53.06

$H_1/D)^{1/2}$

- Average degree of dominance

$H_2/4H_1$

- The proportion of genes with positive and negative effects in in parents

$$K_D/K_r = \frac{(4DH_1)^{1/2} + F}{(4DH_1)^{1/2} - F}$$

- The ratio of dominant and recessive genes in the parents

h^2/H_2

- Number of gene groups

Heritability in narrow sense (%)

4.5.5. Boll weight (g)

The additive component D and the other components H_1 and H_2 were found to be positive but non-significant. The component E was found to be significant and positive. The components F and h^2 were negative and non-significant.

The mean degree of dominance $(H_1/D)^{1/2}$ was less than unity (0.75). The ratio of $H_2/4H_1$ was less than 0.25 (0.06). The ratio of K_D/K_r was found to be less than unity (-0.04). The ratio of h^2/H_2 was -7.28. The narrow sense heritability was moderate (31.65 per cent).

4.5.6. Single plant yield (g)

All the genetic parameters were significant and positive but D and F were non-significant. The value of dominance effect (H_1) was greater than additive effect (D).

The mean degree of dominance $(H_1/D)^{1/2}$ was more than unity (7.09). The ratio of $H_2/4H_1$ was less than 0.25 (0.23). The ratio of K_D/K_r was found to be less than unity (0.17). The ratio of h^2/H_2 was 1.08. The narrow sense heritability was moderate (30.48 per cent).

4.5.7. Ginning outturn (%)

Only H_1 and H_2 were found to be significant and positive. The value of dominance effect (H_1) was greater than additive effect (D).

The mean degree of dominance $(H_1/D)^{1/2}$ was more than unity (3.34) since H_1 was greater than D. The ratio of $H_2/4H_1$ was less than 0.25 (0.20). The ratio of K_D/K_r was found to be more than unity (1.47). The ratio of h^2/H_2 was 0.001. The narrow sense heritability was low (28.75 per cent).

4.5.8. Lint index

The additive component (D) and F were found to be positive but non-significant. The values of other components viz., H_1 , H_2 and E were significant. The component h^2 was negative and non-significant. The value of dominance effect (H_1) was greater than additive effect (D). The estimates of $(H_1/D)^{1/2}$ and K_D/K_r were more than unity. The ratio of $H_2/4H_1$ was less than 0.25 (0.24). The ratio of h^2/H_2 was -0.12. Low heritability was noted for this trait (12.24 per cent).

4.5.9. Seed index

For this trait the genetic parameters viz., D, F, H_1 , H_2 and h^2 were positive but non-significant. Only component E is found to be significant and positive. The mean degree of dominance $(H_1/D)^{1/2}$ was more than unity (1.82). The ratio of $H_2/4H_1$ was less than 0.25 (0.18). The ratio of K_D/K_r was found to be more than unity (2.04). The ratio of h^2/H_2 was 0.33. The narrow sense heritability was low (13.86 per cent).

4.5.10. 2.5% span length (mm)

The estimates of genetic components viz., D, F, H_1 , H_2 and h^2 were positive and significant. The environmental component E exhibited a positive but non-significant value. The value of dominance effect (H_1) was greater than additive effect (D).

The mean degree of dominance $(H_1/D)^{1/2}$ was more than unity (1.18) since H_1 was greater than D. The ratio of $H_2/4H_1$ was less than 0.25 (0.19). The ratio of K_D/K_r was found to be more than unity (2.17). The ratio of h^2/H_2 was 3.17. Moderate heritability was noted for this trait (46.15 per cent).

4.5.11. Bundle strength (g/tex)

In this trait the genetic parameters viz., D, F, H_1 , H_2 and h^2 were positive and non-significant. The value of environmental component E exhibited a positive but non-significant. The value of dominance effect (H_1) was greater than additive effect (D). The estimates of $(H_1/D)^{1/2}$ and K_D/K_r were more than unity. The ratio of $H_2/4H_1$ was less than 0.25 (0.21). The ratio of h^2/H_2 was 1.98. Moderate heritability was noted in this trait (48.34 per cent).

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

In this character the estimates of D, H_1 , H_2 and h^2 were positive and significant. The components F and E were positive but non-significant.

The $(H_1/D)^{1/2}$ ratio exceeded unity (1.14). The ratio of $H_2/4H_1$ (0.20) was below 0.25. The K_D/K_r ratio was more than one (1.31). The h^2/H_2 ratio was 0.20. High heritability was noted for this trait (64.75 per cent).

4.5.13. Uniformity ratio (%)

The estimates of genetic components viz., D, F, H_1 and H_2 were positive and significant. The environmental component (E) and h^2 exhibited a positive but non-significant value. The value of dominance effect (H_1) was greater than additive effect (D).

The mean degree of dominance $(H_1/D)^{1/2}$ was more than unity (1.63). The ratio of $H_2/4H_1$ was less than 0.25 (0.18). The ratio of K_D/K_r was found to be more than unity (2.60). The ratio of h^2/H_2 was very low (0.07). Low heritability was noted (23.17 per cent).

4.5.14. Elongation per cent (%)

In this character the estimates of D, F, h^2 and E were found to be positive and significant. The other components H_1 and H_2 were positive but found to be non-significant. The mean degree of dominance $(H_1/D)^{1/2}$ was less than unity (0.40). The ratio of $H_2/4H_1$ was 0.25. The ratio of K_D/K_r was found to be more than unity (2.64). The ratio of h^2/H_2 was 2.12. The narrow sense heritability was moderate (53.06 per cent).

4.6. Graphical analysis

Graphical analysis measures the genetic diversity of the parents involved in full diallel cross in terms of proportion of dominant and recessive genes along with net directional dominance either with favourable effects or unfavourable effects. The estimated values of array variance (V_r) and co-variances between the parents and their progenies in each arrays (W_r) were plotted in V_r - W_r graph on Y and X ordinates respectively for fourteen characters. They were presented in Figure 6 to 19 and the values of V_r and W_r for parents were given in the Table 41 and 42. The results of graphical data are presented characterwise.

4.6.1. Days to first boll bursting (days)

The regression line in V_r - W_r graph crossed the Y axis just above the point of origin showing partial dominance nature (Figure 6). The parental array points are widely scattered showing the diversity among the parents. The parental array points P_3 (Khandwa 2) and P_5 (KC 2) are located near to origin showing the presence of more dominant genes in these lines. The array point P_9 (G.Cot 16) was found to be contain more of recessive genes.

Table 41. Estimation of Vr and Wr for parents with respect to yield and fibre quality traits in *Gossypium hirsutum* L.

SI. No.	Characters	Suraj		Surabhi		Khandwa 2	
		Vr	Wr	Vr	Wr	Vr	Wr
1.	Days to first boll bursting	0.597	0.690	0.989	0.599	0.261	-0.058
2.	Plant height (cm)	99.885	18.072	56.616	36.494	35.409	-8.452
3.	Number of sympodial branches per plant	2.037	2.708	1.285	0.474	2.403	2.473
4.	Number of bolls per plant	4.758	0.378	4.313	-0.063	6.092	0.425
5.	Boll weight (g)	0.060	0.043	0.033	0.022	0.019	0.012
6.	Single plant yield (g)	77.241	11.417	11.777	-1.110	60.532	-3.042
7.	Ginning outturn (%)	2.438	0.277	1.369	0.858	4.054	0.917
8.	Lint index	0.041	0.048	0.136	0.008	0.318	0.096
9.	Seed index	0.365	0.247	0.331	0.069	0.308	0.264
10.	2.5% span length (mm)	3.773	2.319	1.581	2.232	5.697	4.690
11.	Bundle strength (g/tex)	0.804	0.421	1.349	0.348	0.721	0.376
12.	Micronaire value (µg/inch)	0.085	0.047	0.101	0.110	0.063	0.033
13.	Uniformity ratio (%)	1.106	0.174	0.882	0.455	0.975	0.127
14.	Elongation per cent (%)	0.076	0.096	0.085	0.087	0.071	0.092

Contd...

Table 41. Contd...

Sl. No.	Characters	Anjali		KC 2		KC 3	
		Vr	Wr	Vr	Wr	Vr	Wr
1.	Days to first boll bursting	2.058	-0.003	0.319	-0.155	1.104	0.689
2.	Plant height (cm)	126.256	58.170	92.123	37.775	157.615	25.761
3.	Number of sympodial branches per plant	1.231	1.522	0.991	0.424	2.192	1.524
4.	Number of bolls per plant	3.133	0.689	2.980	0.409	1.492	0.083
5.	Boll weight (g)	0.096	0.059	0.104	0.031	0.018	-0.002
6.	Single plant yield (g)	78.819	29.943	63.154	21.272	22.357	2.888
7.	Ginning outturn (%)	9.025	-0.972	7.586	0.199	4.985	1.392
8.	Lint index	0.136	-0.001	0.259	0.175	0.166	0.086
9.	Seed index	1.187	0.658	1.169	-0.284	0.337	0.279
10.	2.5% span length (mm)	2.622	1.167	7.025	6.205	2.909	2.306
11.	Bundle strength (g/tex)	1.309	1.473	2.252	2.241	1.492	1.220
12.	Micronaire value ($\mu\text{g}/\text{inch}$)	0.118	0.092	0.151	0.115	0.119	0.117
13.	Uniformity ratio (%)	1.061	0.917	0.688	0.357	2.076	1.070
14.	Elongation per cent (%)	0.275	0.333	0.067	0.151	0.179	0.237

Contd...

Table 41. Contd...

SI. No.	Characters	MCU 5		MCU 7		G.Cot 16	
		Vr	Wr	Vr	Wr	Vr	Wr
1.	Days to first boll bursting	1.634	1.166	1.710	0.526	3.458	1.113
2.	Plant height (cm)	83.301	33.859	69.530	46.548	71.237	12.557
3.	Number of sympodial branches per plant	1.531	2.057	0.798	0.121	0.768	0.657
4.	Number of bolls per plant	2.611	0.659	3.459	2.323	0.840	-0.036
5.	Boll weight (g)	0.076	0.035	0.046	0.049	0.063	0.011
6.	Single plant yield (g)	87.034	7.775	102.148	33.328	36.256	4.503
7.	Ginning outturn (%)	3.693	0.756	4.590	0.254	1.781	-0.811
8.	Lint index	0.249	-0.050	0.168	-0.032	0.123	0.050
9.	Seed index	0.557	-0.338	0.747	0.024	0.552	0.309
10.	2.5% span length (mm)	4.101	-0.588	9.007	7.453	2.536	2.587
11.	Bundle strength (g/tex)	1.066	0.927	0.822	1.122	0.376	0.044
12.	Micronaire value (µg/inch)	0.040	0.018	0.115	0.131	0.026	0.017
13.	Uniformity ratio (%)	3.017	0.807	1.071	-0.681	1.394	-0.155
14.	Elongation per cent (%)	0.191	0.240	0.077	0.129	0.157	0.195

Table 42. Estimation of mean and variance of parents, dominance relationship and Y intercept for yield and fibre quality traits in *Gossypium hirsutum* L.

SI. No.	Characters	V_0L_0	W_0L_{01}	V_1L_1	V_0L_{01}	$(M_{L1} - M_{L0})^2$	Y Intercept
1.	Days to first boll bursting	1.367	0.507	1.348	0.343	0.318	0.15
2.	Plant height (cm)	78.077	28.976	87.997	15.165	42.467	9.05
3.	Number of sympodial branches per plant	5.866	1.329	1.471	0.437	0.902	-0.58
4.	Number of bolls per plant	3.238	0.541	3.298	0.286	6.194	0.34
5.	Boll weight (g)	0.093	0.029	0.057	0.022	0.001	0.006
6.	Single plant yield (g)	23.615	11.886	59.924	13.545	40.926	-6.45
7.	Ginning outturn (%)	1.856	0.319	4.391	0.774	0.033	0.72
8.	Lint index	0.195	0.042	0.177	0.021	0.000	-0.001
9.	Seed index	0.964	0.136	0.617	0.099	0.131	0.15
10.	2.5% span length (mm)	11.321	3.152	4.361	1.369	9.027	-0.54
11.	Bundle strength (g/tex)	2.691	0.908	1.132	0.389	1.334	-0.29
12.	Micronaire value ($\mu\text{g}/\text{inch}$)	0.181	0.075	0.091	0.044	0.009	-0.02
13.	Uniformity ratio (%)	2.475	0.341	1.363	0.200	0.089	-0.12
14.	Elongation per cent (%)	0.490	0.173	0.131	0.069	0.043	0.03

Figure 6. Vr-Wr graph for days to first boll bursting

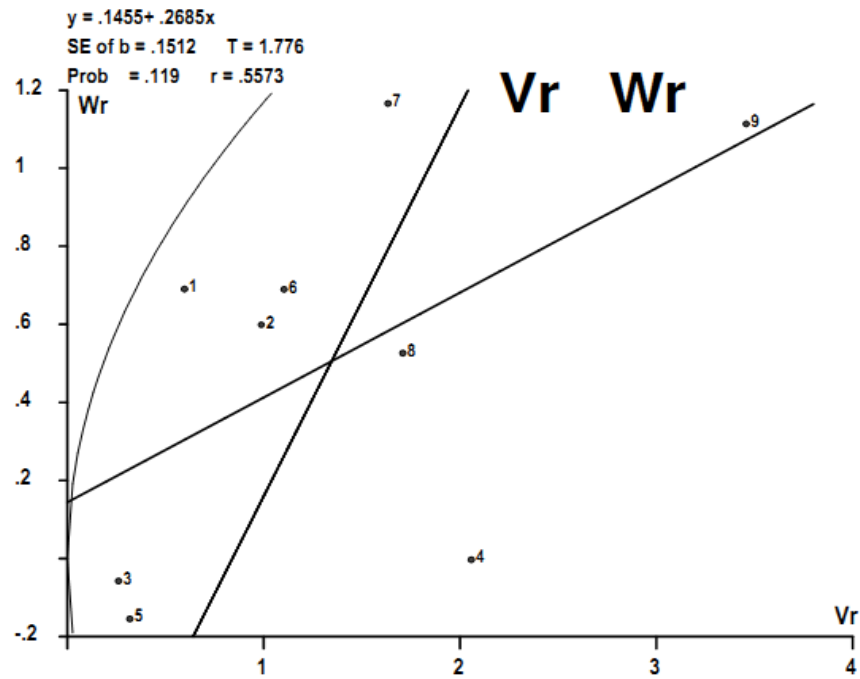
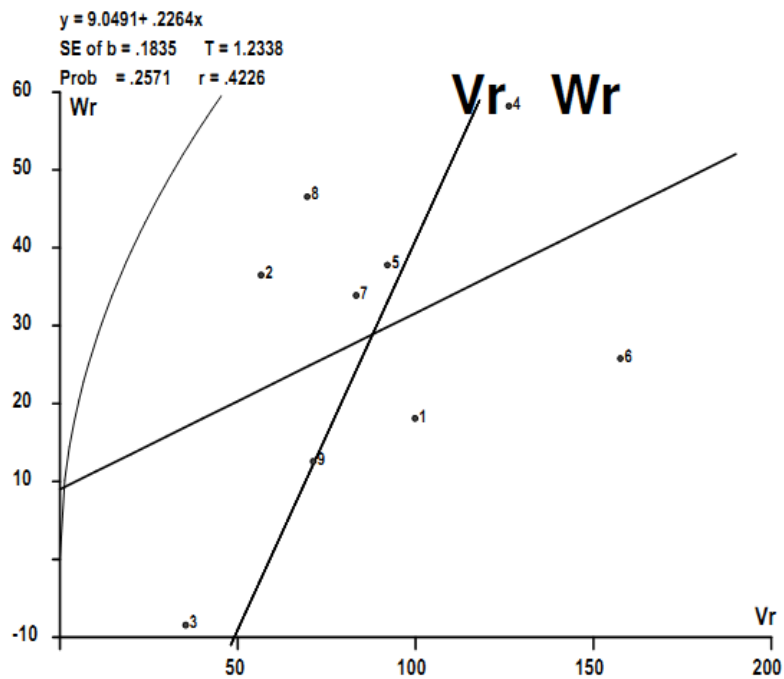


Figure 7. Vr-Wr graph for plant height



4.6.2. Plant height (cm)

The parental array points are widely scattered showing the diversity among the parents. The regression line in Vr-Wr graph crossed the Y axis just above the point of origin showing partial dominance nature (Figure 7). All the array points except P₃ (Khandwa 2) and P₆ (KC 3) were occupied by the intermediate position indicating the equal frequency of dominant and recessive genes.

4.6.3. Number of sympodial branches per plant

The regression line in Vr-Wr graph crossed the Y axis just below the point of origin showing the presence of over dominance. The parental array points are scattered both in above and below the standard line (Figure 8). The array point P₉ (G.Cot 16) located on the regression line and P₃ (Khandwa 2) was found to contain more number of recessive genes.

4.6.4. Number of bolls per plant

The Vr-Wr graph showed that the regression line cuts the Y axis just above the point of origin. The parental array points are widely scattered showing the diversity among the parents. The array points P₄ (Anjali), P₅ (KC 2) and P₇ (MCU 5) were closer to the regression line (Figure 9). The parents KC 3 (P₆) and G.Cot 16 (P₉) were found to contain moderate amount of dominant genes. The array point P₃ (Khandwa 2) was at the distal end.

4.6.5. Boll weight (g)

The parental array points are widely scattered showing the diversity among the parents. The regression line in Vr-Wr graph crossed the Y axis just above the point of origin showing partial dominance nature (Figure 10). The array points P₂ (Surabhi), P₃ (Khandwa 2) and P₇ (MCU 5) were closer to the regression line. The parents Khandwa 2 (P₃) and KC 3 (P₆) were found to contain moderate amount of dominant genes.

4.6.6. Single plant yield (g)

The regression line in Vr-Wr graph crossed the Y axis just below the point of origin showing the presence of over dominance for this trait. The parental array points are widely scattered showing the diversity among the parents for this trait. The array points P₂ (Surabhi) and P₆ (KC 3) were closer to the regression line (Figure 11). The array point P₉

Figure 8. Vr-Wr graph for number of sympodial branches per plant

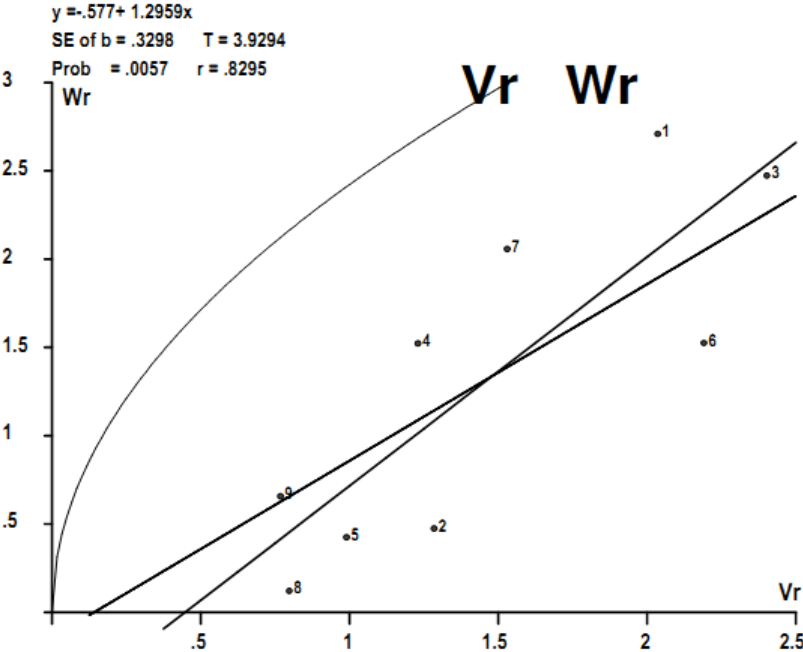


Figure 9. Vr-Wr graph for number of bolls per plant

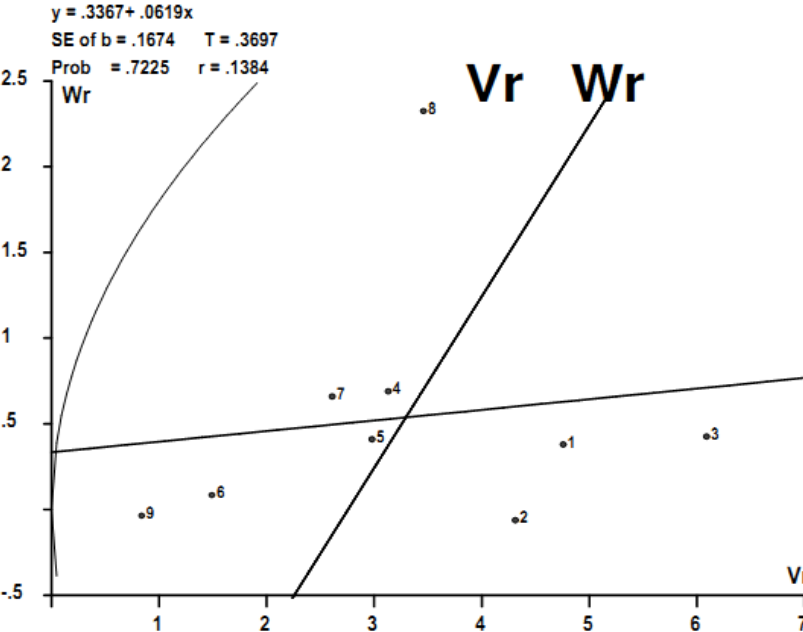


Figure 10. Vr-Wr graph for boll weight

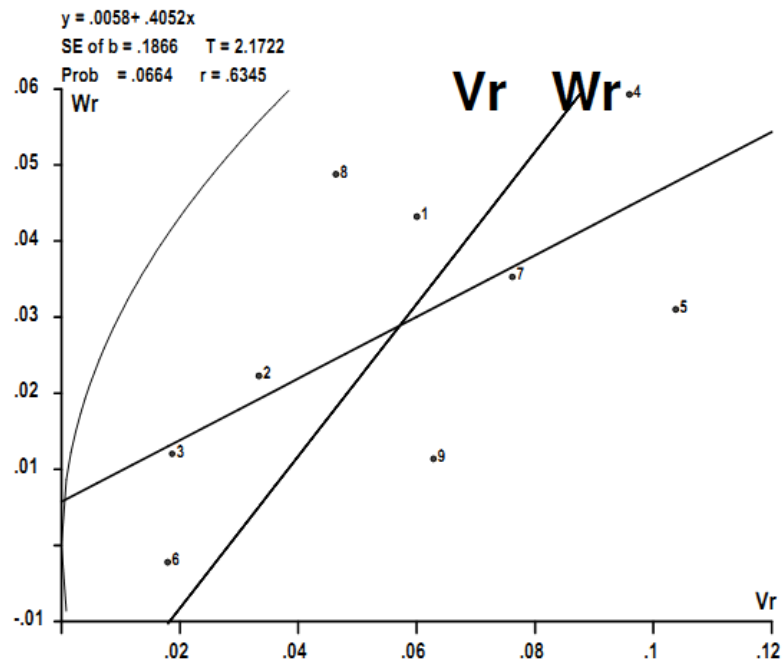
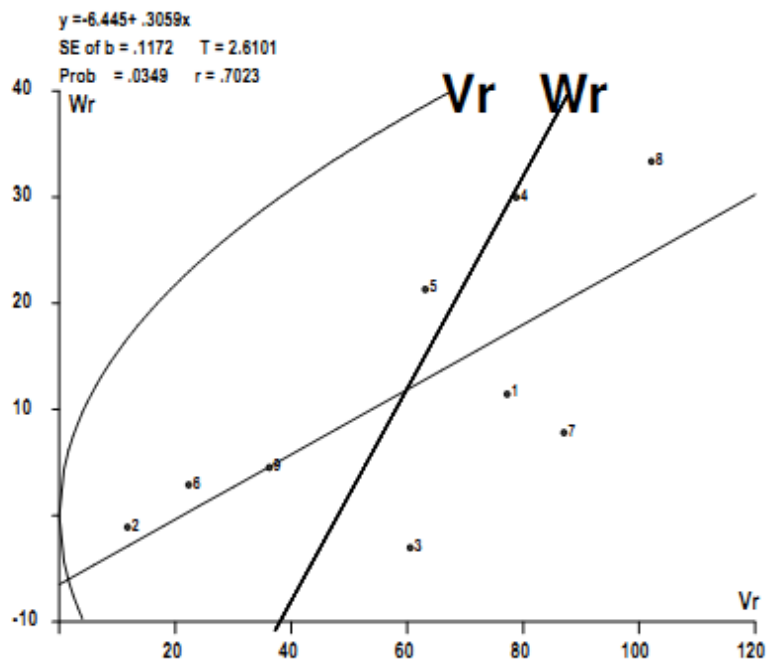


Figure 11. Vr-Wr graph for single plant yield



(G.Cot 16) was located on the regression line and P₈ (MCU 7) was found to contain more number of recessive genes in this trait.

4.6.7. Ginning outturn (%)

The regression line on the Vr-Wr graph passed the Wr axis above the point of origin showing partial dominance nature. The array points P₁ (Suraj), P₅ (KC 2) and P₈ (MCU 7) were close to the regression line. The array points P₂ (Surabhi), P₃ (Khandwa 2), P₅ (KC 2), P₆ (KC 3) and P₇ (MCU 5) were above the regression line (Figure 12). The parental array points P₄ (Anjali) and P₉ (G.Cot 16) are away from the regression line.

4.6.8. Lint index

The regression line cuts the Y axis just below the origin showing the presence of over dominance for this trait. The parental array points are widely scattered showing the diversity among the parents in this trait. The array points P₂ (Surabhi), P₃ (Khandwa 2), P₄ (Anjali) and P₉ (G.Cot 16) were closer to the regression line (Figure 13). The parent Suraj (P₁) was found to contain moderate amount of dominant genes.

4.6.9. Seed index

The regression line intercepted the Y axis above the origin showing partial dominance nature for this trait. The array points are scattered both in above and below the regression line. The array points P₁ (Suraj), P₃ (Khandwa 2), P₄ (Anjali), P₆ (KC 3) and P₉ (G.Cot 16) were above the regression line (Figure 14). The parental array points P₄ (Anjali), P₅ (KC 2) and P₇ (MCU 5) were away from the regression line. The parental lines P₁ (Suraj), P₂ (Surabhi), P₃ (Khandwa 2), P₆ (KC 3), P₈ (MCU 7) and P₉ (G.Cot 16) were occupied by the intermediate position of the graph.

4.6.10. 2.5% span length (mm)

The regression line on the Vr-Wr graph passed the Wr axis below the point of origin showing over dominance nature. The array points P₁ (Suraj), P₄ (Anjali) and P₆ (KC 3) were located near the regression line and P₈ (MCU 7) was found to contain more number of recessive genes (Figure 15).

Figure 12. Vr-Wr graph for ginning outturn

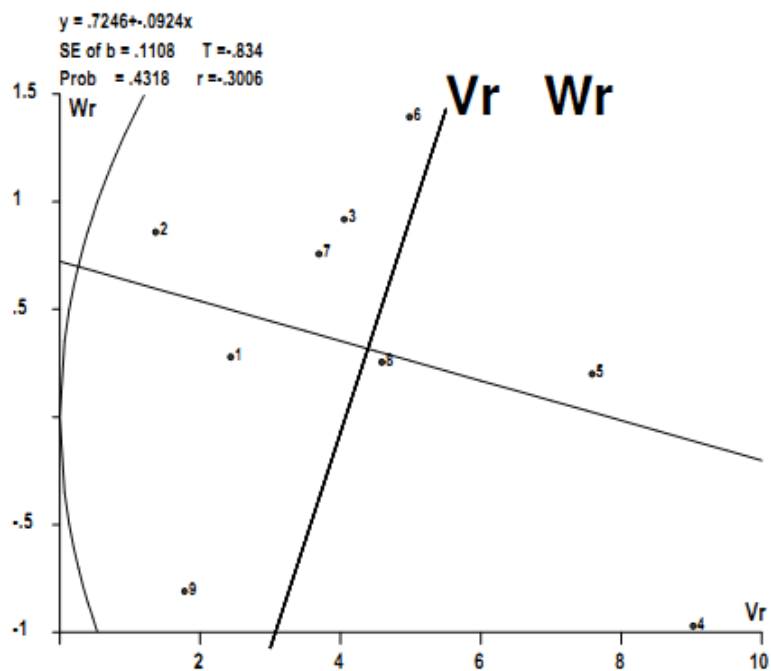


Figure 13. Vr-Wr graph for lint index

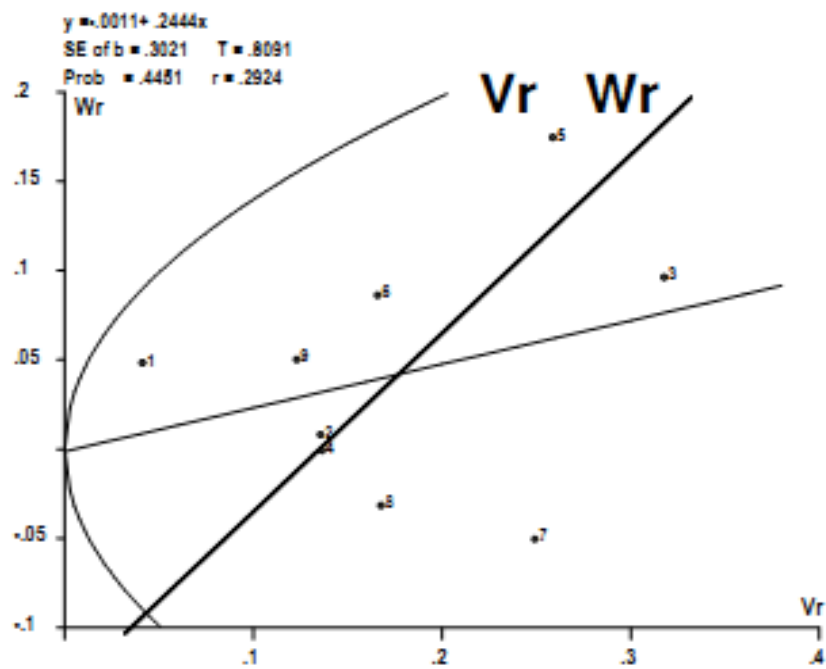


Figure 14. Vr-Wr graph for seed index

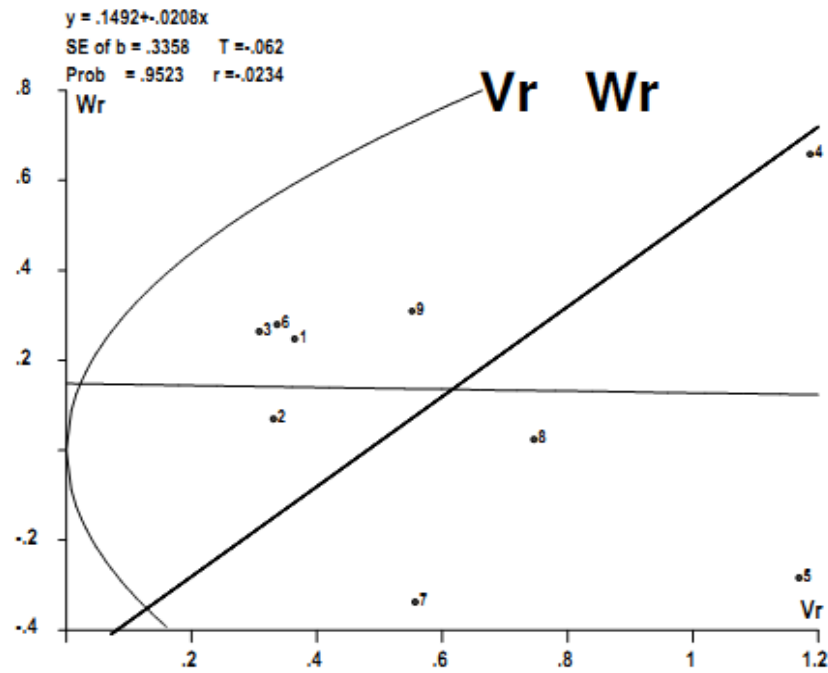
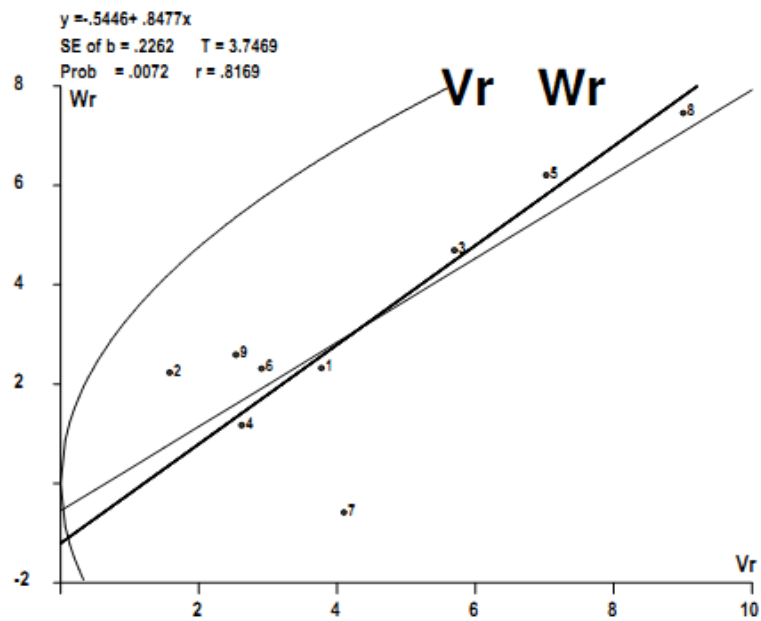


Figure 15. Vr-Wr graph for 2.5 per cent span length



4.6.11. Bundle strength (g/tex)

The regression line passes below the origin showing the presence of over dominance in this character. The parental array point P₉ (G.Cot 16) was located near to the origin showing the presence of more dominant genes in this line (Figure 16). The parent KC 2 (P₅) was located far from origin indicating the presence of more recessive alleles. The array points P₁ (Suraj), P₃ (Khandwa 2), P₆ (KC 3) and P₇ (MCU 5) were located closer to the regression line.

4.6.12. Micronaire value (µg/inch)

The regression line passes below the origin showing the presence of over dominance of this character. The parents MCU 5 (P₇) and G.Cot 16 (P₉) were found to contain moderate amount of dominant genes. The array points P₁ (Suraj), P₃ (Khandwa 2), P₄ (Anjali), P₅ (KC 2), P₆ (KC 3), P₇ (MCU 5) and P₉ (G.Cot 16) were closer to the regression line (Figure 17).

4.6.13. Uniformity ratio (%)

The regression line in Vr-Wr graph crossed the Y axis just below the point of origin showing the presence of over dominance. The parental array points are widely scattered showing the diversity among the parents. The array points P₁ (Suraj) and P₃ (Khandwa 2) were located closer to the regression line (Figure 18). P₇ (MCU 5) was found to contain more number of recessive genes for this trait. The array points viz., P₁ (Suraj), P₂ (Surabhi), P₃ (Khandwa 2), P₅ (KC 2) and P₉ (G.Cot 16) were occupied the intermediate position indicating the equal frequency of dominant and recessive alleles.

4.6.14. Elongation per cent (%)

The regression line in Vr-Wr graph crossed the Y axis just below the point of origin showing over dominance nature. The array points P₆ (KC 3) and P₇ (MCU 5) occupy position along the regression line indicating their same genetic base (Figure 19). The array point P₄ (Anjali) was found to contain more number of recessive genes as it was located far from origin.

Figure 16. Vr-Wr graph for bundle strength

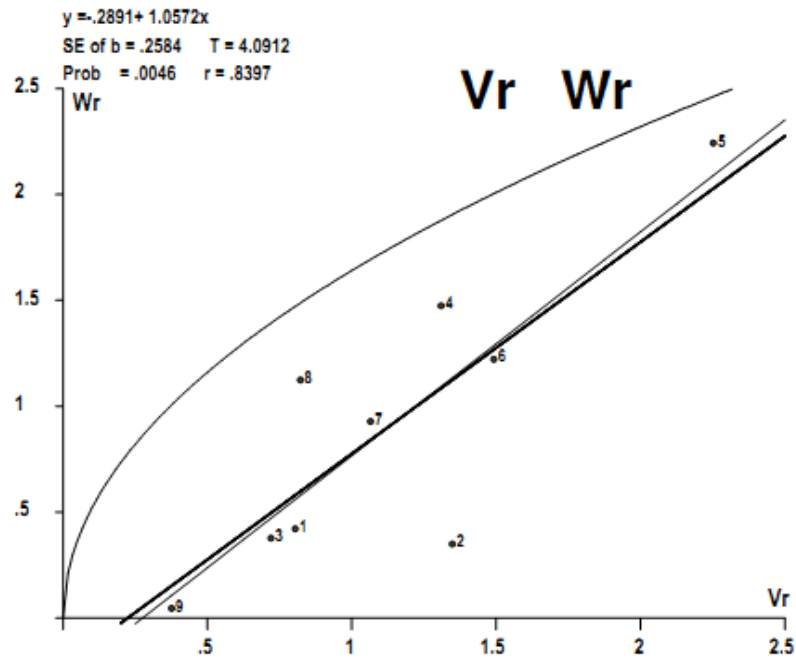


Figure 17. Vr-Wr graph for micronaire value

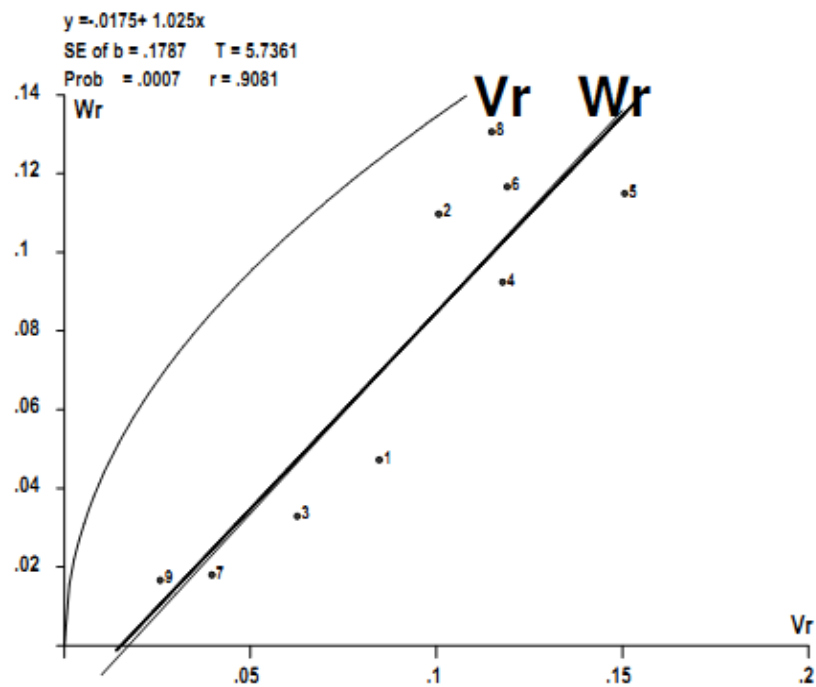


Figure 18. Vr-Wr graph for uniformity ratio

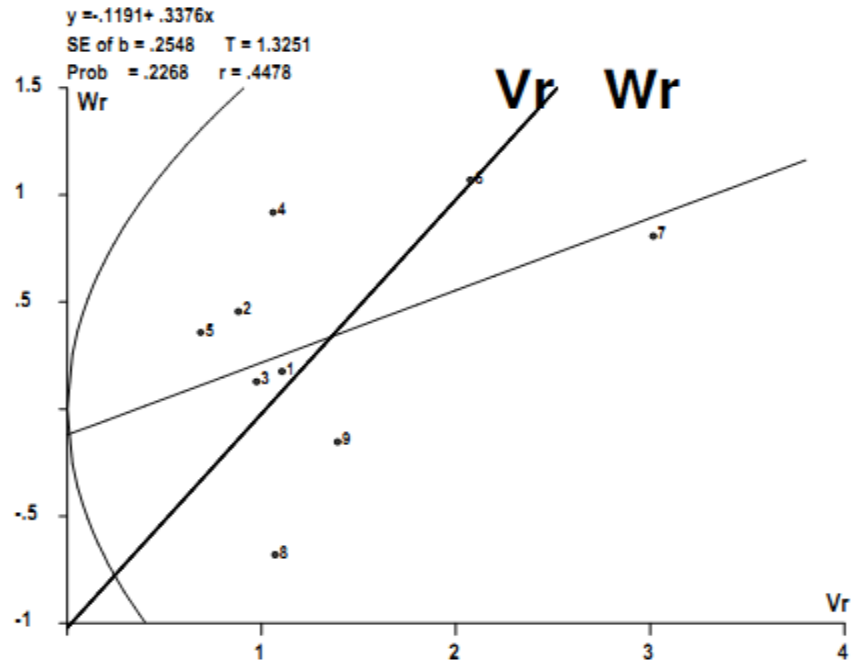
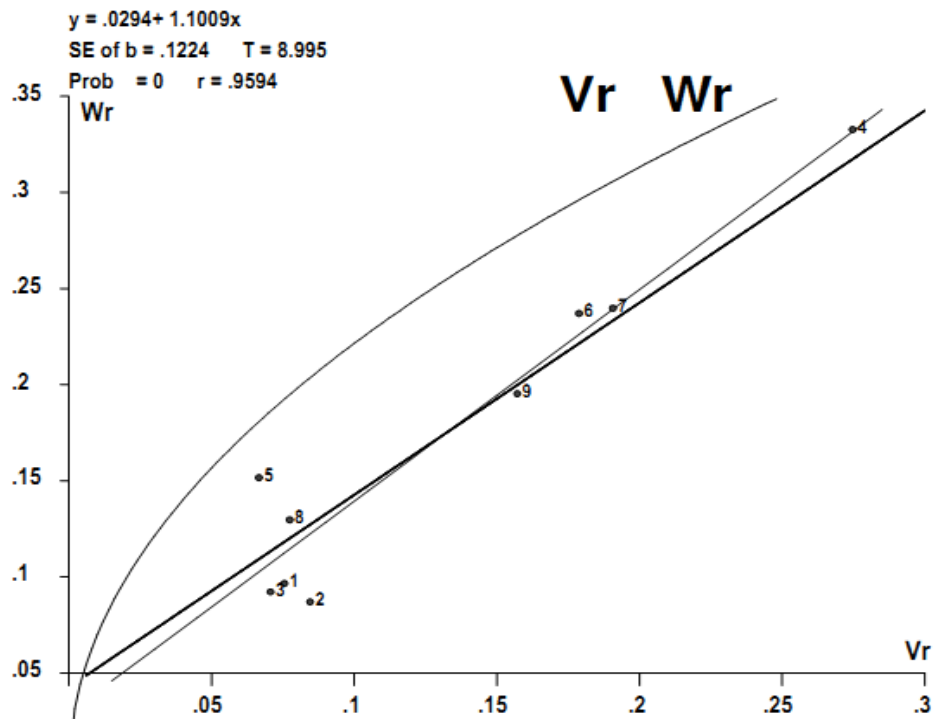


Figure 19. Vr-Wr graph for elongation per cent



Molecular marker analysis

In the present investigation, F₃ progenies derived from an intraspecific cross KC 2 (female parent; abbreviated as P₁) and MCU 5 (male parent; abbreviated as P₂) were evaluated for observing variation and correlation among yield components and fibre quality traits. An attempt has also been made to identify SSR markers linked to the investigated traits by associating the phenotypic data of F₃ progenies with the genotypic data of F₂ segregants, using single marker analysis (SMA) using Anova tool available in Excel. All the F₃ individuals were studied to assess the mean performance, genetic variability, heritability, genetic advance and association analysis of the traits. The results obtained in this study were presented below.

4.7. Mean performance

The mean performance of parents and F₃ progenies for yield and fibre quality traits is presented in Table 43.

The mean values recorded for plant height in P₁, P₂ and F₃ were 95.67cm, 118.67cm and 89.76cm respectively, with a range between 27.00 and 131.33cm in F₃. The F₃ recorded a wide range of 15 to 27 for number of sympodia per plant, with a higher mean value of 19.87 as compared to P₁ (16.33) and P₂ (18.00). Number of bolls per plant ranged from 22 to 38 in F₃ and the mean value recorded in F₃ was higher (27.53) as compared to parents (19.67 and 24.33). The mean boll weight of F₃ was low (2.64g) as compared to the parents P₁ (3.68g) and P₂ (4.00g), with a minimum of 1.25g and a maximum of 4.13g.

The F₃ exhibited a wide range for single plant yield with the highest yield of 115g/plant and the lowest of 23.77g and the mean value recorded for F₃ (73.30g) lie in between P₁ (66.38g) and P₂ (85.09g). The mean values recorded for ginning outturn in P₁, P₂ and F₃ were 33.03%, 34.61% and 31.10% respectively, with a range of 15.07 to 36.67% in F₃. The F₃ recorded a range of 2.09 to 4.99 for lint index, with a lower mean value of 3.77 as compared to parents (5.17 and 4.98). The mean value recorded for seed index in F₃ was lower (8.40) when compared to P₁ (10.47) and P₂ (9.41), with a range of 5.26 to 11.92 in F₃.

Table 43. Mean performance of parents and mean, standard error and range of F₃'s for yield and fibre quality traits

S.No	Characters	Mean			Standard Error	Minimum	Maximum
		KC 2 (P ₁)	MCU 5 (P ₂)	F ₃			
1.	Plant height (cm)	95.67	118.67	89.76	0.62	27.00	131.33
2.	No of sympodia per plant	16.33	18.00	19.87	0.14	15.00	27.33
3.	No. of bolls per plant	19.67	24.33	27.53	0.19	22.00	38.00
4.	Boll weight (g)	3.68	4.00	2.64	0.03	1.25	4.13
5.	Single plant yield (g)	66.38	85.09	73.30	1.37	23.77	115.00
6.	Ginning outturn (%)	33.03	34.61	31.10	0.21	15.07	36.67
7.	Lint index	5.17	4.98	3.77	0.03	2.09	4.99
8.	Seed index	10.47	9.41	8.40	0.09	5.26	11.92
9.	2.5% span length (mm)	24.98	33.54	29.56	0.12	24.50	34.61
10.	Bundle strength (g/tex)	19.08	22.99	21.03	0.13	16.60	26.10
11.	Micronaire value (µg/inch)	4.42	3.80	3.79	0.03	2.50	4.50
12.	Uniformity ratio (%)	49.87	49.19	48.38	0.13	40.30	51.40
13.	Elongation per cent (%)	5.00	5.56	4.70	0.04	3.90	6.20

Among the fibre quality parameters, the mean 2.5% span length of F₃ was intermediate (29.56mm) between the two parents (24.98mm for P₁ and 33.54mm for P₂), with the maximum of 34.61mm and the minimum of 24.50mm. Bundle strength ranged between 16.60 and 26.10 g/tex in F₃ and the mean value recorded in F₃ was intermediate (21.03 g/tex) between P₁ (19.08 g/tex) and P₂ (22.99 g/tex). The F₃ recorded a lower mean value of 3.79 µg/inch for micronaire when compared to parents (4.42 µg/inch and 3.80 µg/inch), with a range of 2.50 to 4.50 µg/inch in F₃. The lower mean value of 48.38% for uniformity ratio was recorded in F₃ as compared to parents P₁ (49.87%) and P₂ (49.19%), with the maximum of 51.40% and the minimum of 40.30% in F₃. Elongation per cent ranged between 3.90% and 6.20% in F₃ and the mean values recorded in P₁, P₂ and F₃ were 5.00%, 5.56% and 4.70% respectively.

4.8. Variability analysis

The variability was estimated for various yield and fibre quality traits in F₃ population. Phenotypic variance (PV), genotypic variance (GV), phenotypic co-efficient of variance (PCV), genotypic co-efficient of variance (GCV), heritability in broad sense and genetic advance as percentage of mean is presented in Table 44. The PCV and GCV estimates are presented graphically in Figure 20. The heritability and genetic advance as percentage of mean are also presented graphically in Figure 21.

4.8.1. Phenotypic and genotypic variances

The analysis showed that single plant yield recorded the highest phenotypic variance (524.48) and genotypic variance (430.67), followed by plant height (127.86 and 79.57) and number of bolls per plant (11.87 and 7.25). Boll weight recorded the lowest phenotypic variance (0.26) and genotypic variance (0.21). In addition, lint index, seed index, micronaire value and elongation per cent also showed a high phenotypic variance and genotypic variance.

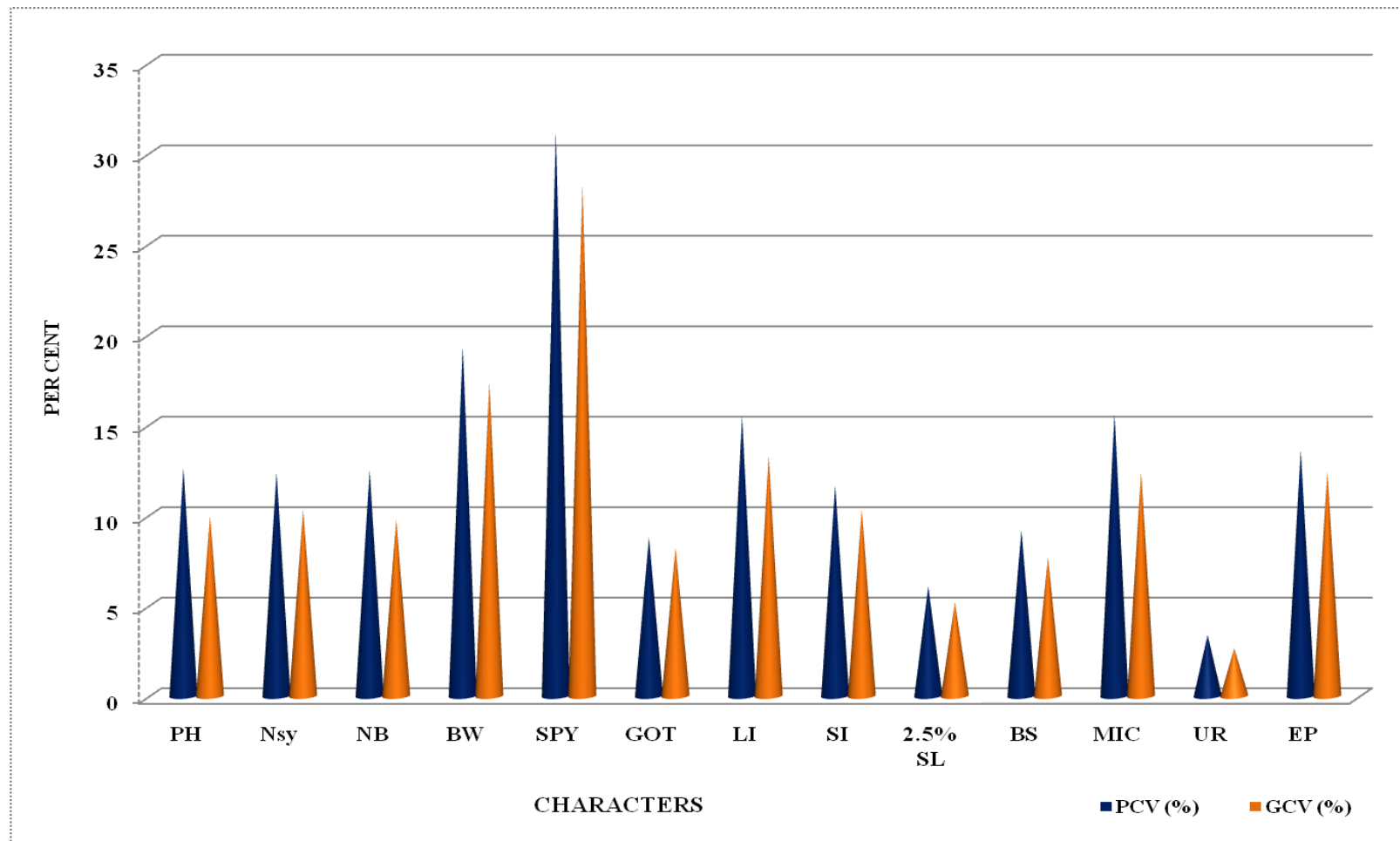
4.8.2. Phenotypic and genotypic co-efficient of variation

The co-efficient of phenotypic and genotypic variance was worked out for valid comparison between different characters. In general, all the characters studied had higher PCV than GCV. The PCV ranged from 3.38 to 31.24 and the highest PCV value of 31.24

Table 44. Components of variance for yield and fibre quality traits

Characters	Phenotypic variance	Genotypic variance	PCV (%)	GCV (%)	Heritability (%)	Genetic advance as percentage of mean
Plant height (cm)	127.86	79.57	12.60	9.94	62.24	16.15
Number of sympodial branches per plant	6.05	4.20	12.38	10.31	69.42	17.68
Number of bolls per plant	11.87	7.25	12.51	9.78	61.08	15.74
Boll weight (g)	0.26	0.21	19.31	17.36	80.77	31.87
Single plant yield (g)	524.48	430.67	31.24	28.31	82.11	52.85
Ginning outturn (%)	7.47	6.50	8.79	8.20	87.01	5.64
Lint index	0.34	0.25	15.47	13.26	73.53	24.91
Seed index	0.96	0.75	11.66	10.31	78.13	14.17
2.5% span length length (mm)	3.22	2.35	6.07	5.19	72.98	4.89
Bundle strength (g/tex)	3.71	2.60	9.16	7.67	70.08	2.78
Micronaire value (µg/inch)	0.35	0.22	15.61	12.38	62.86	21.94
Uniformity ratio (%)	2.67	1.63	3.38	2.64	61.05	2.61
Elongation per cent (%)	0.41	0.34	13.62	12.41	82.93	18.02

Figure 20. PCV and GCV estimates for yield and fibre quality traits



was observed for single plant yield. Moderate PCV values were noticed for boll weight (19.31), micronaire value (15.61), lint index (15.47), elongation per cent (13.62), plant height (12.60), number of bolls per plant (12.51), number of sympodial branches per plant (12.38) and seed index (11.66). Low PCV values were noticed for bundle strength (9.16), ginning outturn (8.79), 2.5% span length (6.07) and uniformity ratio (3.38).

The GCV ranged from 2.64 to 28.31 and the highest GCV value of 28.31 was observed for single plant yield. Moderate GCV values were noticed for boll weight (17.36), lint index (13.26), elongation per cent (12.41), micronaire value (12.38), seed index (10.31) and number of sympodial branches per plant (10.31). Low GCV values were noticed for plant height (9.94), number of bolls per plant (9.78), ginning outturn (8.20), bundle strength (7.67), 2.5% span length (5.19) and uniformity ratio (2.64).

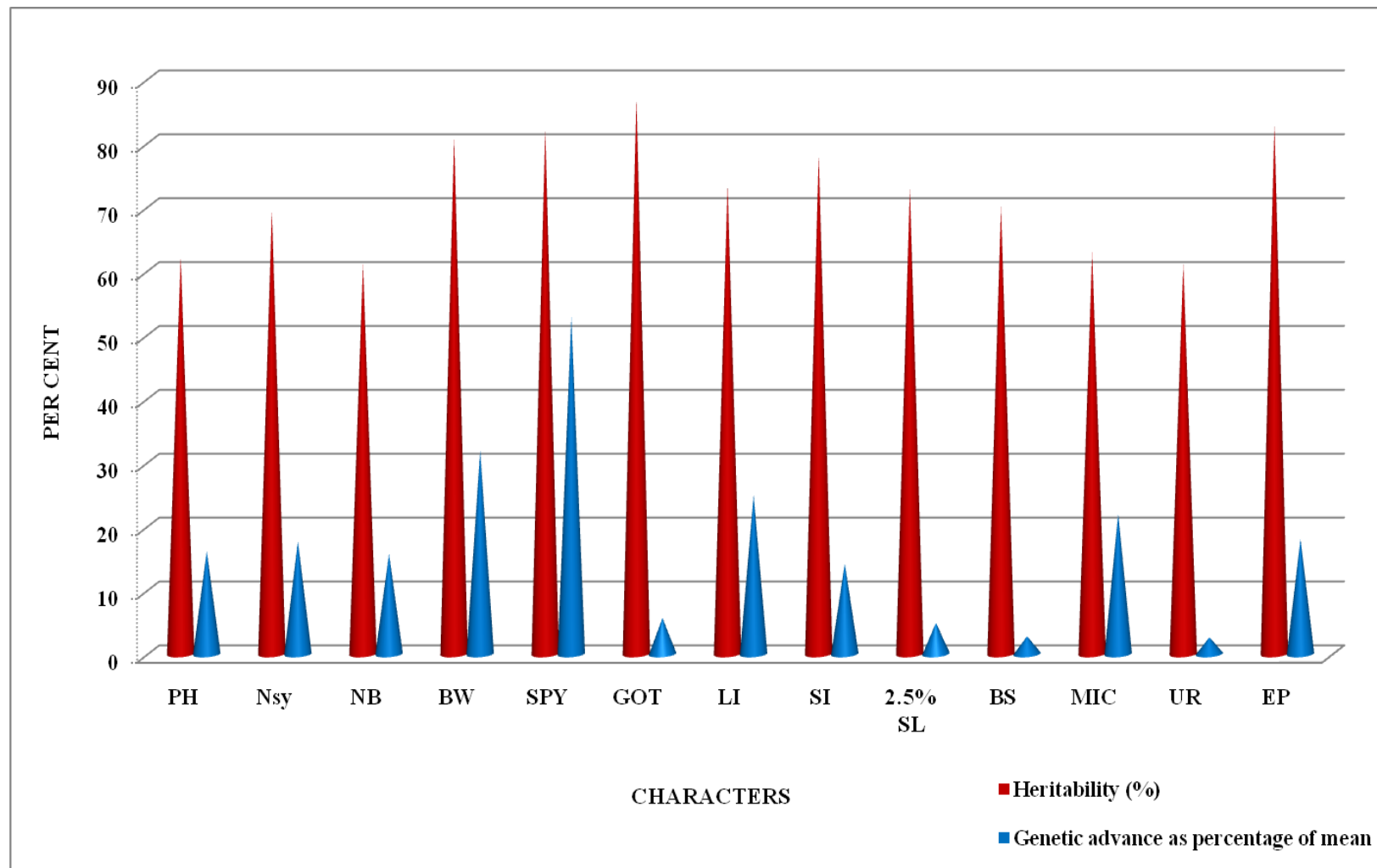
4.8.3. Heritability

The heritability estimates ranged from 61.05 to 87.01 per cent. All the characters showed a high heritability. Ginning outturn exhibited 87.01 per cent heritability, followed by elongation per cent (82.93 per cent), single plant yield (82.11 per cent), boll weight (80.77 per cent), seed index (78.13 per cent), lint index (73.53 per cent) and 2.5% span length (72.98 per cent). Uniformity ratio exhibited 61.05 per cent of heritability.

4.8.4. Genetic advance as percentage of mean

The genetic advance as percentage of mean ranged from 2.61 to 52.85 per cent. The highest genetic advance as percentage of mean was recorded for single plant yield (52.85 per cent), boll weight (31.87 per cent), lint index (24.91 per cent) and micronaire value (21.94 per cent). Moderate values were noticed for elongation per cent (18.02 per cent), number of sympodial branches per plant (17.68 per cent), plant height (16.15 per cent), number of bolls per plant (15.74 per cent) and seed index (14.17 per cent). The lowest genetic advance as percentage of mean was recorded for ginning outturn (5.64 per cent), 2.5% span length (4.89 per cent), bundle strength (2.78 per cent) and uniformity ratio (2.61 per cent).

Figure 21. Heritability and genetic advance as percentage of mean for yield and fibre quality traits



4.9. Association analysis

The nature and extent of association that existed between the seed cotton yield with other yield contributing characters and fibre quality traits were studied through correlation analysis.

4.9.1. Correlation studies

The simple correlation co-efficient between seed cotton yield with twelve biometric characters such as yield and fibre quality components and also among the traits themselves were worked out and presented in Table 45.

4.9.1.1. Correlation between seed cotton yield and its components and fibre quality characters

In the present study, plant height, number of sympodial branches per plant, number of bolls per plant, boll weight, lint index and seed index expressed significantly positive correlation with seed cotton yield. The simple correlation values recorded for these characters were 0.373, 0.318, 0.516, 0.629, 0.543 and 0.797, respectively. The ginning outturn (-0.452) is the only character which showed significantly negative correlation. The quality characters like, 2.5% span length, bundle strength, micronaire value and uniformity ratio exhibited positive correlation whereas, the elongation per cent showed negative correlation with seed cotton yield.

4.9.1.2. Inter correlation among yield and fibre quality component characters

4.9.1.2.1. Plant height

High inter correlation was observed between plant height and characters like number of sympodial branches per plant (0.732), number of bolls per plant (0.562), boll weight (0.152), lint index (0.148), seed index (0.401) and 2.5% span length (0.193). The plant height was positively correlated with bundle strength (0.120) and uniformity ratio (0.004) and negatively correlated with micronaire value (-0.107). This trait had significant and negative correlation with ginning outturn (-0.245) and elongation per cent (-0.150).

Table 45. Simple correlation co-efficients between seed cotton yield with yield components and fibre quality traits

Characters	PH	Nsy	NB	BW	GOT	LI	SI	2.5% SL	BS	MIC	UR	EP	SCY
PH	1.000	0.732**	0.562**	0.152*	-0.245**	0.148*	0.401**	0.193**	0.120	-0.107	0.004	-0.150*	0.373**
Nsy		1.000	0.665**	0.021	-0.221**	0.135*	0.357**	0.158*	0.129*	-0.084	0.030	-0.035	0.318**
NB			1.000	0.026	-0.237**	0.283**	0.432**	0.099	-0.025	0.051	0.045	-0.074	0.516**
BW				1.000	-0.418**	0.431**	0.576**	0.046	0.080	0.011	0.098	0.019	0.629**
GOT					1.000	0.471**	-0.508**	-0.117	-0.117	0.028	0.009	0.080	-0.452**
LI						1.000	0.514**	-0.019	-0.065	0.065	0.091	0.039	0.543**
SI							1.000	0.107	0.054	0.030	0.089	-0.042	0.797**
2.5% SL								1.000	0.430**	-0.170**	-0.206**	-0.460**	0.066
BS									1.000	-0.341**	0.243**	-0.155*	0.036
MIC										1.000	0.042	0.054	0.034
UR											1.000	0.327**	0.108
EP												1.000	-0.006

*significant at 5 per cent level, ** significant at 1 per cent level

4.9.1.2.2. Number of sympodial branches per plant

The trait number of sympodial branches per plant recorded significant and positive correlation with number of bolls per plant (0.665), lint index (0.135), seed index (0.357), 2.5% span length (0.158) and bundle strength (0.129). This trait was positively correlated with boll weight (0.021) and uniformity ratio (0.030) whereas, negatively correlated with micronaire value (-0.084) and elongation per cent (-0.035). The ginning outturn (-0.221) is the only character which showed significantly negative correlation.

4.9.1.2.3. Number of bolls per plant

Number of bolls per plant was significantly and positively correlated with lint index (0.283) and seed index (0.432). It showed a positive relationship with boll weight (0.026), 2.5% span length (0.099), micronaire value (0.051) and uniformity ratio (0.045). This trait had significant negative inter correlation with ginning outturn (-0.237). This trait was negatively correlated with bundle strength (-0.025) and elongation per cent (-0.074).

4.9.1.2.4. Boll weight

Boll weight displayed a positive and significant correlation with lint index (0.431) and seed index (0.576). It showed a positive relationship with 2.5% span length (0.046), bundle strength (0.080), micronaire value (0.011), uniformity ratio (0.098) and elongation per cent (0.019). The ginning outturn (-0.418) is the only character which showed significantly negative correlation.

4.9.1.2.5. Ginning outturn

This character showed a positive significant correlation with lint index (0.471), while positive association with micronaire value (0.028), uniformity ratio (0.009) and elongation per cent (0.080). Seed index (-0.508) showed the significant negative correlation, whereas the negative correlation was exhibited by 2.5% span length (-0.117) and bundle strength (-0.117).

4.9.1.2.6. Lint index

Lint index had significant positive association with seed index (0.514), whereas it had negative correlation with 2.5% span length (-0.019) and bundle strength (-0.065). This trait had positive inter relationship with micronaire value (0.065), uniformity ratio (0.091) and elongation per cent (0.039).

4.9.1.2.7. Seed index

Positive correlation was observed between seed index and characters like 2.5% span length (0.107), bundle strength (0.054), micronaire value (0.030) and uniformity ratio (0.089). This trait was negatively correlated with elongation per cent (-0.042).

4.9.1.2.8. 2.5% span length

This trait showed positive significant correlation with bundle strength (0.430), while negative significant correlation with micronaire value (-0.170), uniformity ratio (-0.206) and elongation per cent (-0.460).

4.9.1.2.9. Bundle strength

Bundle strength had significant positive association with uniformity ratio (0.243) whereas, it had negative significant correlation with micronaire value (-0.341) and elongation per cent (-0.155).

4.9.1.2.10. Micronaire value

Micronaire value exhibited positive association with uniformity ratio (0.042) and elongation ratio (0.054).

4.9.1.2.11. Uniformity ratio

The trait uniformity ratio had significant and positive correlation with elongation per cent (0.327).

4.10. SMA analysis for yield and fibre quality traits

A segregating population of 246 F₂ plants, obtained from an intraspecific cross KC 2 x MCU 5 were used for QTL analysis of agronomic and fibre quality traits. Genotyping of these F₂ progenies with SSR markers and phenotypic data of 246 F₃

progenies on thirteen yield and fibre quality traits were used for SMA analysis. By correlating the phenotypic data on yield and fibre quality traits with the genotypic data, an attempt has been made to identify SSR markers associated with yield and fibre quality traits. Heritability (percentage) for yield and fibre quality traits is given in Table 46.

4.10.1. Parental polymorphism

A total of 708 SSR markers were used to screen polymorphism between the parents KC 2 and MCU 5. Though, 23 SSR primer pairs showed polymorphism between parents, only 12 SSRs (3.25%) yielded unambiguous and scorable polymorphic loci (Plate 5) and hence, they have been used for further analysis (Plate 6). The list of polymorphic primers are given in Table 5 and sequence information is furnished in Annexure I.

4.10.2. Single marker analysis (SMA)

The markers were subjected to single factor ANOVA analysis using the marker as independent and the respective phenotype as dependent. SMA of polymorphic markers, identified in this study, using simple ANOVA revealed significant association of 8 SSR markers with yield and fibre quality traits and were listed in Table 46.

BNL 3563 showed association with plant height with a phenotypic variation of 2.95%. BNL 1161 were found to have relationship with the trait number of sympodial branches per plant with a phenotypic variation of 2.67%. The marker BNL 3623 had associated with number of bolls per plant with an R^2 value of 5.46%. Four SSR markers viz., BNL 3452, BNL 3563, DPL 0234 and DPL 0322 showed association with boll weight and explained the phenotypic variation of 3.42%, 3.54%, 2.89% and 2.83%, respectively. The marker BNL 3563 had associated with three traits viz., single plant yield, ginning outturn and seed index with the phenotypic variation of 2.49%, 6.58% and 2.50%, respectively. Both BNL 1161 and CIR 203 showed association with 2.5% span length and explained the phenotypic variation of 2.49% and 3.33%, respectively. The marker BNL 3563 had associated with bundle strength with an R^2 value of 3.12%. The marker NAU 797 had associated with both micronaire value and elongation per cent with the phenotypic variation of 3.47% and 2.62%, respectively.

Table 46. SSR markers associated with yield and fibre quality traits identified through single marker analysis using simple ANOVA

SI. No	Name of the trait	Primer	Chromosome number *	F-cal.	F-crit.	R ² (%)
1.	Plant height	BNL 3563	10	3.676	3.033	2.95
2.	Number of sympodial branches per plant	BNL 1161	9, 23	3.209	3.034	2.67
3.	Number of bolls per plant	BNL 3623	13	6.818	3.034	5.46
4.	Boll weight	BNL 3452	10, 19	4.248	3.033	3.42
		BNL 3563	10	4.437	3.033	3.54
		DPL 0234	-	3.526	3.034	2.89
		DPL 0322	15	3.434	3.034	2.83
5.	Single plant yield	BNL 3563	10	3.087	3.033	2.49
6.	Ginning outturn	BNL 3563	10	8.520	3.033	6.58
7.	Seed index	BNL 3563	10	3.101	3.033	2.50
8.	2.5% span length	BNL 1161	9, 23	2.988	3.034	2.49
		CIR 203	5	3.983	3.035	3.33
9.	Bundle strength	BNL 3563	10	3.897	3.033	3.12
10.	Micronaire value	NAU 797	-	4.258	3.034	3.47
11.	Elongation per cent	NAU 797	-	3.186	3.034	2.62

*as per the published reports of Cotton Marker Database (CMD) (http://www.cottonmarker.org/cgi-bin/cmd_search_marker.cgi)

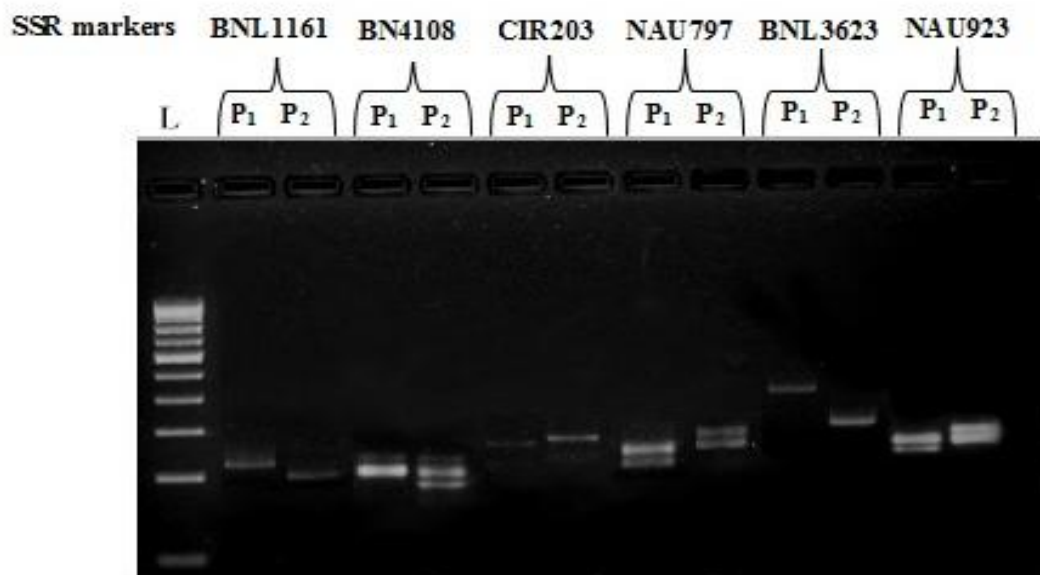
- : Not yet assigned to cotton chromosomes

F-cal : calculated F value

F-crit : F table value

R² (%) : percentage of phenotypic variation

**Plate 5. Parental polymorphism as revealed by SSR markers between the parents
KC 2 and MCU 5**

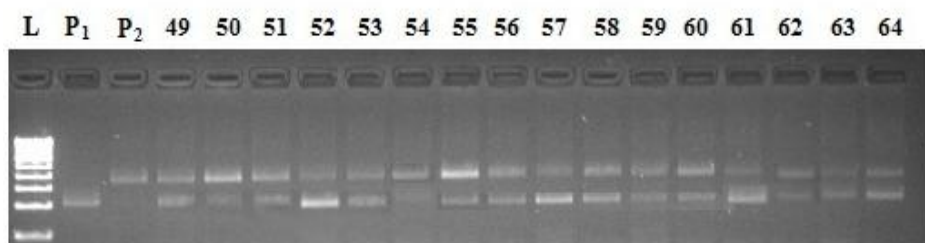
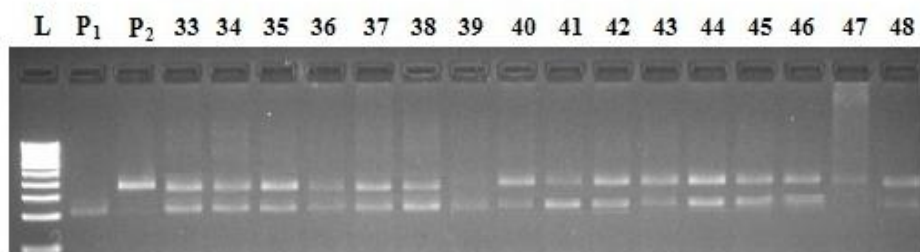
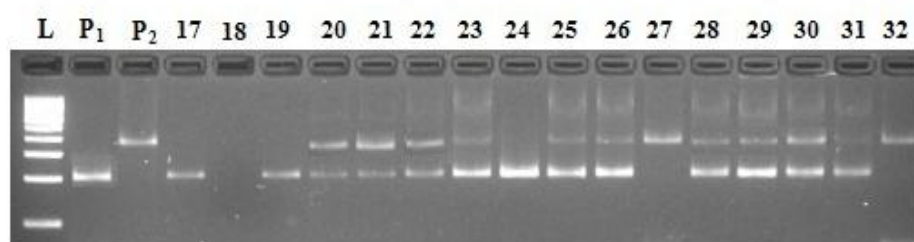
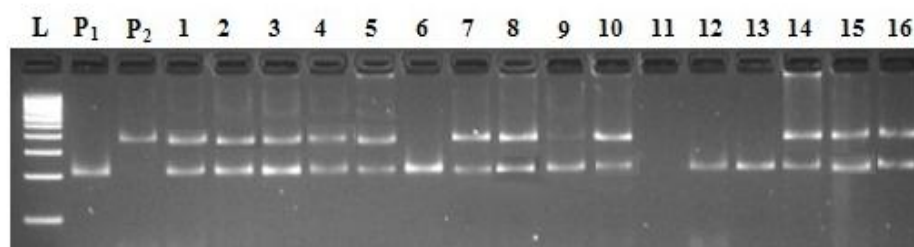


L – 100 bp ladder

P₁ – KC 2

P₂ – MCU 5

**Plate 6. Segregation pattern of BNL3623 among F₂ progenies derived from
KC 2 x MCU 5**



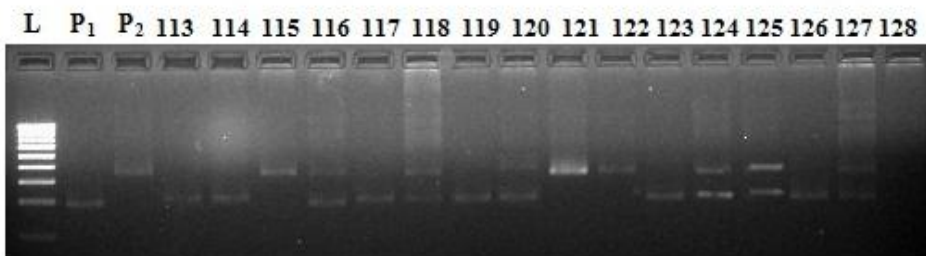
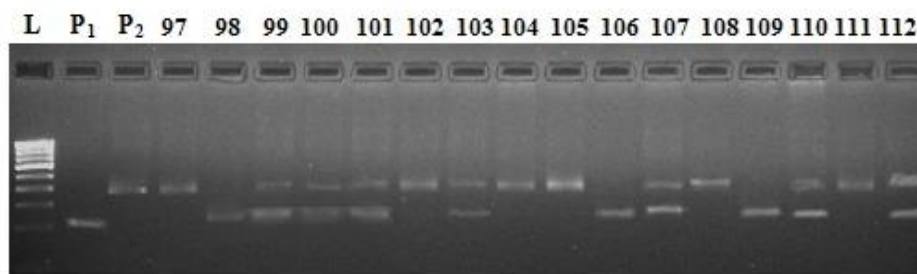
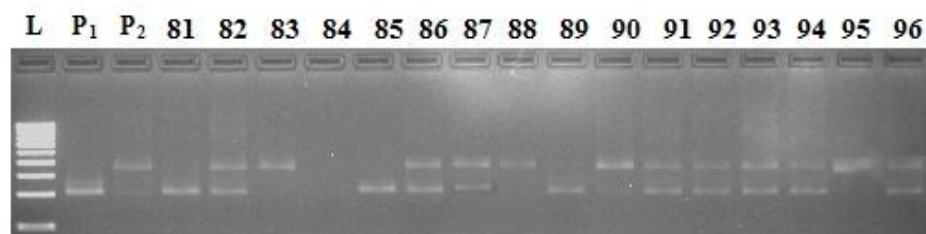
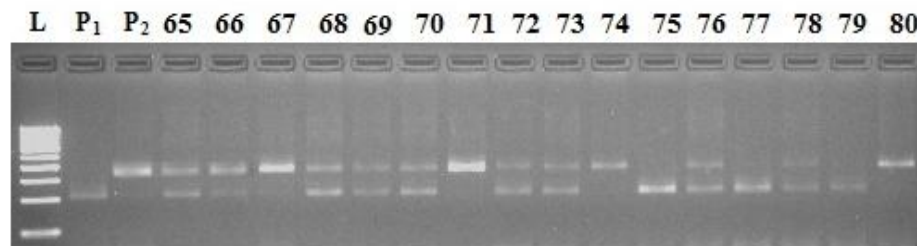
L - 100 base pair ladder

P₁ - KC 2

1 to 64 - F₂ progenies

P₂ - MCU 5

Plate 6. Contd..



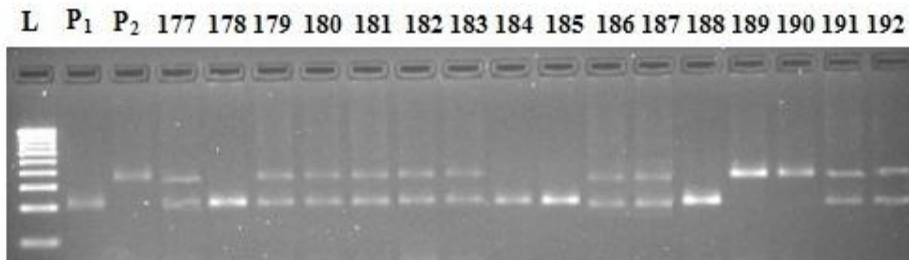
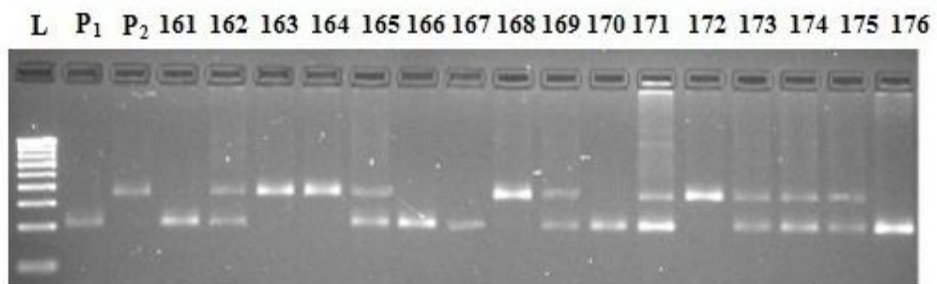
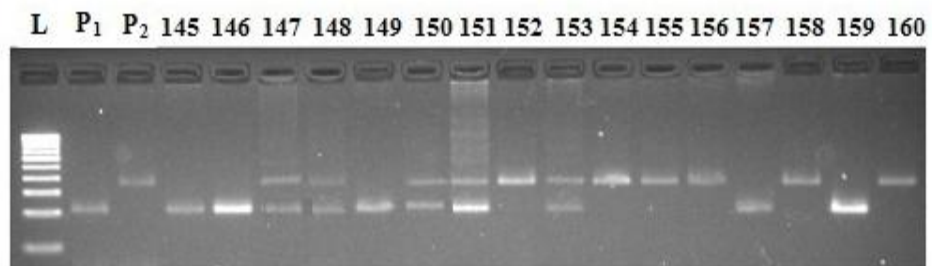
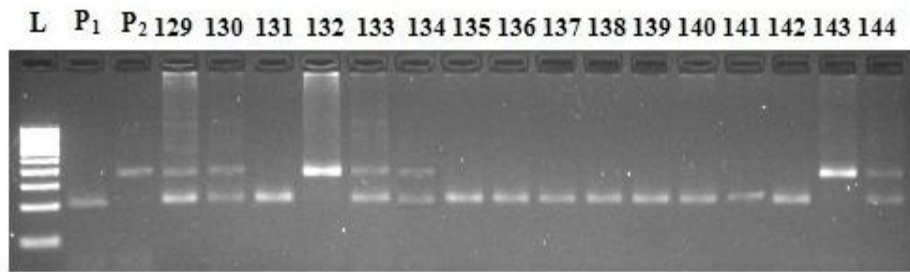
L - 100 base pair ladder

P₁ - KC 2

65 to 128 - F₂ progenies

P₂ - MCU 5

Plate 6. Contd..



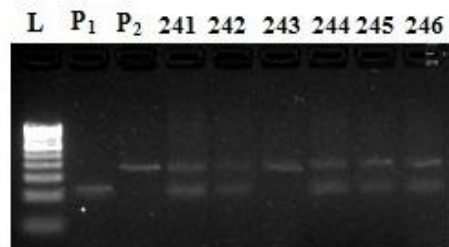
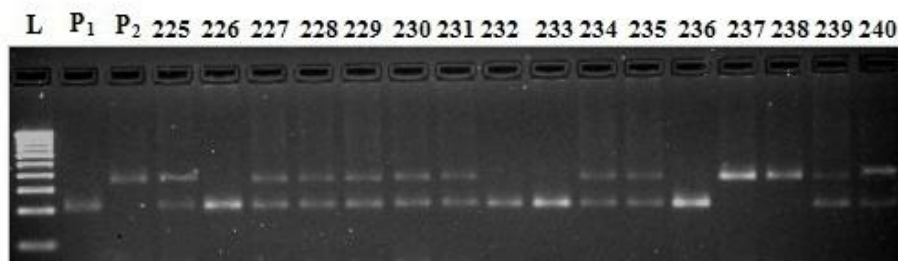
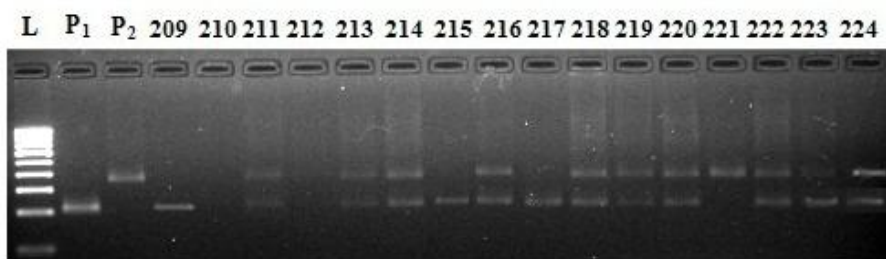
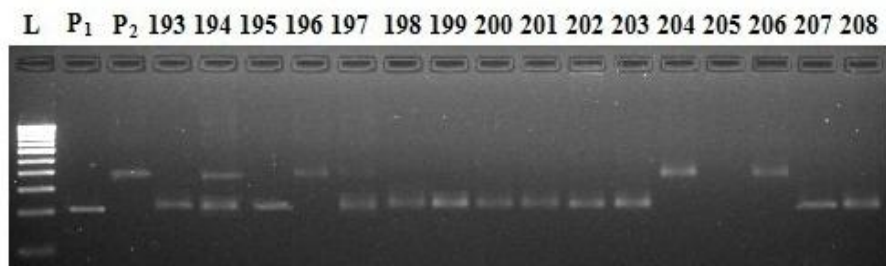
L – 100 base pair ladder

P₁ – KC 2

129 to 192 – F₂ progenies

P₂ – MCU 5

Plate 6. Contd..



L – 100 base pair ladder

P₁ – KC 2

193 to 246 – F₂ progenies

P₂ – MCU 5

Discussion

CHAPTER - V

DISCUSSION

Cotton is the world's leading natural fibre crop and it is a cornerstone for textile industries worldwide. It is a large diverse and economically viable genus, which includes many diploid and tetraploid species indigenous to most of the tropical regions of the world (Fryxell *et al.*, 1992). The cultivated tetraploid species *G. hirsutum*, also referred to as "upland cotton", accounts for about 95% of the global cotton production. Consequently, a great majority of world-wide cotton breeding programs have been focusing on improving upland cotton. With the increasing global demand for textile products, intense competition from synthetic fibres and textile industry's modernization by shifting to high-speed spinning technologies, the need for higher yielding upland cotton cultivars with improved fibre quality has never been more critical (Meredith, 2005).

In breeding high yielding varieties of crop plants for quantitative and qualitative traits, plant breeders often faces the problem of selecting parents and crosses. Hybridization programme has been carried out to create variability for making selections. Knowledge on genetic architecture of parents, in terms of yield and quality related characters would help in identifying superior cross combinations in early generation itself. Combining ability analysis gives us more useful informations regarding the selection in terms of the performance of the hybrids. This analysis elucidates the nature and magnitude of various types of gene action involved in the expression of quantitative traits. Recent developments in the methodologies of biometrical genetics have led to the formulations of a number of effective approaches to understand the genetics of quantitative and qualitative characters.

The first step in cross breeding programme involves the selection of good parents for which the diallel analysis is a tool to identify parents whose hybrids will be amenable to selection response (Khan *et al.*, 2009a). The diallel analysis has been extensively used to understand the genetic architecture of quantitatively inherited traits. The diallel cross among selected parents can provide information on the genetic variances in a population derived by random mating of these parents.

In the present study, nine genotypes were crossed in a diallel analysis model I and method I to produce seventy two hybrids and those along with the parental lines were studied for the manifestation of heterosis in hybrids. The magnitude of heterosis and general as well as specific combining abilities were studied for fourteen characters.

The information on genetics of yield, fibre and its components are discussed here under.

5.1. Analysis of variance

Analysis of variance showed highly significant differences due to genotypes for all the traits indicating the presence of sufficient variability in the experimental materials. Significance of variance in parents V_s hybrids interaction provided adequacy for comparing the heterotic expression for all the characters except boll weight, ginning outturn, lint index and seed index. Parents and hybrids showed significant differences between all the characters studied except number of bolls, boll weight, single plant yield, lint index and seed index. It was also confirmed by the results reported in earlier studies of Jatoi *et al.* (2010) in boll weight and Kumar *et al.* (2014) in single plant yield.

5.2. Evaluation of parents

Information on the *per se* performance and nature of general combining ability of characters is necessary for selection of suitable parents for developing hybrids. Gilbert (1958) suggested that parents with high mean performance would be much useful in producing better offsprings in any breeding programme. According to Spargue and Tatum (1942), the parents having high *gca* effects could be useful since, the *gca* effects is due to additive gene action which is fixable. Therefore, in the present study a total of nine parents were evaluated based on *per se* performance and *gca* effects both individually and in combination.

5.2.1. Based on *per se* performance

The *per se* performance of parents would serve greater importance in production of best offspring. MCU 5 possessed favourable mean values for ten characters viz., days to first boll bursting, plant height, number of sympodial branches per plant, number of bolls per plant, boll weight, single plant yield, 2.5% span length, bundle strength,

micronaire value and elongation per cent; Anjali possessed favourable mean values for seven characters namely plant height, number of bolls per plant, boll weight, single plant yield, micronaire value, uniformity ratio and elongation per cent; Surabhi for days to first boll bursting, plant height, 2.5% span length, bundle strength and micronaire value and KC 3 for days to first boll bursting, number of bolls per plant, ginning outturn, lint index and 2.5% span length; MCU 7 possessed favourable mean values for four characters viz., days to first boll bursting, single plant yield, seed index and micronaire value; G.Cot 16 registered superior mean values for two characters and Suraj for three characters.

Considering the mean performance of all the parents for different traits, MCU 5 had recorded significantly superior mean values for seven traits studied. Anjali and Surabhi registered significantly desirable mean values for five characters each. This was followed by MCU 7 and KC 3 which possessed significantly higher mean values for three traits each. In general, high mean values remain as selection index in the choice of parents and the parents possessing high *per se* performance will result in superior hybrids. Therefore, these parents can be exploited in hybridization for improving concerned character through pedigree breeding as reported by Gul Hassan *et al.* (2000).

5.2.2. Based on *gca* effects

The importance of combining ability in selection of parents for hybridization has been emphasized by many workers in cotton. The potentiality of any line to be used as a parent in hybridization depends on the performance of the F₁ hybrid derived from it and its own *gca* effect. In the estimation of general combining ability effects, none of the parents exhibited significant *gca* effect for all the characters.

Parents with negative and significant *gca* effects were considered desirable for days to first boll bursting and micronaire value while for other traits parents with positively significant *gca* effects were taken into consideration. Shaukat *et al.* (2013) reported that combining ability provides useful information on the choice of parents in terms of expected performance of hybrids and progenies.

Among the parents, MCU 5 possessed good *gca* effects for seven traits namely plant height, number of sympodial branches per plant, single plant yield, ginning outturn, 2.5% span length, bundle strength and micronaire value. The next best general combiner

was Suraj recording desirable *gca* effects for six traits viz., boll weight, ginning outturn, lint index, 2.5% span length, bundle strength and micronaire value. The parent Anjali also recorded desirable *gca* effects for five traits viz., boll weight, ginning outturn, micronaire value, uniformity ratio and elongation per cent. This was followed by MCU 7 having desirable *gca* effects for single plant yield, ginning outturn, micronaire value and uniformity ratio and Surabhi for plant height, 2.5% span length, bundle strength and micronaire value. The parent KC 2 had recorded high significant *gca* effects for days to first boll bursting, boll weight and uniformity ratio. The parent KC 3 having desirable *gca* effects for days to first boll bursting and ginning outturn. Manickam and Gururajan (2004) reported that high *gca* effect in desirable direction for a particular character indicates the presence of additive genes for that character in the parent, it could be expected that when the parents possessing high *gca* effects were combined, larger proportion of progenies would have high *per se* value for the character concerned facilitating easy selection for the character.

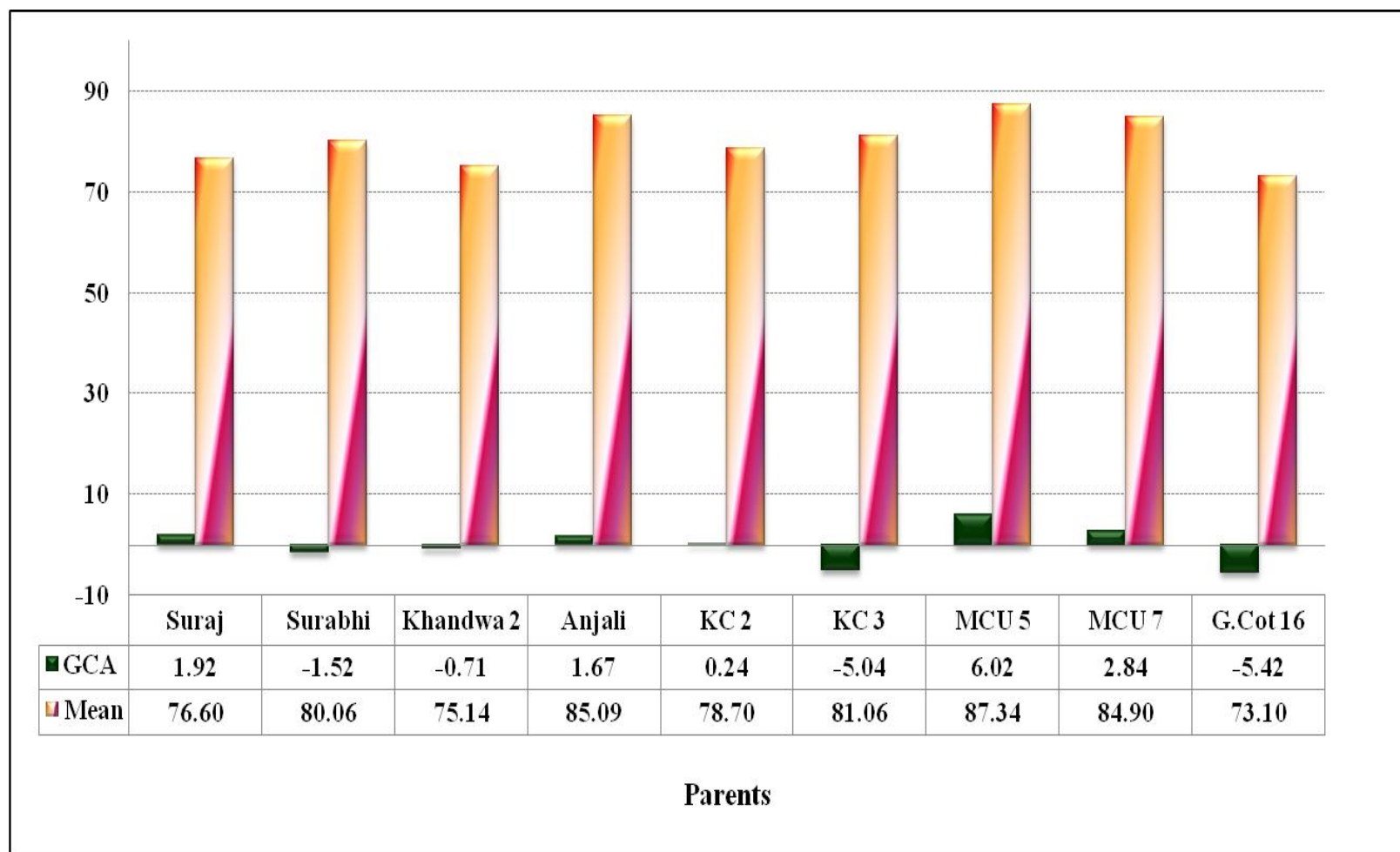
Evaluation of parents based on mean and *gca* separately might result in identification of different sets of parents as promising ones. According to Jatoi *et al.* (2010), Hinze *et al.* (2011) and Kumar *et al.* (2014), the *per se* performance and *gca* effects of parents were directly related to each other. Khan (2013) also reported parallelism between *per se* performance and *gca* effects.

Parents based on mean and *gca* effects for fourteen traits were given in Table 47. Based on mean and *gca* effects, the parent MCU 5 was considered the best, since it had superior mean performance and *gca* effects for six traits viz., plant height, number of sympodial branches per plant, single plant yield, 2.5% span length, bundle strength and micronaire value. The line Surabhi had desirable mean and *gca* effects for plant height and quality traits like 2.5% span length, bundle strength and micronaire value. The parent Anjali also recorded desirable mean and *gca* effects for four traits viz., boll weight, micronaire value, uniformity and elongation per cent. For boll weight, lint index and micronaire value, Suraj had shown better expression for high *per se* and *gca* effects. This was followed by MCU 7 and KC 3 for two traits (Figure 22).

Table 47. Evaluation of parents based on mean performance and *gca*

Characters	Mean performance	<i>gca</i> effects	Mean and <i>gca</i> effects
Days to first boll bursting	MCU 5, MCU 7, KC 3, Khandwa 2, Surabhi,	Khandwa 2, KC 2 and KC 3	Khandwa 2 and KC 3
Plant height (cm)	MCU 5, Anjali and Surabhi	MCU 5 and Surabhi	Surabhi and MCU 5
Number of sympodial branches / plant	MCU 5	MCU 5	MCU 5
Number of bolls/plant	MCU 5, KC 3 and Anjali	-	-
Boll weight (g)	MCU 5, Suraj and Anjali	Suraj, Anjali and KC 2	Suraj and Anjali
Single plant yield (g)	MCU 5, Anjali, and MCU 7	MCU 5 and MCU 7	MCU 5 and MCU 7
Ginning outturn (%)	KC 3	Suraj, MCU 7, KC 3, Anjali and MCU 5	KC 3
Lint index	G.Cot 16, KC 3 and Suraj	Suraj	Suraj
Seed index	G.Cot 16, MCU 7 and KC 2	G.Cot 16	G.Cot 16
2.5% span length (mm)	MCU 5, Surabhi and KC 3	Surabhi, MCU 5 and Suraj	Surabhi and MCU 5
Bundle strength (g/tex)	Surabhi and MCU 5	Surabhi, MCU 5 and Suraj	Surabhi and MCU 5
Micronaire value (µg/inch)	Surabhi, Anjali, MCU 5, Suraj and MCU 7	MCU 5, Surabhi, MCU 7, Anjali and Suraj	Suraj, Surabhi, Anjali, MCU 5 and MCU 7
Uniformity ratio (%)	Anjali	Anjali, MCU 7 and KC 2	Anjali
Elongation per cent (%)	Anjali and MCU 5	Anjali	Anjali

Figure 22. Parental performance for single plant yield using mean and GCA effects



Earlier Arumugampillai and Amirthadevarathinam (1998) reported that identification of parents for breeding programme based on either *per se* performance or *gca* effects alone was misleading in selection programme. In the present study, considering *gca* effects and *per se* performance together, the parents MCU 5, Surabhi, Anjali, Suraj, MCU 7 and KC 3 were identified as desirable parents for further breeding programme. Hence, it could be concluded that, these parents can be utilized in hybridization programmes to identify superior segregants with high yield and good fibre quality traits. Earlier findings like Gul Hassan *et al.* (1999) and Kaushik *et al.* (2006) also concluded that best yielding parents having high *gca* and *per se* produced the best hybrids.

5.3. Evaluation of hybrids

Hybridization is carried out to combine the favourable genes from different parent into a single genotype. These hybrids are utilized in two ways.

1. Directly using the F_1 's to exploit the hybrid vigour
2. Forwarding to further generations and selecting the superior individuals after attaining homozygosity.

The utilization of hybrids in anyone of the two ways will depend upon the genetic constitution of the parents as well as the hybrids. Heterosis breeding has brought out great studies in plant breeding ever since East and Shull put forth the hypothesis on expression of hybrid vigour. During the last century, the hybrid technology was responsible for increasing the production and productivity of many food and commercial crops including cotton. However, *sca* effects and hybrid vigour of the crosses are also considered frequently in cases where non-additive component of genetic variance predominates the inheritance.

To exploit the hybrid vigour, the parameters like *per se* performance of hybrids, *sca* effects and standard heterosis of hybrids have to be taken into account (Shimna Bhaskaran, 2004; Kumar, 2007 and Kanimozhi, 2012). The hybrids, obtained by full diallel fashion in the present investigation, were evaluated for their performance based on mean, *sca* effects and heterosis for each of trait.

5.3.1. Based on mean performance

The primary criterion to evaluate a hybrid is its mean performance. Kadambavanasundaram (1980) and Nadarajan (1986) reported that *per se* performance of hybrids appeared to be useful index for judging the hybrids. Gilbert (1958) suggested that parents with good *per se* performance would result in good hybrids. In the present study, the hybrids Suraj x Surabhi, Surabhi x Anjali, Khandwa 2 x Suraj, Anjali x Suraj, Anjali x MCU 5, KC 2 x MCU 5, KC 3 x Anjali, MCU 5 x MCU 7, G.Cot 16 x Khandwa 2 showed superior mean performance for single plant yield. Among the above hybrids, MCU 5 x MCU 7 and KC 2 x MCU 5 showed desirable mean performance for ten and nine yield and fibre quality traits respectively. The hybrid Anjali x Suraj showed superior mean performance for eight characters. The hybrids Suraj x Surabhi and KC 3 x Anjali showed desirable mean performance for seven yield and fibre quality traits. The hybrids viz., Surabhi x Anjali, Anjali x MCU 5 and G.Cot 16 x Khandwa 2 showed superior mean performance for six different yield characters in addition to quality characters.

Therefore in the present study, based on the mean performance, Suraj x Surabhi, Surabhi x Anjali, Khandwa 2 x Suraj, Anjali x Suraj, Anjali x MCU 5, KC 2 x MCU 5, KC 3 x Anjali, MCU 5 x MCU 7, G.Cot 16 x Khandwa 2 were considered as best ones for improving yield combined with good fibre quality.

5.3.2. Based on *sca* effects

The *sca* effect is an important criterion for the evaluation of hybrids. The specific combining ability is the deviation of F_1 performance from that predicted on the basis of general combining ability (Allard, 1960). According to Spargue and Tatum (1942), the specific combining ability is controlled by non-additive gene action. As per Peng and Virmani (1990), *sca* effect is an index to determine the usefulness of a particular cross combination for the exploitation of heterosis.

In the present study, negative *sca* effects were taken into consideration for days to first boll bursting and micronaire value while for other traits positive *sca* effects were considered. Several hybrids recorded significant *sca* effects for different characters under study. The hybrid MCU 5 x KC 2 showed significant *sca* effects for plant height, number of sympodial branches per plant, number of bolls per plant, single plant yield, ginning

outturn, 2.5% span length and uniformity ratio and the hybrid MCU 7 x KC 3 also showed significant *sca* effects for seven traits viz., plant height, number of bolls per plant, boll weight, single plant yield, ginning outturn, lint index and bundle strength. These two are considered as the best combiner for yield and fibre quality traits. This was followed by the hybrids Surabhi x Suraj, Khandwa 2 x G.Cot 16, KC 2 x KC 3, MCU 5 x Anjali, MCU 5 x MCU 7 and G.Cot 16 x Suraj which showed significant *sca* effects for five yield and fibre quality traits. The hybrids Suraj x Khandwa 2, MCU 7 x Surabhi and MCU 7 x MCU 5 showed significant *sca* effects for four different characters.

Significant *sca* effects were also reported for days to 50% flowering (Deosarkar *et al.*, 2009), plant height (Waldia *et al.*, 1980; Nirania *et al.*, 1992; Kaushik *et al.*, 2006; Deosarkar *et al.*, 2009 and Jatoi *et al.*, 2010), monopodia and sympodia per plant (Bhatade and Bhale, 1983; Kaushik *et al.*, 2006; Deosarkar *et al.*, 2009 and Jatoi *et al.*, 2010), bolls per plant (Waldia *et al.*, 1980, Jatoi *et al.*, 2010 and Javaid *et al.*, 2014), boll weight (Singh *et al.*, 2010; Jatoi *et al.*, 2010 and Javaid *et al.*, 2014), number of seeds per boll (Kaushik *et al.*, 2006), ginning outturn (Kaushik *et al.*, 2006; Karademir and Gencer, 2010 and Singh *et al.*, 2010), seed cotton yield (Karademir and Gencer, 2010; Jatoi *et al.*, 2010; Natera *et al.*, 2012 and Javaid *et al.*, 2014), lint yield (Chaudhari *et al.*, 1990 and Deosarkar *et al.*, 2009), seed index (Kaushik *et al.*, 2006; Deosarkar *et al.*, 2009 and Hinze *et al.*, 2011), lint index (Bhatade and Bhale, 1983 and Singh *et al.*, 2010), 2.5% span length (Kaushik *et al.*, 2006; Karademir and Gencer, 2010, Singh *et al.*, 2010; Natera *et al.*, 2012 and Shaukat *et al.*, 2013), micronaire value (Kaushik *et al.*, 2006; Karademir and Gencer, 2010; Singh *et al.*, 2010; Natera *et al.*, 2012; Shaukat *et al.*, 2013 and Ng *et al.*, 2014), bundle strength (Karademir and Gencer, 2010; Singh *et al.*, 2010; Hinze *et al.*, 2011; Natera *et al.*, 2012 and Shaukat *et al.*, 2013), elongation per cent (Karademir and Gencer, 2010; Singh *et al.*, 2010; Shaukat *et al.*, 2013 and Ng *et al.*, 2014) and uniformity ratio (Karademir and Gencer, 2010; Hinze *et al.*, 2011; Shaukat *et al.*, 2013 and Ng *et al.*, 2014).

From the foregoing discussion, the specific combining effects of the hybrids revealed that the hybrids viz., MCU 5 x KC 2, MCU 7 x KC 3, Surabhi x Suraj, Khandwa 2 x G.Cot 16, KC 2 x KC 3, MCU 5 x Anjali, MCU 5 x MCU 7, G.Cot 16 x Suraj,

Suraj x Khandwa 2, MCU 7 x Surabhi and MCU 7 x MCU 5 were found to be good combiner for exploitation of yield, yield contributing traits and quality traits.

An examination of the *gca* effects of the parents and the *sca* effects of the resultant hybrid revealed that it may not be possible to find a definite trend for all the traits on all the hybrids. However, in the present study, when both the parents possessed the significant *gca* effects, positive *sca* effects were discernible in the hybrids involving them in at least a few hybrids. This could be exemplified by the hybrids, MCU 5 x MCU 7 for single plant yield, MCU 7 x KC 3, MCU 5 x Anjali and MCU 7 x MCU 5 for ginning outturn, Khandwa 2 x G.Cot 16 and KC 2 x KC 3 for micronaire value and Surabhi x Suraj for 2.5% span length, parents with high x high *gca* effects indicating the presence of additive x additive type of gene action between the favourable alleles contributed by the two parents which was considered to be fixable type of nature (Subba Reddy and Nadarajan, 2006). Thus these hybrids would be very much useful for further testing.

Significant positive *gca* effect on any one of the parents and negative or non significant *gca* effects on the other parents leading to significant positive *sca* effects in the hybrids could be observed for most of the traits as was seen on the following crosses MCU 5 x KC 2, G.Cot 16 x Suraj and MCU 7 x Surabhi for single plant yield with yield components and fibre quality related parent traits with high x low or low x high *gca* effects produced crosses with significant *sca* effects, indicating the presence of the additive x dominance type of genic interaction. Therefore, the above crosses could throw desirable transgressive segregants of the additive genetic systems and present in one general combiner and complementary epistatic effects in the other that act in the same direction to maximize the desirable plant attributes (Kalsy and Garg, 1980; Gururajan and Basu, 1992b; Muthu *et al.*, 2005). In general, the study indicated that a combination of good general combiners were not necessarily the best cross combinations nor was a low x low cross always a poor combinations. Similar results were reported by Kumar (2007).

5.4. Evaluation of hybrids based on magnitude of heterosis

As for as heterosis is concerned, high positive *sca* effect alone may not be the appropriate criterion for the exploitation of a hybrid because hybrids having high *sca* effects may exhibit poor *per se* performance also. The examination of heterosis is

actually based on the mean performance of the parents and hybrids rather than the *gca* and *sca* effects of the parents and hybrids. Ashokkumar *et al.* (2013) and Abro *et al.* (2014) reported that scope for exploitation of hybrid vigour would largely depend on *per se* performance of hybrid and the magnitude of heterosis.

Solanki *et al.* (2014) emphasized the need for computing heterosis over the standard variety or hybrid. Hence in the present study, the hybrids were evaluated for their heterotic performance over the standard variety MCU 13. The hybrids with high mean, significant specific combining ability effects and standard heterosis are listed in Table 48.

Based on standard heterosis, the hybrid KC 2 x MCU 5 performed well for seven different traits *viz.*, number of sympodial branches per plant, number of bolls per plant, single plant yield, 2.5% span length, bundle strength, micronaire value and uniformity ratio. The hybrid MCU 5 x MCU 7 also showed significant heterosis over standard variety for seven different yield contributing and quality traits. The next best were Anjali x Suraj, Anjali x MCU 5 and Surabhi x Anjali which showed significant heterosis for five different traits. This was followed by the hybrid KC 2 x Suraj which showed significant standard heterosis for five different traits *viz.*, days to first boll bursting, number of bolls per plant, boll weight, micronaire value and uniformity ratio. Hence, the hybrids *viz.*, KC 2 x MCU 5, MCU 5 x MCU 7, Anjali x Suraj, Anjali x MCU 5, Surabhi x Anjali and KC 2 x Suraj may be highly suitable for heterosis breeding.

Positive and significant heterosis were also reported for number of sympodial branches per plant (Tuteja *et al.*, 2005b; Verma *et al.*, 2006; Abro *et al.*, 2009 and Geddam *et al.*, 2011), number of bolls per plant (Nirania *et al.*, 1992; Gencer and Kaynak, 1994), boll weight (Solanki *et al.*, 2014), single plant yield (Abro *et al.*, 2009; Jyotiba *et al.*, 2010; Basal *et al.*, 2011; Geddam *et al.*, 2011 and Patil *et al.*, 2011b), seed index (Pole *et al.*, 2008 and Jyotiba *et al.*, 2010), ginning outturn (Nirania *et al.*, 2004; Rauf *et al.*, 2005; Preetha and Raveendaran, 2008; Patel *et al.*, 2009 and Geddam *et al.*, 2011), 2.5% span length (Kumar, 2007 and Ashokkumar *et al.*, 2013), bundle strength (Shimna Bhaskaran, 2004; Kumar, 2007 and Ashokkumar *et al.*, 2013), micronaire value (Shimna Bhaskaran, 2004; Kumar, 2007; Kanimozhi, 2012 and Ashokkumar *et al.*, 2013)

Table 48. Evaluation of hybrids based on mean and significant effects of *sca* and standard heterosis

Character	Mean performance	SCA based on significance	Standard heterosis based on significance	Mean + SCA + Standard heterosis
Days to first boll bursting	Suraj x Surabi, Suraj x Khandwa 2, Suraj x Anjali, Suraj x KC 2, Suraj x KC 3, Suraj x MCU 5, Suraj x MCU 7, Suraj x G.Cot 16, Surabi x Suraj, Surabi x Khandwa 2, Surabi x KC 2, Surabi x KC 3, Surabi x MCU 5, Surabi x MCU 7, Surabi x G.Cot 16, Khandwa 2 x Suraj, Khandwa 2 x Surabi, Khandwa 2 x Anjali, Khandwa 2 x KC 2, Khandwa 2 x KC 3, Khandwa 2 x MCU 5, Khandwa 2 x MCU 7, Khandwa 2 x G.Cot 16, Anjali x Surabi, Anjali x Khandwa 2, Anjali x KC 2, Anjali x KC 3, Anjali x MCU 5, Anjali x MCU 7, Anjali x G.Cot 16, KC 2 x Suraj, KC 2 x Khandwa 2, KC 2 x Anjali, KC 2 x KC 3, KC 2 x MCU 5, KC 2 x MCU 7, KC 2 x G.Cot 16, KC 3 x Suraj, KC 3 x Surabi, KC 3 x Khandwa 2, KC 3 x KC 2, KC 3 x MCU 7, KC 3 x G.Cot 16, MCU 5 x Suraj, MCU 5 x Surabi, MCU 5 x Khandwa 2, MCU 5 x KC 2, MCU 5 x KC 3, MCU 5 x MCU 7, MCU 5 x G.Cot 16, MCU 7 x Suraj, MCU 7 x Surabi, MCU 7 x Khandwa 2, MCU 7 x Anjali, MCU 7 x KC 2, MCU 7 x KC 3, MCU 7 x MCU 5, MCU 7 x G.Cot 16, G.Cot 16 x Suraj, G.Cot 16 x Surabi, G.Cot 16 x Khandwa 2, G.Cot 16 x KC 2, G.Cot 16 x KC 3, G.Cot 16 x MCU 5	Surabi x MCU 7, Surabi x G.Cot 16, Khardwa 2 x Anjali, Khardwa 2 x G.Cot 16, Anjali x Suraj, Anjali x KC 2, KC 2 x Surabi, KC 3 x Anjali, KC 3 x G.Cot 16, MCU 5 x Anjali, G.Cot 16 x Anjali, G.Cot 16 x MCU 7	Suraj x KC 3, Surabi x G.Cot 16, Anjali x KC 2, KC 2 x Suraj, KC 2 x Khardwa 2, G.Cot 16 x Khardwa 2	Surabi x G.Cot 16 Anjali x KC 2

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Table 48. Contd..

Characters	Mean performance	SCA based on significance	Standard heterosis based on significance	Mean + SCA + Standard heterosis
Plant height (cm)	Suraj x MCU 5, Suraj x G.Cot 16, Surabi x Anjali, Surabi x KC 3, Khandwa 2 x Surabi, Khandwa 2 x MCU 5, Anjali x Suraj, Anjali x KC 3, Anjali x MCU 5, KC 2 x Suraj, KC 2 x Surabi, KC 2 x Anjali, KC 2 x MCU 5, KC 3 x Anjali, KC 3 x KC 2, MCU 5 x Surabi, MCU 7 x Anjali, MCU 7 x KC 2, MCU 7 x MCU 5, G.Cot 16 x Khandwa 2, G.Cot 16 x MCU 5	Suraj x Surabi, Suraj x KC 2, Suraj x MCU 5, Suraj x G.Cot 16, Surabi x MCU 5, Khandwa 2 x G.Cot 16, Anjali x Surabi, Anjali x KC 3, KC 2 x Khandwa 2, KC 2 x KC 3, KC 2 x MCU 7, MCU 5 x Suraj, MCU 5 x Anjali, MCU 5 x KC 2, MCU 5 x G.Cot 16, MCU 7 x KC 3, G.Cot 16 x Suraj, G.Cot 16 x MCU 7	---	---
Number of sympodial branches/plant	Suraj x Surabi, Suraj x MCU 5, Surabi x Anjali, Surabi x KC 3, Khandwa 2 x Surabi, Khandwa 2 x Anjali, Khandwa 2 x MCU 5, Anjali x Suraj, Anjali x KC 2, Anjali x MCU 5, Anjali x MCU 7, KC 2 x Suraj, KC 2 x Surabi, KC 2 x KC 3, KC 2 x MCU 5, KC 3 x Anjali, KC 3 x KC 2, KC 3 x MCU 7, MCU 5 x Surabi, MCU 5 x KC 3, MCU 5 x MCU 7, MCU 7 x Suraj, MCU 7 x Anjali, G.Cot 16 x MCU 5	Surabi x Suraj, Surabi x Khandwa 2, KC 2 x KC 3, KC 3 x Surabi, MCU 5 x Khandwa 2, MCU 5 x KC 2, G.Cot 16 x Surabi	Suraj x MCU 5, Surabi x Anjali, Surabi x KC 3, Khandwa 2 x Surabi, Khandwa 2 x MCU 5, Anjali x MCU 5, KC 2 x MCU 5, KC 3 x Anjali, KC 3 x KC 2, KC 3 x MCU 7, MCU 5 x Surabi, MCU 7 x Anjali	---
Number of bolls/plant	Suraj x KC 3, Suraj x MCU 5, Surabi x Khandwa 2, Surabi x Anjali, Surabi x KC 3, Surabi x MCU 7, Khandwa 2 x Suraj, Khandwa 2 x Surabi, Khandwa 2 x Anjali, Anjali x Suraj, Anjali x Surabi, Anjali x KC 3, Anjali x MCU 5, KC 2 x Suraj, KC 2 x	Suraj x Khandwa 2, MCU 5 x Anjali, MCU 5 x KC 2, MCU 5 x KC 3, MCU 5 x MCU 7, Anjali x Khandwa 2, MCU 7 x KC 3	Surabi x Anjali, Khandwa 2 x Suraj, Khandwa 2 x Anjali, Anjali x MCU 5, KC 2 x Suraj, KC 2 x Khandwa 2, KC 2 x MCU 5, KC 3 x Anjali,	MCU 5 x MCU 7

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Table 48. Contd..

	Surabi, KC 2 x Khandwa 2, KC 2 x MCU 5, KC 3 x Anjali, KC 3 x KC 2, KC 3 x MCU 5, KC 3 x MCU 7, MCU 5 x Suraj, MCU 5 x Khandwa 2, MCU 5 x MCU 7, MCU 7 x Anjali, MCU 7 x MCU 5, G.Cot 16 x Khandwa 2, G.Cot 16 x KC 2, G.Cot 16 x MCU 5, G.Cot 16 x MCU 7		KC 3 x MCU 7, MCU 5 x Suraj, MCU 5 x MCU 7, MCU 7 x Anjali, G.Cot 16 x MCU 7	
Boll weight (g)	Suraj x Surabi, Suraj x Anjali, Suraj x KC 2, Suraj x MCU 7, Suraj x G.Cot 16, Surabi x KC 3, Surabi x MCU 7, Khandwa 2 x Suraj, Khandwa 2 x MCU 7, Anjali x Suraj, Anjali x Khandwa 2, Anjali x KC 2, Anjali x G.Cot 16, KC 2 x Suraj, KC 2 x Surabi, KC 2 x Khandwa 2, KC 2 x Anjali, KC 2 x MCU 7, KC 2 x G.Cot 16, KC 3 x MCU 7, MCU 5 x Suraj, MCU 5 x Surabi, MCU 5 x KC 2, MCU 5 x MCU 7, MCU 7 x Surabi, MCU 7 x Anjali, MCU 7 x MCU 5, G.Cot 16 x Anjali, G.Cot 16 x KC 3	Surabi x Suraj, KC 3 x Surabi, MCU 7 x KC 2, MCU 7 x KC 3	Suraj x Surabi, Suraj x Anjali, Suraj x KC 2, Suraj x G.Cot 16, Anjali x Suraj, Anjali x KC 2, KC 2 x Suraj, KC 2 x Surabi, KC 2 x MCU 7	---
Single plant yield (g)	Suraj x Surabi, Surabi x Anjali, Khandwa 2 x Suraj, Anjali x Suraj, Anjali x MCU 5, KC 2 x MCU 5, KC 3 x Anjali, MCU 5 x MCU 7, G.Cot 16 x Khandwa 2	Suraj x Khandwa 2, Surabi x Suraj, Khandwa 2 x G.Cot 16, Anjali x Surabi, Anjali x Khandwa 2, Anjali x MCU 5, Anjali x MCU 7, KC 2 x KC 3, KC 2 x MCU 7, KC 3 x Surabi, MCU 5 x Anjali, MCU 5 x KC 2, MCU 5 x MCU 7, MCU 7 x Surabi, MCU 7 x KC 3, MCU 7 x MCU 5, G.Cot 16 x Suraj	Anjali x Suraj, Anjali x MCU 5, KC 2 x MCU 5, MCU 5 x MCU 7	Anjali x MCU 5 MCU 5 x MCU 7

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Table 48. Contd..

Characters	Mean performance	SCA based on significance	Standard heterosis based on significance	Mean + SCA + Standard heterosis
Ginning outturn (%)	Suraj x Anjali, Suraj x MCU 7, Surabi x KC 2, Surabi x MCU 5, Khandwa 2 x Anjali, Khandwa 2 x KC 3, Anjali x Suraj, Anjali x Khandwa 2, Anjali x MCU 7, KC 2 x KC 3, KC 2 x MCU 7, KC 3 x Suraj, KC 3 x Anjali, KC 3 x MCU 5, KC 3 x MCU 7, MCU 5 x Suraj, MCU 5 x Khandwa 2, MCU 5 x KC 3, MCU 5 x G.Cot 16, MCU 7 x Khandwa 2, MCU 7 x Anjali, MCU 7 x KC 2, MCU 7 x MCU 5, G.Cot 16 x Khandwa 2, G.Cot 16 x Anjali, G.Cot 16 x KC 3, G.Cot 16 x MCU 7	Suraj x Anjali, Suraj x MCU 7, Surabi x MCU 5, Khandwa 2 x Anjali, Khandwa 2 x MCU 5, Anjali x MCU 7, Anjali x G.Cot 16, KC 2 x Surabi, KC 2 x Anjali, KC 2 x KC 3, KC 2 x MCU 7, KC 2 x G.Cot 16, KC 3 x Khandwa 2, KC 3 x KC 2, KC 3 x MCU 5, MCU 5 x Surabi, MCU 5 x KC 2, MCU 7 x Suraj, MCU 7 x Surabi, MCU 7 x KC 3, G.Cot 16 x Suraj, G.Cot 16 x Surabi, G.Cot 16 x MCU 5	Suraj x Anjali, Suraj x MCU 7, Surabi x KC 2, Khandwa 2 x Anjali, Anjali x Suraj, Anjali x Khandwa 2, Anjali x MCU 7, KC 2 x KC 3, KC 3 x Suraj, KC 3 x Anjali, KC 3 x MCU 5, KC 3 x MCU 7, MCU 5 x Khandwa 2, MCU 5 x KC 3, MCU 5 x G.Cot 16, MCU 7 x Khandwa 2, MCU 7 x Anjali, MCU 7 x KC 2, MCU 7 x MCU 5, G.Cot 16 x Anjali, G.Cot 16 x MCU 7	Suraj x Anjali, Suraj x MCU 7 Khandwa 2 x Anjali Anjali x MCU 7 KC 2 x KC 3 KC 3 x MCU 5
Lint index	Anjali x Suraj, KC 3 x Anjali	Surabi x MCU 5, Khandwa 2 x Anjali, Khandwa 2 x MCU 5, Khandwa 2 x MCU 7, KC 2 x KC 3, KC 2 x G.Cot 16, MCU 7 x Suraj, MCU 7 x Surabi, MCU 7 x KC 3, G.Cot 16 x MCU 5	---	---
Seed index	KC 2 x Surabi, KC 3 x G.Cot 16, MCU 5 x Surabi, G.Cot 16 x Suraj	Surabi x MCU 5, Khandwa 2 x MCU 7, Anjali x KC 2, MCU 7 x MCU 5, G.Cot 16 x KC 3	KC 3 x G.Cot 16	---

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Characters	Mean performance	SCA based on significance	Standard heterosis based on significance	Mean + SCA + Standard heterosis
2.5% span length (mm)	Suraj x Surabi, Suraj x Khandwa 2, Suraj x Anjali, Suraj x KC 3, Suraj x MCU 5, Suraj x MCU 7, Suraj x G.Cot 16, Surabi x KC 2, Surabi x MCU 5, Surabi x G.Cot 16, Anjali x Surabi, KC 2 x MCU 5, KC 3 x Surabi, MCU 5 x Suraj, MCU 5 x Surabi, MCU 5 x Khandwa 2, MCU 5 x MCU 7, MCU 5 x G.Cot 16, MCU 7 x Surabi, MCU 7 x MCU 5	Suraj x Khandwa 2, Suraj x KC 3, Suraj x MCU 7, Suraj x G.Cot 16, Surabi x Suraj, Surabi x Anjali, Surabi x KC 2, Surabi x KC 3, Khandwa 2 x Suraj, Khandwa 2 x Anjali, Khandwa 2 x KC 3, Khandwa 2 x MCU 5, Khandwa 2 x G.Cot 16, Anjali x Suraj, Anjali x KC 2, Anjali x G.Cot 16, KC 2 x Anjali, KC 2 x MCU 5, KC 3 x Suraj, MCU 5 x Suraj, MCU 5 x KC 2, MCU 5 x MCU 7, MCU 7 x Suraj, G.Cot 16 x Suraj, G.Cot 16 x Surabi, G.Cot 16 x KC 3, G.Cot 16 x MCU 5	Suraj x Surabi, Suraj x Khandwa 2, Suraj x Anjali, Suraj x KC 2, Suraj x KC 3, Suraj x MCU 5, Suraj x MCU 7, Suraj x G.Cot 16, Surabi x Suraj, Surabi x Anjali, Surabi x KC 2, Surabi x KC 3, Surabi x MCU 5, Surabi x MCU 7, Surabi x G.Cot 16, Khandwa 2 x Suraj, Khandwa 2 x Surabi, Khandwa 2 x MCU 5, Anjali x Surabi, Anjali x Khandwa 2, Anjali x KC 2, KC 2 x Surabi, KC 2 x MCU 5, KC 3 x Suraj, KC 3 x Surabi, KC 3 x Khandwa 2, MCU 5 x Suraj, MCU 5 x Surabi, MCU 5 x Khandwa 2, MCU 5 x Anjali, MCU 5 x KC 2, MCU 5 x KC 3, MCU 5 x MCU 7, MCU 5 x G.Cot 16, MCU 7 x Suraj, MCU 7 x Surabi, MCU 7 x Anjali, MCU 7 x MCU 5, G.Cot 16 x Anjali	Suraj x Khandwa 2 Suraj x KC 3 Suraj x G.Cot 16 Surabi x KC 2 KC 2 x MCU 5 MCU 5 x Suraj MCU 5 x MCU 7
Bundle strength (g/tex)	Suraj x Surabi, Suraj x KC 3, Suraj x MCU 7, Suraj x G.Cot 16, Surabi x Anjali, Surabi x MCU 5, Khandwa 2 x MCU 5, Anjali x	Suraj x KC 3, Surabi x Anjali, Surabi x KC 2, Surabi x KC 3, Surabi x MCU 5, Khandwa 2 x Suraj, Khandwa 2 x KC 2,	Suraj x Surabi, Suraj x Khandwa 2, Suraj x Anjali, Suraj x KC 3, Suraj x MCU 7, Suraj x G.Cot 16, Surabi x	Suraj x KC 3 Surabi x Anjali Surabi x MCU 5

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	Surabi, KC 2 x MCU 5, KC 3 x Surabi, MCU 5 x Suraj, MCU 5 x Surabi, MCU 5 x Khandwa 2, MCU 5 x MCU 7, MCU 7 x MCU 5	Khandwa 2 x MCU 5, Khandwa 2 x MCU 7, Anjali x Khandwa 2, KC 2 x Anjali, KC 2 x MCU 5, KC 2 x G.Cot 16, KC 3 x G.Cot 16, MCU 5 x MCU 7, MCU 7 x Suraj, MCU 7 x KC 3, G.Cot 16 x Suraj, G.Cot 16 x Khandwa 2, G.Cot 16 x MCU 5	Suraj, Surabi x Anjali, Surabi x KC 2, Surabi x KC 3, Surabi x MCU 5, Khandwa 2 x Anjali, Khandwa 2 x MCU 5, Khandwa 2 x MCU 7, Khandwa 2 x G.Cot 16, Anjali x Surabi, Anjali x MCU 5, Anjali x MCU 7, KC 2 x Surabi, KC 2 x MCU 5, KC 3 x Suraj, KC 3 x Surabi, KC 3 x G.Cot 16, MCU 5 x Suraj, MCU 5 x Surabi, MCU 5 x Khandwa 2, MCU 5 x Anjali, MCU 5 x KC 3, MCU 5 x MCU 7, MCU 5 x G.Cot 16, MCU 7 x Surabi, MCU 7 x MCU 5, MCU 7 x G.Cot 16, G.Cot 16 x KC 3	Khandwa 2 x MCU 5 KC 2 x MCU 5 MCU 5 x MCU 7
Micronaire value (µg/inch)	Suraj x Surabi, Suraj x KC 3, Suraj x MCU 5, Suraj x MCU 7, Surabi x Suraj, Surabi x Anjali, Surabi x KC 2, Surabi x KC 3, Surabi x MCU 5, Surabi x MCU 7, Khandwa 2 x Surabi, Khandwa 2 x MCU 5, Khandwa 2 x G.Cot 16, Anjali x Suraj, Anjali x Surabi, Anjali x KC 2, Anjali x KC 3, Anjali x MCU 7, Anjali x G.Cot 16, KC 2 x Suraj, KC 2 x MCU 5, KC 2 x MCU 7,	Suraj x KC 3, Surabi x Anjali, Surabi x KC 3, Surabi x MCU 7, Khandwa 2 x MCU 5, Khandwa 2 x G.Cot 16, Anjali x KC 3, Anjali x MCU 7, Anjali x G.Cot 16, KC 2 x Surabi, KC 2 x Anjali, KC 2 x MCU 5, KC 3 x Suraj, KC 3 x Anjali, KC 3 x G.Cot 16, MCU 7 x G.Cot 16, G.Cot 16 x Anjali, G.Cot 16 x MCU 7	Suraj x Surabi, Suraj x KC 3, Suraj x MCU 5, Suraj x MCU 7, Surabi x Suraj, Surabi x Anjali, Surabi x KC 2, Surabi x MCU 5, Surabi x MCU 7, Khandwa 2 x Surabi, Khandwa 2 x MCU 5, Anjali x Suraj, Anjali x Surabi, Anjali x KC 2, Anjali x KC 3, Anjali x MCU 7, Anjali x G.Cot 16, KC 2 x Suraj, KC 2 x MCU 5, KC 3 x Surabi, MCU 5 x Suraj, MCU	Surabi x Anjali Surabi x MCU 7 Khandwa 2 x MCU 5 Anjali x KC 3 Anjali x MCU 7 Anjali x G.Cot 16 KC 2 x MCU 5 MCU 7 x G.Cot 16

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	KC 2 x G.Cot 16, KC 3 x Surabi, MCU 5 x Suraj, MCU 5 x Surabi, MCU 5 x Khandwa 2, MCU 5 x Anjali, MCU 5 x KC 2, MCU 5 x KC 3, MCU 5 x MCU 7, MCU 5 x G.Cot 16, MCU 7 x Suraj, MCU 7 x Surabi, MCU 7 x Anjali, MCU 7 x KC 2, MCU 7 x KC 3, MCU 7 x MCU 5, MCU 7 x G.Cot 16, G.Cot 16 x Surabi, G.Cot 16 x Khandwa 2, G.Cot 16 x MCU 5, G.Cot 16 x MCU 7		5 x Surabi, MCU 5 x Khandwa 2, MCU 5 x Anjali, MCU 5 x KC 2, MCU 5 x KC 3, MCU 5 x MCU 7, MCU 7 x Suraj, MCU 7 x Surabi, MCU 7 x Anjali, MCU 7 x KC 2, MCU 7 x MCU 5, MCU 7 x G.Cot 16, G.Cot 16 x MCU 5	
Uniformity ratio (%)	Suraj x MCU 7, Khandwa 2 x Suraj, Khandwa 2 x KC 2, Anjali x Surabi, Anjali x Khandwa 2, Anjali x KC 2, KC 2 x Surabi, KC 2 x Anjali, KC 2 x MCU 5, KC 3 x Surabi, KC 3 x Anjali, KC 3 x KC 2, KC 3 x MCU 7, MCU 5 x Surabi, MCU 5 x MCU 7, MCU 7 x Suraj, MCU 7 x KC 3, MCU 7 x MCU 5, G.Cot 16 x Anjali	Suraj x Khandwa 2, Suraj x KC 3, Suraj x MCU 7, Suraj x G.Cot 16, Surabi x Suraj, Surabi x KC 3, Khandwa 2 x KC 2, Anjali x KC 2, Anjali x G.Cot 16, KC 2 x MCU 5, KC 3 x MCU 7, KC 3 x G.Cot 16, MCU 5 x Khandwa 2, MCU 5 x Anjali, MCU 5 x KC 2, MCU 5 x MCU 7, MCU 7 x Khandwa 2, MCU 7 x Anjali, MCU 7 x MCU 5, G.Cot 16 x KC 2	Suraj x MCU 7, Khandwa 2 x Suraj, Khandwa 2 x KC 2, Anjali x Surabi, Anjali x Khandwa 2, Anjali x KC 2, Anjali x MCU 7, Anjali x G.Cot 16, KC 2 x Suraj, KC 2 x Surabi, KC 2 x Anjali, KC 2 x MCU 5, KC 3 x Surabi, KC 3 x Anjali, KC 3 x KC 2, KC 3 x MCU 7, MCU 5 x Surabi, MCU 5 x MCU 7, MCU 7 x Suraj, MCU 7 x KC 3, MCU 7 x MCU 5, G.Cot 16 x Anjali, G.Cot 16 x KC 3, G.Cot 16 x MCU 7	Suraj x MCU 7 Khandwa 2 x KC 2 Anjali x KC 2 KC 2 x MCU 5 KC 3 x MCU 7 MCU 5 x MCU 7 MCU 7 x MCU 5

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Table 48. Contd..

Character	Mean performance	SCA based on significance	Standard heterosis based on significance	Mean + SCA + Standard heterosis
Elongation per cent (%)	Anjali x Surabi, Anjali x Khardwa 2, Anjali x KC 2, Anjali x KC 3, Anjali x MCU 5, Anjali x MCU 7, Anjali x G.cot 16, MCU 5 x MCU 7, MCU 5 x G.Cot 16, MCU 7 x Khardwa 2, G.cot 16 x KC 3, G.cot 16 x MCU 5	Suraj x Surabi, Khardwa 2 x MCU 7, MCU 5 x G.Cot 16, MCU 7 x MCU 5, G.Cot 16 x Anjali	Anjali x Suraj, Anjali x Surabi, Anjali x Khardwa 2, Anjali x KC 2, Anjali x KC 3, Anjali x MCU 5, Anjali x MCU 7, Anjali x G.cot 16, KC 2 x MCU 5, KC 3 x Anjali, MCU 5 x Khardwa 2, MCU 5 x MCU 7, MCU 5 x G.cot 16, MCU 7 x Khardwa 2, MCU 7 x Anjali, MCU 7 x KC 3, G.cot 16 x KC 3, G.cot 16 x MCU 5	MCU 5 x G.cot 16

and elongation per cent (Shimna Bhaskaran, 2004; Kanimozhi, 2012 and Ashokkumar *et al.*, 2013). Hybrids with high *per se* performance, significant *sca* and heterosis for yield and fibre quality traits have been reported by (Shimna Bhaskaran, 2004; Kumar, 2007 and Kanimozhi, 2012).

5.5. Superior hybrids based on *per se* performance, *sca* effects and heterosis

Identification of superior heterotic hybrid is mostly done based on the high *per se* performance, high *sca* effect associated with high heterotic effect (standard heterosis). If all these parameters are associated for the expression of character, it will be a boon to the breeder to screen such parental combination to exploit them for hybrids development. The following hybrids were registered to have good performance through all the three aforesaid parameters (Table 48).

The hybrids Anjali x MCU 5 and MCU 5 x MCU 7 for single plant yield; the hybrids Surabhi x G.Cot 16 and Anjali x KC 2 for days to first boll bursting; MCU 5 x MCU 7 for number of bolls/plant, Suraj x Anjali, Suraj x MCU 7, Khandwa 2 x Anjali, Anjali x MCU 7, KC 2 x KC 3 and KC 3 x MCU 5 for ginning outturn; Suraj x Khandwa 2, Suraj x KC 3, Suraj x G.Cot 16, Surabhi x KC 2, KC 2 x MCU 5, MCU 5 x Suraj and MCU 5 x MCU 7 for 2.5% span length; Suraj x KC 3, Surabhi x Anjali, Surabhi x MCU 5, Khandwa 2 x MCU 5, KC 2 x MCU 5 and MCU 5 x MCU 7 for bundle strength; Surabhi x Anjali, Surabhi x MCU 7, Khandwa 2 x MCU 5, Anjali x KC 3, Anjali x MCU 7, Anjali x G.Cot 16, KC 2 x MCU 5 and MCU 7 x G.Cot 16 for micronaire value, Suraj x MCU 7, Khandwa 2 x KC 2, Anjali x KC 2, KC 2 x MCU 5, KC 3 x MCU 7, MCU 5 x MCU 7 and MCU 7 x MCU 5 for uniformity ratio, MCU 5 x G.Cot 16 for elongation per cent exhibited their supremacy through *per se*, *sca* and standard heterosis.

From this investigation, three hybrids viz., MCU 5 x MCU 7, Anjali x MCU 5 and KC 2 x MCU 5 were identified as promising and these hybrids are superior than the check MCU 13 in both yield and fibre quality traits. These hybrids could be exploited for commercial cultivation after ascertaining the genetic potential through multilocation trials. The *sca* effects along with *per se* performance of the hybrids gave an idea about the practical utility of hybrid combinations for heterosis breeding.

In general, none of the hybrids in this study were found to be consistently performing good for all the characters. Hence, multiple crosses among the parents can be made to get homozygous lines through recombination breeding and could be used for developments of hybrids.

5.6. Gene action

The success of a plant breeding programme greatly depends on correct choice of parents for hybridization and the gene action of different economic traits. Combining ability analysis provides such information so as to chalk out the breeding programme effectively. The diallel analysis gives reliable information about the nature and magnitude of gene action and combining ability effects present in the genetic materials. Dhillon (1975) pointed out that the combining ability gives useful information on the choice of parents in terms of expected performance of the hybrids and their progenies.

The performance of parent may not necessarily reveal it to be a good or poor combiner. Therefore, gathering information on nature of gene effects and their expression in terms of combining ability is necessary. At the same time, it also elucidates the nature of gene action involved in the inheritance of characters.

Nature of gene action as measured by GCA and SCA variances is of great importance in deciding the inheritance of a character. Spargue and Tatum (1942) defined the term general combining ability as the performance of a line or a population in several hybrid combinations and specific combining ability was used to designate dose effects in specific combinations which significantly departed from what could be expected on the basis of the average performance of the lines involved. General combining ability is a reflection of additive effect of genes and specific combining ability is due to dominance deviation and epistatic interactions. Baker (1978) and Shaukat *et al.* (2013) suggested that the relative importance of general and specific combining ability should be assessed by estimating the components of variance and expresses as ratio between GCA and SCA.

According to Panse (1942), selection of genotypes for any character under the control of additive gene action will be easier than those trait governed by non-additive gene action. In this situation, simple selection is enough to identify a good genotype for a trait controlled by additive gene action, as it is fixable. When non-additive gene action is

predominant for a character, which is non-fixable, heterosis breeding may be recommended or the selection has to be postponed to later generations after complete attainment of homozygosity.

In the present investigation with cotton, nine parents and seventy two hybrids were studied for combining ability through complete diallel analysis. The GCA variance was larger than those of SCA for all the traits except number of bolls per plant, indicating the preponderance of additive gene action. Similar findings were also reported by Jatoi *et al.* (2010) for plant height, number of sympodia per plant, number of bolls per plant, boll weight and seed cotton yield per plant, Iyanar *et al.* (2005) for kapas yield, lint index, seed index and boll weight. Preponderance of additive type of gene effects suggested directional selection for isolating better homozygous lines from segregating population for these traits. These observations are in conformity with findings obtained by Yuan *et al.* (2002), Khan *et al.* (2005) and Aguiar *et al.* (2007) in upland cotton. The higher SCA variance than GCA variance for number of bolls per plant indicates the preponderance of non-additive gene action. These observations are in conformity with findings obtained Imran *et al.* (2012) in upland cotton.

It may be concluded that since additive gene action was predominant for most of the characters studied, which could be exploited for the improvement of these traits by mass selection or pedigree method of breeding. However, non-additive gene action was also observed for number of bolls per plant for which selection of superior segregants has to be postponed to later generations until homozygosity is achieved.

5.7. Genetical and Graphical analysis

Hayman's (1954) method of diallel technique is subjected to several assumptions namely (1) diploid segregation, (2) homozygosity of the parents, (3) absence of reciprocal difference, (4) non epistasis, (5) absence of multiple allelism, (6) uncorrelated gene distribution and (7) no non allelic interaction. It is important to test the validity of these assumptions before proceeding to the genetic analysis.

The parental lines used for crossing showed a diploid segregation and satisfy the primary assumption required for diallel analysis. The parental homozygosity was valid as the parents were maintained over several generations by selfing. The assumption of non

epistasis, no multiple allelism and uncorrelated gene distribution are difficult to evaluate independently. The validity of all these assumptions were tested by t^2 values and regression co-efficients of V_r and W_r values i.e., $b-0$ and $1-b$. Non significant deviation from unity was observed for number of sympodial branches per plant, 2.5% span length, bundle strength and micronaire value which indicated the absence of non-allelic interactions for this trait. Similar results were recorded by Ali *et al.* (2010). The t^2 estimates were not significant for boll weight, lint index, seed index, 2.5% span length, bundle strength, micronaire value, uniformity ratio and elongation per cent. The validity of hypothesis did not fulfill some of the assumptions in case of a few characters. In such cases, the estimates may not be reliable as they ought to be. Crumpacker and Allard (1962) explained that such partial failure of certain assumptions will not have much impact on genetic analysis. The results of the present study must be considered in the light of these limitations (Hayman, 1954; Baker, 1978).

5.7.1. Genetic analysis

The proper understanding of genetic architecture of characters of the parents involved in hybridization is essential to genetically improve the crop plants. The genetic analysis of different characters was estimated adopting the method suggested by Hayman (1954) and Griffing (1956b). This analysis provides certain additional information such as

- a) Mean degree of dominance
- b) Proportion of genes with positive and negative effects in parents
- c) The proportion of dominant and recessive genes in parents
- d) Heritability estimate in narrow sense

The data obtained gives more information about the genetic behavior of the agronomic traits under investigation. The mean values of each cross were used to estimate the different genetic components of variation viz., D , H_1 , H_2 , E and F as defined by Hayman (1954). It is clear that the additive component (D) was highly significant for plant height, number of sympodial branches per plant, 2.5% span length, bundle strength, micronaire value, uniformity ratio and elongation per cent. Similar results were reported by Ali *et al.* (2010), Khan and Hassan (2011) for lint percentage, Khan and Qasim (2012)

for seed cotton yield, Raza *et al.* (2013) for plant height, number of sympodial branches, boll weight, bundle strength and micronaire value. Meanwhile dominant genetic components (H_1 and H_2) were significant for all the traits studied except number of sympodial branches per plant, number of bolls per plant, boll weight, seed index and elongation per cent. H_1 and H_2 were greater in their magnitude than the corresponding additive genetic variation (D) for all the traits except number of sympodial branches per plant, boll weight and elongation per cent under investigation. It may be concluded that the dominance genetic variation had a greater role in inheritance for all the traits studied. In case of seed weight per boll and seed index, the variability was accounted for by dominance effects, which conform to the previous studies in cotton (Subhan *et al.*, 2001; Chandio *et al.*, 2003; Cheatham *et al.*, 2003; Mahmoud *et al.*, 2004; Mehetre *et al.*, 2004; Murtaza *et al.*, 2005).

Significant environmental component of variation (E) is observed for number of sympodial branches per plant, number of bolls per plant, boll weight, single plant yield, lint index, seed index and elongation per cent. However, similar significant variation in environmental sensitivity were lacking for the other important traits. These results are in conformity with findings of Ali and Awan (2009).

The F value measuring the covariance of additive and dominant effect point to the fact that dominant and recessive alleles were almost equal in distribution among parents. It was positive for all the characters except number of bolls per plant, boll weight and single plant yield. The positive F values showed that there are more dominant alleles present in the parental lines than recessive alleles.

The mean degree of dominance was found to be more than one indicating over dominance for days to first boll bursting, plant height, number of bolls per plant, single plant yield, ginning outturn, lint index, seed index, 2.5% span length, bundle strength, micronaire value and uniformity ratio. These results were supported by Mahmoud *et al.* (2004) and Basal and Turgut (2005) for seed index.

The value $H_2/4H_1$ was less than 0.25 for all the characters studied except for the number of bolls per plant and elongation per cent and also it was suggested unequal mean allelic frequencies at effective loci among the parents. Khan and Hassan (2011) and

Raza *et al.* (2013) also reported similar results for boll weight, seed cotton yield and 2.5% span length. The value of $H_2/4H_1$ was 0.25 for elongation per cent, which was due to the fact that dominant genes would be in equal proportions (Singh and Choudhary, 1985).

The ratio of dominant and recessive genes in the parents (K_D/K_r) is greater than one for all the characters except number of bolls per plant, boll weight and single plant yield. It indicated the presence of excess of dominant genes. Similar results were previously obtained by Khan and Hassan (2011).

The high estimates of heritability in narrow sense were found for micronaire value. The characters *viz.*, days to first boll bursting, plant height, boll weight, single plant yield, 2.5 per cent span length, bundle strength and elongation per cent recorded medium estimates of heritability. However, number of sympodial branches per plant, number of bolls per plant, ginning outturn, lint index, seed index and uniformity ratio demonstrated lower heritability estimates due to the involvement of dominance effects in their inheritance (Ahmad *et al.*, 1997; Iqbal *et al.*, 2003). It also showed that there is preponderance of non-additive gene action and heterosis breeding may be useful.

5.7.2. Graphical analysis

Graphical analysis of experimental data recorded was done in order to get information about allelic constitution of the parents used in the diallel cross. The graphical analysis was carried out as suggested by Hayman (1954).

The characters *viz.*, number of sympodial branches per plant, single plant yield, lint index, 2.5% span length, bundle strength, micronaire value and uniformity ratio showed over dominance type of gene action in the variance (V_r) covariance (W_r) graph. Similar results were previously obtained by Khan and Hassan (2011) for sympodial branches and yield, Khan and Qasim (2012) for monopodial branches.

A partial dominance type of gene action was desirable for days to first boll bursting, plant height, number of bolls per plant, boll weight, ginning outturn, seed index and elongation per cent. The results are in harmony with the results obtained by Khan and Qasim (2012) and Raza *et al.* (2013) for plant height, number of sympodial branches, boll weight and yield of seed cotton.

The position of the parental points along the regression line indicates the dominance order of the parents. For the trait, days to first boll bursting, the parents Khandwa 2 and KC 2 had more dominant genes and the parent G.Cot 16 had more number of recessive genes, since it occupied at the end of the regression line. The parental lines Suraj, Surabhi, Anjali, KC 2, MCU 5, MCU 7 and G.Cot 16 occupied the intermediate position indicating the equal frequency of dominant and recessive alleles for plant height trait. The parent Khandwa 2 occupied at the end of the regression line with more number of recessive genes for number of sympodial branches per plant.

For number of bolls per plant, the parents KC 3 and G.Cot 16 were found to contain moderate amount of dominant genes and the parent Khandwa 2 occupied distal end. For the trait boll weight also, the parents Khandwa 2 and KC 3 were found to contain moderate amount of dominant genes. Similar observations were reported by Sarwar *et al.* (2011) in different genotypes.

The position of the parental points for single plant yield showed that the parent Surabhi occupied near to the origin having more dominant genes and the parent MCU 7 occupied extreme right position away from the origin. Khan and Hassan (2011) also reported that dominant genes were responsible for number of sympodia, lint percentage and yield.

In case of lint index, the parent Suraj occupied near to the origin and the parent KC 2 occupied the end of the regression line.

The parental lines Suraj, Surabhi, Khandwa 2, KC 3, MCU 7 and G.Cot 16 occupied the intermediate position indicating the equal frequency of dominant and recessive genes for seed index trait.

The parent MCU 7 was found to contain more number of recessive genes for 2.5% span length. In case of bundle strength, G.Cot 16 was located near to the origin showing the presence of more dominant genes in this line and KC 2 was located far from the origin with more number of recessive genes. For micronaire value, the parents MCU 5 and G.Cot 16 were found to contain moderate amount of dominant genes.

For uniformity ratio, MCU 5 was found to contain more number of recessive genes and the parents viz., Suraj, Surabhi, Khandwa 2, KC 2 and G.Cot 16 occupied the intermediate position. In case of elongation per cent, Khandwa 2 and G.Cot 16 occupied near to the origin with more dominant genes and the parent MCU 5 occupied extreme position. Similar observations were reported by Ali *et al.* (2008) in different genotypes.

Genetic and SMA analysis for yield and fibre quality components

Plant breeders are continuously developing new crop varieties to satisfy farmers and consumers preference. Conventional cotton breeding programmes, primarily rely on crossing adapted genotypes and selecting novel allele combinations based on phenotypes, have greatly contributed to the success of the cotton industry in the past century (Green and Culp, 1990; Zhang *et al.*, 2012). However, the very complex quantitative inheritance of yield and fiber quality traits and the negative associations between them as described above require cotton breeders to develop more effective strategies in order to develop superior cultivars.

The use of DNA marker technology in plant breeding has opened new way and it has enormous potential to improve conventional plant breeding through marker assisted selection (MAS). The simple sequence repeats (SSRs) are now considered as the marker of choice even in narrow genetic based intraspecific crosses such as *G. hirsutum* x *G. hirsutum* and the total pool of SSRs present in the cotton genome is sufficiently abundant to satisfy the requirement of extensive genome mapping and MAS (Reddy *et al.*, 2001). Hence, SSRs are being used regularly to study the extent of genetic diversity between cultivars, construct genetic linkage maps, identification of QTLs linked to yield, fibre quality and other important agronomic traits in cotton. Identification of multiple QTLs with varying genetic effects for an individual trait provides evidence of quantitative nature of the genes influencing the trait. When QTLs are closely linked with the molecular markers, the conditions open up the opportunity for MAS. Among the different mapping populations used for molecular genetic studies, F₂ progenies are the most preferred population since they are easy to construct and it requires only a short time for development and can be developed with the minimum efforts as compared to

other populations. Further, genetics of F₂ progenies reveal all the allelic combinations and the intergenic and intragenic interactions (Haley and Anderson, 1997).

The extent of variability available in any crop is the result of genetic and environmental factors. An assessment of variability is a pre-requisite to select desirable genotypes, revealing a wide range of mean expression for almost all the characters. Development of an effective breeding programme depends on the existence of genetic variability for various economic characters. Selection is effective only when there is enough magnitude of variability in the breeding population. Hence, an insight into the magnitude of genetic variability present in the genotypes to determine heritable components of variability is of utmost importance to a plant breeder for starting a judicious plant breeding programme (Percy *et al.*, 2006).

Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone. Estimates of heritability and genetic advance as percentage of mean together provides an idea about the gene action involved in the expression of various polygenic traits.

An idea on the extent of association between yield components and fibre quality traits conferring seed cotton yield would be much helpful to decide the traits to be given importance in selection for high yield. Correlation provides information on the nature and extent of relationships among characters. Selection for yield will be effective when it is based on its contributing components rather than relying on yield alone (Grafius, 1960). When the selection pressure is applied for a trait, the population being improved for that trait also gets improved in respect of all the other characters associated with it. Thus, a correlation study facilitates simultaneous improvement of two or more characters. Knowledge of the relationship among yield components is essential for formulation of breeding programmes aimed at achieving the desired combinations of various components of yield.

With this information in background, the present investigation was carried out by using intraspecific (*G. hirsutum* x *G. hirsutum*) F₂ and F₃ populations to study and detect the genomic regions associated with yield and fibre quality traits in cotton. The population of the present study which was developed from intraspecific cross, would

carry new gene combinations for superior yield and fibre quality traits that are transferred from donor parent (MCU 5 - *G. hirsutum*) to the widely cultivated recipient parent (KC 2 - *G. hirsutum*). In order to exploit these gene combinations, F_3 progenies were evaluated for yield and fibre quality traits. The first and foremost criterion to be considered while evaluating a population is the magnitude of genetic variation. Simple measures of variability viz., range, variance and standard error were computed in F_3 progenies. In cotton breeding, these parameters are commonly used to assess the variability for seed cotton yield (Ahuja and Tuteja, 2000; Gururajan, 2000; Rao and Reddy, 2001; Dheva and Potdukhe, 2002) and fibre properties (Dheva and Potdukhe, 2002). The results of the studies conducted on genetic variability, heritability and genetic advance, association studies *i.e.*, correlation analysis and molecular marker analysis for yield and fibre quality traits were discussed hereunder.

5.8. Variability studies

Most of the characters of economic importance are highly influenced by environmental conditions, whereas the improvement of crop mainly depends upon the nature and magnitude of genetic variability present in the base population. The heritable (genotypic) variation is usually masked by non-heritable variation creating difficulty in exercising selection. Hence, it becomes necessary to partition overall variability into heritable and non-heritable components to enable the breeders to plan for proper breeding programme.

In the present study there was a close correspondence between phenotypic and genotypic variance for number of sympodial branches per plant, boll weight, ginning outturn, lint index, seed index, 2.5% span length, bundle strength, micronaire value and elongation per cent indicating less environmental influence. The plant height, number of bolls per plant, single plant yield and uniformity ratio showed higher difference indicating the influence of environment on these characters.

Since the variations are influenced by the magnitude of the units of measurements of different traits, a measure of co-efficient of variation which is independent of the unit of measurement is more useful in comparison between the characters. The PCV, which measures total variation, was found to be greater than GCV for all the characters,

indicating some degree of environmental influence on these traits. Similar results were also reported by Tomar and Singh (1991), Tomar *et al.* (1992), Krishnadoss and Kadambavanasundaram (1993) and Sakthi *et al.* (2007).

High PCV and GCV estimates are obtained for single plant yield indicating the presence of sufficient genetic variability for this character and hence it is amenable for selection. Earlier studies of Punitha (2001), Ahmad (2003), Saeed Ahmad *et al.* (2003), Preetha and Raveendran (2007), Santoshkumar *et al.* (2012) and Dhivya *et al.* (2014) also indicated the presence of high variability for this character.

Among the characters studied boll weight, micronaire value, lint index, elongation per cent, number of sympodial branches per plant and seed index showed moderate PCV and GCV values. This suggests that the best possibilities for improvement are through selection. Similar results were also reported by Ganesan and Raveendran (2007) and Santoshkumar *et al.* (2012) for boll weight, Preetha and Raveendran (2007) and Dhivya *et al.* (2014) for number of sympodial branches per plant, Ahmad (2003) and Prasad *et al.* (2005) for seed index, Ganesan and Raveendran (2007) for lint index, Dheva and Potdukhe (2002) for micronaire value and Santoshkumar *et al.* (2012) for elongation per cent.

Bundle strength, ginning outturn, 2.5% span length and uniformity ratio showed low PCV and GCV estimates, which indicated that one has to create or locate source of high variability of a wider spectrum for effective selection for improvement in these characters. Observations of similar nature were reported by Dheva and Potdukhe (2002), Ahmad (2003), Preetha and Raveendran (2007), Ali *et al.* (2009), Santoshkumar *et al.* (2012) and Dhivya *et al.* (2014).

Genotypic co-efficient of variation does not give an exact idea on total variation that is heritable. The relative amount of heritable portion of variation could be assessed generally by heritability estimates. Generally, the magnitude of heritability is influenced by the variability existing between the population and the extent to which a particular character is affected by the prevailing environmental conditions.

The heritability indicates the effectiveness of selection based on phenotypes but heritability does not provide information regarding gain that is expected by selection.

Estimates of heritability and genetic advance together provide an idea about the gene action involved in the expression of various polygenic traits.

In the present study, high heritability coupled with high genetic advance as percentage of mean was observed for boll weight, single plant yield, lint index and micronaire value. This indicates that the additive gene effects are probably more important for these characters. Similar results were reported by Preetha and Raveendran (2007) and Dinakaran *et al.* (2012) for boll weight, Ganesan and Raveendran (2007), Venkatesan (2008), Dinakaran *et al.* (2012) and Dhivya *et al.* (2014) for single plant yield, Gururajan (2000) and Santoshkumar *et al.* (2012) for lint index and Preetha and Raveendran (2007) for micronaire value. Therefore, simple selection method will be effective for improvement of these traits.

High heritability coupled with low genetic advance was observed for ginning outturn, 2.5% span length, bundle strength and uniformity ratio. This suggests that these characters were under the control of non additive gene action and heterosis breeding can be resorted for improving these characters. The reports of Rao and Reddy (2001), Dheva and Potdukhe (2002), Ahmad (2003) and Santoshkumar *et al.* (2012) for ginning outturn, Ahmad (2003) and Santoshkumar *et al.* (2012) for 2.5% span length and Preetha and Raveendran (2007), Venkatesan (2008) and Dinakaran *et al.* (2012) for uniformity ratio were also in accordance with the results obtained in the present study.

Estimates of high heritability and moderate genetic advance were observed for elongation per cent, number of sympodial branches per plant, plant height, number of bolls per plant and seed index. Similar results were reported by Dinakaran *et al.* (2012) and Santoshkumar *et al.* (2012) for elongation per cent, Venkatesan (2008) for number of sympodial branches per plant, Dhivya *et al.* (2014) for plant height and Preetha and Raveendran (2007), Venkatesan (2008) and Santoshkumar *et al.* (2012) for seed index. Hence, for identifying the plant having greater number of bolls from base population, the cotton breeder is required to make rigorous selection as mentioned by Bhatade and Bhale (1984), Khan and Tariq (1984).

However, Falconer and Mackey (1996) suggested that estimates of heritability are subject to environmental conditions, and therefore may be used with great care and caution in plant improvement programme.

5.9. Correlation studies

Seed cotton yield is a complex quantitative characters governed by many genes and these were greatly affected by environmental factors, hence, the selection of superior genotypes based on yield is a rational approach towards the improvement of yield. Association of yield and other attributes assumed special importance as basis for selection of desired strains. The biometric traits which are directly associated with yield can be used as a *scale* for selecting genotypes as parents for the future hybridization programme. Studying the relationship between those traits is important so as to identify the protocol for applying selection pressure to make the breeding programme successful.

The estimates of correlation co-efficient among the different fibre quality traits indicate the extent of direction of association. The correlation co-efficient provides a reliable measure of association among the traits and that helps to differentiate vital associates useful in breeding from those of the non vital ones (Falconer, 1981). When the breeder applies selection pressure for a trait, besides the population being improved for that trait, it will also improve simultaneously all other characters associated with it. Seed cotton yield per plant is the resultant product of component character, which is not under direct control of any gene. Thus, an improvement of component characters leads to the improvement of yield.

In the present investigation, correlation co-efficient was worked out in the F_3 population between 12 yield and fibre quality related characters with seed cotton yield per plant. Six characters namely plant height, number of sympodial branches per plant, number of bolls per plant, boll weight, lint index and seed index had positive significant association with seed cotton yield per plant. Hence, selection for these characters will help in selecting genotypes with high seed cotton yield per plant. Similar results of positive correlation between yield and fibre quality related traits were already reported by Annapurva *et al.* (2007), Sakthi *et al.* (2007), Aguado *et al.* (2008), Kalpande *et al.* (2008b),

Rasheed *et al.* (2009), Thiyagu *et al.* (2010), Dinakaran *et al.* (2012), Tamilselvam *et al.* (2013) and Gul *et al.* (2014).

The inter correlation among the important component traits is also important in order to decide upon which trait to be given due weightage in exercising selection. The inter correlation between the quantitative yield contributing traits *viz.*, plant height with number of sympodial branches per plant, number of bolls per plant, boll weight, lint index and seed index; number of sympodial branches per plant with number of bolls per plant, lint index and seed index; number of bolls per plant and boll weight with lint index and seed index were positive and significant indicating the possibility of simultaneous improvement of these traits by concentrating on any of these traits. Similar results were reported by Altaher and Singh (2003), Sambamurthy and Chamundeswari (2006), Basbag and Gencer (2007), Leela Pratap *et al.* (2007), Kalpande *et al.* (2008b), Thiyagu *et al.* (2010) and Rao and Gopinath (2013).

It is interesting to note that the yield contributing trait such as ginning outturn had significant negative inter correlation with seed index. The fibre quality traits exhibited positive inter correlation among themselves with some of them showing significance. The 2.5 per cent span length had significant negative inter correlation with micronaire value, uniformity ratio and elongation per cent. This is in conformity with the findings of Altaher and Singh (2003), Ulloa (2006), Turley *et al.* (2007), Thiyagu *et al.* (2010), Dinakaran *et al.* (2012) and Rao and Gopinath (2013).

Hence for undertaking a selection programme in intraspecific cross combinations, the selection based on important yield contributing traits *viz.*, plant height, number of sympodial branches per plant, number of bolls per plant, boll weight, lint index, seed index along with 2.5 per cent span length, bundle strength and elongation per cent will bring about breakthrough in cotton yields under wide hybridization. Enough care should also be taken to select genotypes showing high ginning percentage and micronaire.

5.10. Molecular marker analysis for yield and fibre quality traits

The present investigation was attempted to utilize F₂ and F₃ progenies for detecting the genomic regions associated with fibre quality traits. An intraspecific F₂ population derived from *G. hirsutum* var. KC 2 (medium duration, jassid resistant but

medium staple variety) and *G. hirsutum* var. MCU 5 (extra long staple and strong fibre cultivar) were used to generate mapping population. Using these two cultivars, F₂ and F₃ population of 246 individuals segregating for fibre quality traits were developed to record the genotypic (F₂) and phenotypic (F₃) data in order to identify SSR markers linked to the investigated traits. Many intraspecific studies of *G. hirsutum* have already been reported by (Ulloa *et al.*, 1999; Ulloa and Meredith, 2000; Zhang *et al.*, 2005b; Wang *et al.*, 2006b; Shen *et al.*, 2007; Zhang *et al.*, 2009; Lin *et al.*, 2009; Zhang *et al.*, 2012; Byers *et al.*, 2012 and Gore *et al.*, 2014) to investigate cotton genome and identify molecular markers linked to agriculturally important genes/QTLs.

In the present study, a population size of 246 was used for SMA analysis. The earlier studies by He *et al.* (2005), Lin *et al.* (2005) and He *et al.* (2007) have used 69 individuals of F_{2:3} populations. There is no specific study relating to the ideal number of individuals in a given population required to establish accurate genetic maps. A segregating population consisting of 50 to 250 individuals is required to construct the linkage map (Mohan *et al.*, 1997), but high resolution fine mapping is possible only with a larger population size. Ferreira *et al.* (2006) performed simulation studies using F₂, BC, RILs and DHs populations with varying sample size (50 - 1000) and indicated that more accurate maps were obtained for RIL and F₂ population with co-dominant markers and lowest number of individuals provided several fragmented linkage groups and inaccurate locus order. Hence, a population size of 246 individuals, as used in this study to identify SSR markers linked to the investigated traits.

SSR markers have been used for molecular marker analysis in this research program. SSR markers are regarded as useful markers for map construction in cotton as there is one microsatellite marker for every 170 kb DNA on an average (Zhao *et al.*, 1998). SSRs identify loci that are sub genome (A or D) specific and they can also be used as anchors to combine linkage map produced with different populations to generate more comprehensive genetic linkage representations. Moreover, this marker is simple, informative and prompt. Hence, SSRs were employed in this study for molecular marker analysis. Out of 708 SSR primer pairs, 23 SSRs revealed (3.25 per cent) polymorphism between KC 2 and MCU 5 which was in accordance with polymorphism rate of 2.97 per cent between *G. hirsutum* cv. P 56-4 and *G. hirsutum* cv. RS 2013 (Chaudhary *et al.*,

2013), 4.56 per cent between *G. hirsutum* cv. FM966 and *G. hirsutum* cv. ST V474 (Fang *et al.*, 2014) and 13 per cent between *G. hirsutum* var. L-70 and *G. hirsutum* var. L-47 (Abdurakhmonov *et al.*, 2007).

There are some constraints to construct linkage groups with few polymorphic markers (Young, 2000). There is no linkage map formation in this present study due to poor polymorphism between the parents. However, the polymorphic SSR markers were used for their association with yield and fibre quality traits in SMA. The linkage studies by Ulloa and Meredith Jr. (2000), Bolek *et al.* (2005), He *et al.* (2005), Wang *et al.* (2006a), Guo *et al.* (2008) and Lu *et al.* (2008) have shown poor coverage of cotton genome due to sparse distribution of markers and less number of total linkage groups. Inadequate coverage of cotton genome has been reported due to poor polymorphism, lack of informative recombinants etc. For example, eleven linkage groups were identified from a tri-specific F₂ population that spanned 521.7 cM with an average distance of 16.8 cM (Altaf *et al.*, 1997). Han *et al.* (2006) constructed a linkage map from BC₁F₁ population which contains only six linkage groups. He *et al.* (2007) have published such a map with F₂ and F_{2:3} populations (*G. hirsutum* x *G. barbadense*) which include 1029 genetic loci mapped to 26 linkage groups that covered 5472.3 cM with an average distance of 5.31 cM between loci. Hence, identification and incorporation of additional SSRs or other kinds of markers are required to construct a sufficiently dense linkage map for reasonably good QTL analysis.

5.10.1. QTL analysis

Despite the poor parental polymorphism, an attempt was made for a preliminary QTL analysis by performing single marker analysis to find out the SSR markers linked to yield and fibre quality traits in cotton.

5.10.1.1. Single marker analysis (SMA)

Map based QTL analysis is efficient in detecting QTL, but it is time consuming and laborious. On the other hand, single marker analysis, based on association of a marker with the phenotype, is the simplest method and does not require a complete linkage map. Single marker analysis has been used for QTL study in many crops including cotton (Roy *et al.*, 2006; Wu *et al.*, 2007b).

SMA is considered preliminary and least informative as it does not reveal the location and effects of detected QTLs precisely. However, this is the first step in QTL mapping study where the complete map information is not available (Edwards *et al.*, 1987). The marker data of F₂ individuals for 12 markers identified in this study and their F₃ phenotypic data were subjected to SMA to detect the markers associated with yield and fibre quality traits using Anova tool available in Excel.

The results revealed an association of 8 SSR markers with eleven yield and fibre quality traits. The marker, BNL 3563 was found to be linked to yield contributing traits viz., plant height, boll weight, single plant yield, ginning outturn and seed index. Similar kind of association of BNL3482 with plant height has already been reported (Valarmathi, 2012). Another interesting point of this study is that BNL 1161 which was observed to be associated with number of sympodial branches per plant, was shown to be linked with the number of bolls per plant by Valarmathi (2012). Further, the marker BNL 3623 was found to be linked to the number of bolls per plant in this study, whereas in a previous study, the trait number of bolls per plant was found to be associated with the marker BNL1665 (Valarmathi, 2012). The markers, BNL 1161 and CIR 203 were found to be linked to 2.5 percent span length. Similar kind of association of BNL 1161 with micronaire value, elongation per cent and uniformity ratio and CIR 203 with bundle strength has already been reported (Valarmathi, 2012). Further, the marker BNL 3563 was found to be linked to bundle strength in this study, whereas in a previous study, the marker BNL 3441 was found to be associated with elongation per cent (Urbi, 2010). The marker NAU 797 had associated with both micronaire value and elongation per cent. Similar kind of associations of NAU 2175 and NAU 3934 were found to be linked to micronaire value and elongation per cent, respectively has already been reported by Zhi *et al.* (2013). This indicates that the markers identified across the genetic backgrounds and environments have the potential in future breeding programs through MAS.

In summary, an effort has been made in the current study to develop molecular association between yield and fibre quality traits in intra-*hirsutum* KC 2 x MCU 5. In the present study only limited amount of polymorphic primers were exhibited which necessitates integration of more number of markers to generate a dense genetic map which would be valuable resource for dissecting the voluminous information.

This study has identified genomic regions linked to yield and fibre quality traits across the genetic backgrounds despite the poor coverage of genome. Use of these markers in MAS may improve yield and fibre quality traits in cotton. MAS is an attractive option for improvement of traits for which phenotypic evaluation is often expensive or unreliable. MAS provide a potential for increasing selection efficiency by allowing earlier selection and reducing population size at the early generations. Hence, markers identified in this study could be useful in future cotton breeding programme.

Summary

CHAPTER VI

SUMMARY

An investigation was undertaken at Department of Cotton, Centre for Plant Breeding and Genetics, Tamil Nadu Agricultural University, Coimbatore, during 2012-2014 to identify the potential parents and superior cross combinations to evolve breeding strategies for yield and fibre quality improvements in cotton, based on the genetic architecture of major yield component characters namely days to first boll bursting, plant height, number of sympodial branches per plant, number of bolls per plant, boll weight, single plant yield, ginning outturn, lint index and seed index and fibre quality characters namely 2.5% span length, bundle strength, micronaire value, uniformity ratio and elongation per cent through complete diallel mating design. The experimental findings are summarized below.

- The analysis of variance had showed highly significant differences due to genotypes for all the traits indicating the presence of sufficient variability in the experimental materials.
- The analysis of variance for combining ability revealed out that the variances for the GCA were larger than those for all the traits except number of bolls per plant indicating the preponderance of additive action which could be exploited for the improvement of these traits by mass selection or pedigree breeding.
- Based on *per se* performance, the parent MCU 5 recorded significant mean value for days to first boll bursting, plant height, number of sympodial branches per plant, single plant yield, 2.5% span length, bundle strength and uniformity ratio. The parent, Anjali recorded significant mean value for plant height, single plant yield, micronaire value, uniformity ratio and elongation per cent. The parent, Surabhi also recorded significant mean value for days to first boll bursting, plant height, 2.5% span length, bundle strength and micronaire value. Hence, the above parents can be utilized for recombination breeding or pedigree breeding to improve the traits of interest.

- In case of general combining ability, the parent MCU 5 was found to be a good general combiner for plant height, number of sympodial branches per plant, single plant yield, ginning outturn, 2.5% span length, bundle strength and micronaire value. The parent Anjali was also found to be a good combiner for boll weight, ginning outturn, micronaire value, uniformity ratio and elongation per cent and Surabhi for plant height, 2.5% span length, bundle strength and micronaire value.
- Based on *per se* performance and *gca* effect MCU 5, Anjali and Surabhi were identified as good parents for most of the traits. Hence, these parents can be utilized for recombination breeding in future.
- Hybrids, MCU 5 x MCU 7 and KC 2 x MCU 5 showed a desirable mean performance for ten and nine yield and fibre quality traits respectively. The hybrid Anjali x Suraj showed superior mean performance for eight characters. The hybrids Suraj x Surabi and KC 3 x Anjali showed desirable mean performance for seven yield and fibre quality traits. The hybrids viz., Surabi x Anjali, Anjali x MCU 5 and G.Cot 16 x Khandwa 2 showed superior mean performance for six different yield characters in addition to quality characters. These crosses can be advanced further and selection of desirable plant types can be made in later generations.
- Considering the specific combining ability, the hybrid MCU 5 x KC 2 showed significant *sca* effects for plant height, number of sympodial branches per plant, number of bolls per plant, single plant yield, ginning outturn, 2.5% span length and uniformity ratio. This was followed by MCU 5 x MCU 7 which showed significant *sca* effect for number of bolls per plant, single plant yield, 2.5% span length, bundle strength and uniformity ratio. The hybrid Anjali x MCU 5 showed significant *sca* effect for most of the characters. The hybrid KC 2 x MCU 5 showed significant *sca* effects for 2.5% span length, bundle strength, micronaire value and uniformity ratio.
- The hybrid, KC 2 x MCU 5 also exhibited significant standard heterosis for number of sympodial branches per plant, number of bolls per plant, single plant yield, 2.5% span length, bundle strength, micronaire value, uniformity ratio and elongation per cent followed by the hybrid MCU 5 x MCU 7 recorded the high

magnitude of standard heterosis for number of bolls per plant, single plant yield, 2.5% span length, bundle strength, micronaire value, uniformity ratio and elongation per cent. The hybrid, Anjali x MCU 5 also recorded high standard heterosis for number of bolls per plant, single plant yield, bundle strength and elongation per cent.

- In the present study, MCU 5 x MCU 7, Anjali x MCU 5 and KC 2 x MCU 5 were identified as promising hybrids for yield and fibre quality traits. Based on their *per se* performance and combining ability effects these hybrids can be exploited through heterosis breeding for commercial cultivation after testing their stability in different environments. These crosses can also be used to derive superior segregants in further generations.
- From the genetic analysis, it showed that additive component (D) was highly significant for plant height, number of sympodial branches per plant, 2.5% span length, bundle strength, micronaire value, uniformity ratio and elongation per cent. Meanwhile, dominant genetic components (H_1 and H_2) were significant for all the traits studied except the number of sympodial branches per plant, number of bolls per plant, boll weight and seed index.
- The mean degree of dominance was found to be more than one indicating over dominance for days to first boll bursting, plant height, number of bolls per plant, single plant yield, ginning outturn, lint index, seed index, 2.5% span length, bundle strength, micronaire value and uniformity ratio. The value $H_2/4H_1$ was less than 0.25 for all the characters studied except for the number of bolls per plant and elongation per cent and also it was suggested unequal mean allelic frequencies at effective loci among the parents.
- The ratio of dominant and recessive genes in the parents (K_D/K_r) is greater than one for all the characters except number of bolls per plant, boll weight and single plant yield. It indicated a presence of excess of dominant genes.
- The graphical analysis indicated that the characters number of sympodial branches per plant, single plant yield, lint index, 2.5% span length, bundle

strength, micronaire value and uniformity ratio showed over dominance type of gene action. A partial dominance was desirable for days to first boll bursting, plant height, number of bolls per plant, boll weight, ginning outturn, seed index and elongation per cent.

In the present investigation, F_3 progenies derived from an intraspecific cross KC 2 and MCU 5 were evaluated for observing variation and correlation among yield components and fibre quality traits. An attempt has also been made to identify SSR markers linked to the investigated traits by associating the phenotypic data of F_3 progenies with the genotypic data of F_2 segregants, using single marker analysis (SMA) using ANOVA tool available in Excel. All the F_3 individuals were studied to assess the mean performance, genetic variability, heritability, genetic advance and association analysis of the traits.

- In the present study there was a close correspondence between phenotypic and genotypic variance for number of sympodial branches per plant, boll weight, ginning outturn, lint index, seed index, 2.5% span length, bundle strength, micronaire value and elongation per cent indicating less environmental influence.
- Among the characters studied boll weight, micronaire value, lint index, elongation per cent, number of sympodial branches per plant and seed index showed moderate GCV values. This suggests that the best possibilities of improvements are through selection.
- A combination of high heritability coupled with high genetic advance as percentage of mean was observed for boll weight, single plant yield, lint index and micronaire value. This indicates that these traits are under the control of additive gene action and directional selection for these traits could be effective for desired genetic improvement. Ginning outturn, 2.5% span length, bundle strength and uniformity ratio showed high heritability coupled with low genetic advance. This indicated that these characters are controlled by non-additive gene action and heterosis breeding can be employed for improving these traits.
- The correlation studies revealed out that plant height, number of sympodial branches per plant, number of bolls per plant, boll weight, lint index and seed

index have positive significant association with seed cotton yield per plant. Hence, selection for these characters will help in selecting genotypes with high seed cotton yield per plant.

- In the molecular studies through SSR analysis, out of 708 SSR primer pairs used, 23 SSR primer pairs showed polymorphism between the parents KC 2 and MCU 5. However, only 12 (3.25%) SSR primer pairs yielded unambiguous and scorable polymorphic loci and they were used in genotyping of F₂ progenies.
- Marker-phenotypic association based on single marker analysis showed that 8 SSR markers viz., BNL 3563, BNL 1161, BNL 3623, BNL 3452, DPL 0234, DPL 0322, CIR 203 and NAU 797 exhibited a significant association with yield and fibre quality traits.
- This study has identified genomic regions linked to yield and fibre quality traits across the genetic backgrounds despite the poor coverage of genome. Use of these markers in MAS may improve yield and fibre quality traits in cotton. MAS provide a potential for increasing selection efficiency by allowing earlier selection and reducing population size at early generations. Hence, markers identified in this study could be useful in future cotton breeding programme.

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<http://www.cottonmarker.org>

* Originals not seen

Annexure

ANNEXURE - I

Details of chromosome wise simple sequence repeat (SSR) primer pairs used in this study

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
CHROMOSOME 1			
1	BNL1693	CCCTTGGGAATAGCAGGTG	CATGTGTCTCCGTGTGTGTGTG
2	BNL2440	TGTTAAGCATACATTAGTTTCACTCG	CCGGCACCACAAAAGTAAAT
3	BNL3090	GAAATCATTGGAAGAACATATACTACA	TTGCTCCGTATTTTCCAGCT
4	CIR009	GTGGGTATGGAGTTGTTT	CCGTTAGGTGTCTTTTCTC
5	CIR018	TCAACTATCAGTCCAAT	AAAGAGACCCACAAG
6	CIR055	AACCATTGTCGAGTAAGTAA	CCGAGTAGGTCATTGTCT
7	CIR089	CTCCATTCCCTCGTTTG	AGATTTTCGTTTCCCATT
8	CIR110	GCTTTCTTCTTCGGTTT	CAGTGATGCTTGAGTTTC
9	CIR114	TTGTAATGGAAC TTTGGTC	GGTGAGTAAATAAACGGG
10	CIR184	TACACGGAAGACAACAAG	CTTTGTTACTGAAATGGGT
11	CIR199	CAGAATTTGACCGTTTC	GCCATGATATTTTCGGT
12	CIR241	TCTTGTTTACATTCCCTTC	CGTGTTGTTTATCCGTC
13	CIR376	ATACACAAGTCATTACACA	TGACTATGACACGAGTGG
14	CIR381	TTTCCATCCTTTTGTGA	AAGGAGAAGAACAAGCAA
15	CIR401	TGGCGACTCCCTTTT	AAAAGATGTTACACACACACAC
16	DPL0094	CCCAAACCACATTCATTTTCG	AGATGTCTGTGATGAGTTTGGAGA
17	DPL0216	AAGGAACTGTCACCAGAGGTAAAG	TAAATTCTCCAACGCTTCGACT
18	DPL0490	AGTATCGTCACTTGTCAAAGTCCA	CTCATGCATGCTTATCACACATC
19	MUSB0399	GGATCGAACCAAGATTTTTTC	AGTTGTAACGCCCCAACAAT
20	MUCS399	TCTCAGTCAGTCCTCCTCAGC	GCTGAAGAAGAAGAAAAC TTGG

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
21	MUSS161	AGAGGAATCGGACAATGACG	CCCAAGAATCTGAAGCATCC
22	MUSS422	TGGTTTTGCCCATCTTTACG	GAAAGGGAAGATGAGGAGGG
23	NAU1246	TGCGCACTAAAGAAAAAGAA	GAACAAAATGAATACCCCACA
24	NAU2265	CAATCACATTGATGCCAACT	CGGTTAAGCTTCCAGACATT
25	NAU2419	TCAAAACATTGGCATTGAAC	CACCAAATTCAGG TTCACAA
26	NAU2474	CTATTACCTCCGCCGTAGTG	CTGAGCTAATGCAAGAAGCA
27	NAU2741	AGTCCACGTCCACAGACTTT	GGCACCTTGGAATACATCTC
28	NAU2798	TTCCTCGCAATTTCTTCTTC	GTTTCAGTGTGGTGGCAGTA
29	NAU2817	CTCGATAGCGATCCCTGTAT	GTGAAGGCTGGTTCAGTTTT
30	NAU2858	AGGCCCTATTTCCAATTTTT	TCCCCAAGAATCACTCTGTT
31	NAU2896	ACAATGGCCATACTTGAACC	GGGTTATTGACCCCTGTAAA
32	NAU2994	GGCGATTTGGTAAGGAGTAA	CTGAAATTACAACAAAGACG
33	NAU3022	AACGGAATGCTTTCTTTTCA	GTTGAATTGGGGTTAGCATT
34	NAU3433	GCACTGTGTTCAAGCTTCTG	AGCTTGTCTCCTTTTGGCTA
35	NAU3419	AGAATCTGCAACCACATTGA	CGGTTAAGCTTCCAGACATT
36	NAU3684	TCCATTTGTCCCTTGAATCT	CAGTGACCATTGATGAAGGA
37	NAU3875	ATTTTCCACTCCCTCCAATC	TGATGGAAGAGCCTCTCATT
38	NAU3485	GTTCAAAGTCGGGTATTGG	AGTGCAACGGCTTAGGATAC
39	NAU3911	GCGGAGAATAAAAGCATGAC	CCAATTCACACGTATTTGGA
40	NAU4073	CCCACCCTTTTCTTCTTTTT	GCTGCCAAATTCATCTCTT
41	NAU5100	ATCATTGGCTTCAAAGGACT	GTCACAAACCCCAAAAACCTC
42	NAU5107	CGATGAAGACGATGCTATTG	GTAGCCTTTGGTCTTCGTGT
43	NAU5163	GACTCCCACCCTAACACAG	TTTTGCAAGAATCCTTCTCC

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
CHROMOSOME 2			
44	NAU1489	GGCAATCGGTTGAACTAAAA	AAATCAGCTAATTCCAATCATGT
CHROMOSOME 3			
45	BNL2443	TTTATTGGTCGGTCTTTGCC	TTAGGGTGTTCTTTGGGCAC
46	BNL3034	AAAGGAAATGGTCATTGGCA	AGTACCCGCCATTTCAAGTG
47	BNL3140	CACCATTGTGGCAACTGAGT	GGAAAAGGGAAAGCCATTGT
48	BNL3259	TTTTGAAATTCCAGCGAAGG	GTCAATACCTGCTTCTCCACG
49	BNL3267	GTCAAACAGCAACAGGCAAA	CCAAATGTCCACCCTTTAGC
50	BNL3408	ATCCAAACCATTGCACCACT	GTGTACGTTGAGAAGTCATCTGC
51	BNL3441	CGTCATAAACCGTGCTTG TG	GGCCACTTTAAGGCTGTCAC
52	BNL3463	GCACTCATTCAGTCAAGGCA	TGCCAATGTGGCATCAAC
53	BNL3627	TATGGGCCTGTCCACCTAAG	CAAAGCAACATGCACACACA
54	BNL3989	ACTGTCTCCAATGAAACGCC	TAGAGAGAAATGAGGGGCGA
55	BNL4017	CATGTGCTTCGCAGTTGATT	CAGTGTCCCTCACCATCCTT
56	CIR030	CAATATCTCACTTGGACCT	TGCTACACATCATAGTTGG
57	CIR058	CCATCTTCCTTTCATACC	AGCTGAAGAACTATACCCA
58	CIR062	TTTAGAGGAGAAGTTTAGG	CAGTCTCTTG TAGTTTCATT
59	CIR068	TAGCCATCCAAATCATC	TGTACCTTG GTTAATTCCT
60	CIR133	TAGCCATTCTCACCCA	AGGCAGTCAGAGTCAAAG
61	CIR212	ATGAACGCTACTGGGA	ACAAGCAAACAACCTGA
62	CIR228	TCCAGGTAAACTCAACAA	TCATCAGTTCAATCACAAG
63	CIR245	TCCCATCATTACCCT	GTGAGTTTAGTTCATCTTTC
64	CIR263	ACAGATGATGGATGGATAG	TTCAGGAGTTCAGCGT
65	CIR332	CTACGCATGAGACGATAC	CAACGCCAATAACAATAC

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
66	DPL0605	CAATATATCAATCTGAAGCCCAGC	GTTTAGGCATAGGATGGTGTGA
67	DPL0631	TTATCTTCCTCTGCTTTCTCCATC	CAAAGAAGATAAACATAGTGCCCAG
68	DPL0733	GGCTACTATGGTGTTCGTTTCAAT	GTATCGCCTTGATGCAGAACTAC
69	MUCS585	GCAGAGACACAAGAAATCAATCC	TGCTGACGACGAGTATGAGG
70	MUSB1101	TTCCACCGATTTCACCTAAGTGC	ACAAGCTGATACAATCTTGCCTCGA
71	MUSS162	TTGGTTGGTTAATTACGGGG	GGCTTGTATCTCCCAGCAAG
72	NAU884	AGAGCTGGAGGACATAACAAA	CGCAGATAAAGGATGGATTT
73	NAU1070	CCCTCCATAACCAAAAGTTG	ACCAACAATGGTGACCTCTT
74	NAU1167	CTGACTTGACCGAGAACTT	AAGAGCCCTGGACAATGATA
75	NAU1179	GCTTGCAAGTGGGTAATCTT	CTTGGTCCCCCATAATTAAA
76	NAU1248	AATGTCAGCTGCCTATTTCC	AAGACAGGCGATGTCATCTT
77	NAU2161	GGGAACAAATGGAGACAAAG	ATGACCATTGGATTTTCTGG
78	NAU3016	TATGGTCGAGATGAAAAGCA	GCTTGCCATGTTTCATACAGA
79	NAU3083	TTTCAGTTGTTTTGCTCGAA	CCTTGGGTTTTTCTTCTTCA
80	NAU3309	ACATCGTCTGCGAGATAGAA	TGTGGTTGAATATTGCCTTG
81	NAU3394	CCTGGGATTGGAACATACAT	CCAGAATATCTGCAGCAGTG
82	NAU3439	CTGCCAAAAATAACCCAAAG	TTCAGAAAAGGAATGGAAGG
83	NAU3541	ATCCCACATTGCCTTCTTAT	CTTTCCCCTCTCAAATACCC
84	NAU3639	TGCAAAATCTGCCTTCAATA	CCAGTCACCAAGACAAATGA
85	NAU3671	CACCAATTTTAAACTGCATCTG	ACAGTTGTCCCTGGTGACTT
86	NAU3808	GATTCATACCCTCCCAATCA	GGTTTAAGGCATGCTTTGTT
87	NAU3839	GGGTAGGGGAAAAGTTTGTT	CGTGAATTCCATCTCTCACA
88	NAU3995	CTGACTTGACCGAGAACTT	AAGAGCCCTGGACAATGATA
89	NAU5035	TCCTCTGCTTTCTCCATCTC	TAAATGGATTCTCCGACACC

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
90	NAU5233	GGCCTAAGCCAAATACACAG	AGCCTATCATAATCGCGAAG
91	NAU5444	TGAAATGAACCTCAAACCTCCT	TCAAGAACCAAGGAAGAACC
92	NAU5469	CCCCTTTAAGGCTAAACCTC	ACCACCTCAGCCTTCATTTA
CHROMOSOME 4			
93	BNL3255	GACAGTCAAACAGAACAGATATGC	GACAGTCAAACAGAACAGATATGC
94	CIR027	CGTTAGAATACCAAGCTG	AGGAGGATTTGTAAAGG
95	CIR048	AATCTTCTCAAACCTCCTT	TGCTCTGTTTCCCATC
96	CIR122	AATGTGGGCTGATACG	CAGACACAATCCACAAAG
97	CIR142	ACCCTGCTCTGTTTCTC	GAAGTCTATCATTGTTGGC
98	CIR218	GCGAAGCAAAGGAAG	CTCCAACATCGTCTCAA
99	CIR222	TCATCAACAATCCTTCC	TACTGTCCCTCTTGCAT
100	CIR249	TGCATACCAACATGACC	GACTCAATTTCAACTCAACA
101	CIR291	TTTGGTGACTCGGTTT	GCATTTCGGCTCTTAC
102	CIR381	TTTCCATCCTTTTGTGA	AAGGAGAAGAACAAGCAA
103	DPL0196	CACATTTGGTGGGTATTGAGAAG	ACCATACACGTGCTAATGTCAAAG
104	DPL0273	ACCATTTCTTCCATAGACTTGCTG	AGATGAATATGGAGGTGATCCTGT
105	DPL0299	CTTCTTCTTTGGTCCCTAATTCTTC	GATGATGATGAGGATGTTGGTAGA
106	DPL0573	ATCCTCTTCTTCGTCAGATGTCTC	CGATCCTTGAGTTATATGCAAGTG
107	NAU1158	ACAAAGCATTTCATTCGCTTC	AAAACCTTGGGTGAGGAAAT
108	NAU1267	TGCGCACTAAAGAAAAAGAA	GAACAAAATGAATACCCACA
109	NAU2235	AGCTCACACAGATGAGTTTGTT	CCATGGGTATGGATTTCTTC
CHROMOSOME 5			
110	BNL2448	TAACTTTATCCGCGGAATCG	TAGTTTGATCAGTTTGATGATTAGC
111	BNL2609	GTTCCCATGCATGCTTTCTT	ATAGCAGTGCAAGCAACGTG

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
112	BNL2884	TCAACTCATACCAAATCAATTCC	CCCTGTTTTGTTCAATGGGT
113	BNL3955	AGAGATGCAATGGGATCGAC	ATGTGATAATGCGGGGAATG
114	BNL3995	ATATTTTATTCTTTTAATAGCTTTATTCCC	TTGGAAAAACCCATGGTGAT
115	BNL4108	TCCACCATTCCCGTAAATGT	TGGCCAAGTCATTAGGCTTT
116	CIR017	CATTTTCGGGTTCATTC	GATTTTCATCCATTCCAAC
117	CIR033	CTATCCAGCCTTCGATT	TGCATGACACAACATGA
118	CIR034	TTGAACCAAGAATGGAA	TGTCACGCCATATACACT
119	CIR048	AATCTTCTCAAACCTCCTT	TGCTCTGTTTCCCATC
120	CIR062	TTTAGAGGAGAAGTTTAGG	CAGTCTCTTGTAGTTTCATT
121	CIR067	AAATGCAAAGCATGGA	TCTGGAAGCAAACCTGAA
122	CIR079	TCCTCGTAGCTCGGT	GCTGAGCTGAACCATT
123	CIR102	TAACAACCTGGATGAGATGA	CATAACTGCAAAGGAGAA
124	CIR128	AACAAACATGCGTGC	TGATGAGTGTAATGGGA
125	CIR179	ATGGGTCCAAAGTAAGAG	GATTTGGGAAGCAGAA
126	CIR185	GCATTTGTATTTCCCTGT	GATCAAGTCCAGAGTCCA
127	CIR203	AGTTCAAGGGCACAAA	ATCTCCAAGTCCCACC
128	CIR235	GCTAGTGCCTGACGAC	CCCACACCCGTATTT
129	CIR253	CCAACCAAGAAACCAG	GTAAGCATGGGCATTT
130	CIR267	GCAAGTTTGAATGGTTG	CTTGGTTCTGCTTGGA
131	CIR280	ACTGCGTTCATTACACC	GCTTCACCCATTTCATC
132	CIR291	TTTGGTGACTCGGTTT	GCATTTTCGGCTCTTAC
133	CIR294	GTTCGTAGGGTCTTCTTC	GATCAACCTGGGAAACT
134	CIR298	TCTACAATGAACCCAACA	TCCTTGCTCCCATTC
135	CIR301	ACCTTTAGTTTCTGGTCTTT	TTTACCGTTTAGTCCATTC

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
136	CIR328	ATCCCTATGCTTGTTCATC	ATTACCATTTCATTACCAC
137	CIR364	ACTTTCATTTTCGTGTGGT	TGTTTCATGCTTGTATCGT
138	CIR373	ACCATTGACTTCCCTGT	CCCTCTTGGTGTTATGTC
139	CIR376	ATACACAAGTCATTCACACA	TGACTATGACACGAGTGG
140	CIR405	AGATGTATCATGTGTGTG	ACGTTACTGTAGCCTTAT
141	DPL0101	ACTTCAAGGAACAAGCCGAGTA	ACATTCCGGTATGACAATCCTTAG
142	DPL0153	CCACGATTACCCCTACAGCTT	GGACTGTGTCATAAGGCAAGATTT
143	DPL0156	GGATTGTTTtagcATTAGGGACAAG	AACTCTGTTCTTAAAGGTGCAAGC
144	DPL0238	GTGGAGGTGTATTTCTATCGATCC	GTTGCTAACAGGCGAGACATAAA
145	DPL0328	GGAACCAAAGGGATGAAGGT	CTCTTTCATTCTACCCAAAGCATC
146	DPL0368	ATGAACCACCTTTACATGAACCAG	ACAGCCTGTAGTGGTGAAGTTGT
147	DPL0588	CAACTTCCATATTAGGAGACCGAA	CTAGTGTTTtagggCAGTGATGATG
148	DPL0665	GCAGAAACCCACCTAATTTAAGAAG	GTAGAGGTTGGAGCACTTGTCATT
149	DPL0681	AAATGGACAAATTCGACTCCC	TTCGACTCGACTGAATCGTAACTA
150	DPL0810	ACTTCAACTCCATTTCTGGTGTCT	ACTGGTATGGCAATAATAACCACC
151	MUSB0399	GGATCGAACCAAGATTTTTCC	AGTTGTAACGCCCCAACAAT
152	NAU905	TGGCTGAACTTTGCAATTTA	AAGCAAGGGAGGTAATCCTT
153	NAU922	GGAGTTTGGGAAACCCTATC	CCATGACTTGAAGCAGATGA
154	NAU1218	TGTGATGAAGAACCCTCTCA	CACTCAACCCAATGAAACAA
155	NAU1272	ACGCTCTTAAGTACCGCAAG	CCGGCCATAAATATGAAAAC
156	NAU2128	TAGGTCGAGGGGATCGATAG	CTAACAGGGGTGACATAGGG
157	NAU2156	CCGGCCATAAATATGAAAAC	GGCAGAGGAGGAGTAAAACA
158	NAU2238	TTTTTCATGGCTGAACTTTG	ATTTCCATTGCTCGCTTTAC
159	NAU2278	CCGGGAAAAATAAAACAACA	TCTGGCAGAGGAGTAAAACA

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
160	NAU2580	CCTTCTCCTTCTCCTCCTTC	CACAGACGCTTACCTCACAC
161	NAU2611	TTCTGGAAGAGGAATTGAGC	TTCTCCTTCCCCTTCTTCTT
162	NAU2773	CCCTTTCAATCACAAAAACC	CAAGGGCAGTCAATTTATCA
163	NAU3206	CCCTTTTCTTGTTGCTTGAT	TCTCTTCTGCTCCTTTCACC
164	NAU3489	GTCATCATAATGGGGGTGAT	TTTCAAAGGCTCTCAAGTCC
165	NAU3677	TGATACAATCAGCCAAACACA	GGCATTTCAGGTTTTATTT
166	NAU3900	AATGGAAGATGTGGAGATGG	TGCTAACCTTTGGAAGATCC
167	NAU5088	ATAAGCAAAAACGGCAACTC	CGTTCCCTTCATATTCGTCT
168	NAU5149	CTGAGCCTGGTAGCTTCAAT	AAGGCAAATCTCACAGAGG
169	NAU5160	GGAAAAGGAAAAAGCAATGG	TCCTGCAGTTGTTGTTGTTT
170	NAU5269	TTCTCTTCCTCCTCTTCCT	GCTGGGAAATAACAACCATC
171	NAU5347	AAAGAAGTTCCGTTCAAGG	ACTGCATACTGTTTGCTCCA
172	NAU5400	TCAGATTCTCTCCCGTTTCT	AAGAACCCTTGTGAGTTTGG
CHROMOSOME 6			
173	NAU2971	TAACATAAGGGGGTGTTTGG	AGAAGCGATATGAGGTCCAG
CHROMOSOME 7			
174	CIR 028	CACGAATCTCCAATC	ATAGATGCCTTCTCTTT
175	CIR141	CGCACAAGGAATAGAAG	ACCCAACATAAGGACTAAA
176	CIR169	GAAGCACAATAAGGCAA	CAAACAAGCGATGAAAC
177	CIR262	ACTTTCACATTTGTACCC	TAGTCCCTAAAGAATCAAC
178	CIR320	CCTCCATAAACCTCTT	TCACATACGAAGACAACC
179	CIR335	TACCAAAACAAAGAGTAACC	AGCACCAAGCAAAATC
180	CIR393	GACCACACAGACAGACAA	TCCACAACCAAACTAACA
181	CIR412	CAGTTTATATCCCCTAAATG	AGTCACTAATTCAACACACA

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
182	CM 0066	GGATACGTAGGCTCCACATATTC	GCTGCCTGCTGTTGAATGCTG
183	CML 60	GAAGATTCCATCTGCAGACCCAG	CCAACAAAACCATAAACATGAACTC
184	DPL0136	TGCTCGTATCATAAGAACCCTAGC	AGATTCAATGGAGTTGCCTTAGAG
185	DPL0292	GGTGATTGCATCAATGAGTCCT	GGAATCATTACATCCAGCAGAAGA
186	DPL0403	CGATGACCACTTGACCAATATCT	TAGAGTCTTAAATCGAACCCAAGC
187	MUSB0139	ATGCAGCATGCAAATGTCC	GGCGGAGAGAGTAGAGAACG
188	MUSB 0463	CCAAGAGAAAAACGGCAAGG	CCTCGTACTCGAAATTGACG
189	NAU1043	GTATCCGCCACAAATAAAG	GCATCGTGAGAGAAAGTGAA
190	NAU1048	GGCCATATTATTGCAGAACC	ACAGCCTTGAGTTGAGCTTT
191	NAU1222	ATAGGCCCATGTTGGAATTA	GTAGCCAGAAGTCCATGGTT
192	NAU1305	CCCATCAGAAGGAGTGCTAT	TGCTGATGTCTGAATGATACC
193	NAU2002	GCCCTTTTGGTAGATGAAC	ATCACTTCAGCTGGGGTTT
194	NAU2186	CAAAACGCTTTCGAATACAA	GATTACACCGCAGAGTCCTT
195	NAU2657	CCATCTTTGGGTTTTTCTTC	TGAAGAGCTCAGAGGTGACA
196	NAU2887	CACCATGAGCCACTAATTCA	ACACATTTTTCCCTTTTTGG
197	NAU2995	CGCTTTTATGCATGTAATCCT	CACAAGCTACAATTCCACCA
198	NAU3380	CACCATGAGCCACTAATTCA	GAGAGACAGTGAGCAAACGA
199	NAU3654	TTACCAGCAGCCAACACTAA	TCCCCTTCAACATCTTCTTC
200	NAU3735	AATACCCGGTTTCAGTTTCA	CTCAGCTCACATTCACCAAG
201	NAU3918	TGTGAACCAGGACCCTATCT	TCAAACGCCACAAAATTAAG
202	NAU4082	CTTGCTTGAGGAAAGGTTA	GGTTGCGACAAAGAGAAGAT
203	NAU5152	TCCTTTCTACCCATGCCTAC	GTCACGAGAAGCAGAGGACT
204	NAU5406	CCCTCCTAGGAATTCCATTT	CATTAGTTCTCAGCCGTTCC
205	NAU5439	GTTGGTGTGGGTCAAGAAAT	AGCATAGTTCCCCAAAAACA

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
CHROMOSOME 8			
206	BNL3255	GACAGTCAAACAGAACAGATATGC	TTACACGACTTGTTCCCACG
207	BNL3792	TTCGAGATCCCCTGTTCTGA	CATATTCCAGTCAAACCAAACG
208	CIR119	GGACCATGCAAAGAAG	AAAGGCTGTTTCTACCC
209	CIR176	TTTACCTCACAAGACTCTCA	ATTTGAGCAATGAACACTAC
210	CIR187	TGGTTCTTCTTGATTGG	TTGGGAAACTTGTAGGA
211	CIR209	TGCATGGATTTCCTTATT	TTCCAGTCAAACCAAAC
212	CIR244	TGGAAGGTGATGTTCTAA	GATCAAAGAGCAAACCTAATC
213	CIR278	TCCTCCAAGAACCCTC	GGCACCTTCATAACCTC
214	CIR343	CCAACAAGACCGACA	GAGGGTGAAAGAGAGAGA
215	CIR354	CACAATCCTCAGCCA	AGAGAAGGAAAGAGGAAA
216	CM43	GCGCAGATATTATTATCACAGC	TATATAAATTTGCATCAGTTGGC
217	DPL0176	GAAACTGGGAGTGAAAGAACAAGT	TGGATGTTAGCTTTGGTTTACCC
218	MUSB0139	ATGCAGCATGCAAATGTCC	GGCGGAGAGAGTAGAGAACG
219	MUSB0818	ACTCCGCGAACCACAGTG	GTCGCCAGGCCGTGTAAC
220	MUSB0958	CGAAACCACTTCCCGACTAGG	GGTTGCATTTCGGCAACTTGC
221	MUSS250	TGCACTTGCTGCAGTTTACC	TGCAGTTCAACACAACAAAGG
222	NAU1209	ACCGACAATTATGTGGCTTT	TAGGCAGCACAACTCCAGTA
223	NAU1254	AAACAGTTGAAATAAATTGAAAAC	CGGCAAAGAGAGGTACAAAT
224	NAU1336	TCGCTAATTCTACCTCCTTATT	GCGGGTAATTGTAGTACATGC
225	NAU1505	TATTGCTACGCACAACCACT	GATACCGTCTGGCAGAACTT
CHROMOSOME 9			
226	BNL1161	CATCTCCTCTGGAAAGAGCG	ATGAAGCAGCACATTCCATG
227	BNL1414	AAAAACCCCTTTCCATCCAT	GGGTGTCCTTCCCAAAAATT

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
228	BNL1423	AAAAACCAATTGCCTCCAAA	CTCCTAACGATCAATGGGGA
229	BNL1707	TCCTAGGCTGAGTGAGGGCT	AATGACGTCGTTTTATGCCC
230	BNL2590	GAAAAACCAAAAAGGAAAATCG	CTCCCTCTCTCTAACCGGCT
231	BNL3031	AGGCTGACCCTTTAAGGAGC	AACCAACTTTTCCAACACCG
232	BNL3383	GTGTTGTCATCGGCACTGAC	TGCAATGGTTCAGTGGTGAT
233	BNL686	ATTTTTCCTTGGTGGTCCT	ACATGATAGAAATATAAACCAAACACG
234	CIR077	TGCCTTGGGATGACT	AATGGATGTTTCGGG
235	CIR227	ATCAGCCATCCAGAAA	TAAGATTGAAGTGAAGGTGT
236	CIR353	CGAATGCTACTTTCATCTT	GAACTTGCTTCCTCACC
237	DPL0222	GCTGATTTGTATAGAGAGTATGCTTCC	CAGTTGATTTAAGACGATCAAGCTC
238	DPL0395	GTAACATCTTTCATCTTGCTCCC	TACCTGTGTTAGACCCTGAGATGA
239	DPL0541	GAAATGCTTGTGGGAAGTGAAT	GCTTCCTCCCTTACAATCAAATCT
240	DPL0659	ATCTTCCTCTTCTCCTTCTCCATC	GGTTAGGTGGTTGTATTCTGTTCC
241	DPL0679	AGAGACTCAAGAAGTTTGAAACCG	TAGTACACTCAGTTTGGATGTGCC
242	MUSS547	AAGACAGATGCAAAAACGGC	CTCTGCATCTTCATCCTCGG
243	MUSB0818	ACTCCGCGAACCACAGTG	GTCGCCAGGCCGTGTAAC
244	MUSB0958	CGAAACCACTTCCCGACTAGG	GGTTGCATTCGGCAACTTGC
245	MUSB1040	AAAAGCGGTATTGCACCGAATCA	GCAGAAACCTTGGAGCCTAACC
CHROMOSOME 10			
246	BNL1161	CATCTCCTCTGGAAAGAGCG	ATGAAGCAGCACATTCCATG
247	BNL1665	CAGAACCAACATACTTTCTACGG	ATGTGCAAAAAGTTGATGTGG
248	BNL2440	TGTTAAGCATAATTAGTTTCACTCG	CCGGCACCACAAAAGTAAAT
249	BNL2560	TTTTGCTCCATTTTTTTGCC	TTTATTAATTTTCGTTTAGCTTCCG
250	BNL2705	TGGTGACTGAACTTTGTCCG	CGACGTCGTTTTGCTTTTAC

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
251	BNL2960	TAAGCTCTGGAGGCCAAAAA	CCATTTCAATTTCAAGCATACG
252	BNL3452	TGTAAGTCTGAGCAGCCGTACG	GCCAAAGCAGAGTGAGATCC
253	BNL3563	AAGCATAAACTTGACACAAGCC	AATGGGCAAGAAAAGGGAAC
254	BNL3895	CGCTCTTGGTCATGGATTTT	GCCAAGCTCACTGGAAGAAC
255	CIR009	GTGGGTATGGAGTTGTTT	CCGTTAGGTGTCTTTCTC
256	CIR055	AACCATTGTCTGAGTAAGTAA	CCGAGTAGGTCATTGTCT
257	CIR082	GCAGAAAGTTGAAGCAGA	GCAAAGAGGCCAAATAAA
258	CIR104	GAGAGCATTGATTCCTT	GAAGTCTAACACCACCT
259	CIR166	CTACTCTTTCTTCTTTGTGG	ACTTGTGGAACTATTCTTG
260	CIR171	GAAATCCAAATCCAACC	AACCACCCGACTCTTT
261	CIR372	CTTCGGTATCATTCTTTTC	GATGGACTCGCTACTCTC
262	CIR400	TACTGAATATGTGTGTGTG	CAATTTGCTTCAACCT
263	DPL0026	CAGAAATCCCTAAATCCAAGAACC	ATGCTACTTCTTCAGCTTCTGCTT
264	DPL0431	CTATCACCCCTTCTCTAGTTGCGTT	ATCGGGCTCACAAACATCA
265	MUSS096	TCTGATAAACAGCGACAAAAGG	AAGAAATGAACTCTCACATGGC
266	NAU1169	GGGTAGTAGCTTTTATGATAGGG	CCATTCCTTCCCCTAATTCT
CHROMOSOME 11			
267	BNL1231	TAATAAAAGGGAAAGGAAAGAGTT	TATGGCTCTAGAATATTCCCTCG
268	BNL2805	AGTTTGGAATTACAATAAATGTACTCG	CCAAGGTCGGTCGGTTACTA
269	BNL3254	CACACAGTGTCTTTGGGTG	AGCCTCAAAGGCCAAAAGTT
270	BNL3431	TCAACCAAGCAACCAATTCA	ATGTATAGAGATAGATTGAAAAGGGG
271	CIR003	AAACCAACAGGAATATGAG	GGGGAAGATAACACGA
272	CIR051	AGAGATTAGTTGCTGGAGA	TCACAGACGAAGGCA
273	CIR069	GTCAGTCTATACACTTTCC	TATTGGGCTTTGATTG

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
274	CIR196	TGAGTGGTTGTTTGTTTC	TTAGACAGAGGGAATGCT
275	CIR207	AACAAGAGAAGGTGAAGG	ATCTCAAAGGGCACAA
276	CIR304	AACACCTCAATAAAGGACT	GCGTTTCACCACTTG
277	CIR399	ACACACACACACACACAA	AGAGGTTACATTTCTCC
278	CIR416	TATATGTGTGTGTGTGTG	TTCTTCCCTCTATTTTCTTT
279	DPL0199	CGAAATTGATTTTCATGCCG	ACAACATACAGCTCCCACATGAT
280	DPL0209	GAAGGAACCTCGTGATTATTTGAG	GACCGGTAGACAGAGATGAGAAAT
281	DPL0270	GGTTGGACCCTAATTTAGTTGATG	AAGTTTAACCTTAGCATCACTGGC
282	DPL0325	AGTCAGAAGCAATGGAAAGAGAAC	CCCTAATAGCAGCAACAGAATAAGA
283	DPL0338	GAGAGAAATCTAATTGGGTCATGC	CCCTCAACCAACAGAACAGTAAA
284	DPL0472	ATAGATGTTTCCGAGTTTGTGGAC	TCAACGCATCGCGTTAGTAAA
285	DPL0585	AACACAAATCCTGTCATGGAGTAAC	GTTGATAAGATTGTTCTTCGGAGC
286	DPL0675	CACTCTCGCAACTAAAGACTCAGA	TGCTACTACAAACACCAAAGCAAG
287	GH 0199	CGAAATTGATTTTCATGCCG	ACAACATACAGCTCCCACATGAT
288	MUCS399	TCTCAGTCAGTCCTCCTCAGC	GCTGAAGAAGAAGAAACTTGG
289	NAU922	GGAGTTTGGGAAACCCTATC	CCATGACTTGAAGCAGATGA
CHROMOSOME 12			
290	BNL1227	CATCAAGATCTATCTCTCTATACCG	TTTACCCTCCGATCTCAACG
291	BNL1679	AATTGAGTGATACTAGCATTTTCAGC	AAAGGGATTTGCTGGCAGTA
292	BNL1707	TCCTAGGCTGAGTGAGGGCT	AATGACGTCGTTTTATGCCC
293	BNL3281	GGCGCCATAATTTCCACA	CATGTGCAGCGTATGCTCTC
294	CIR042	GGGTAGTTCTCAGCTTT	CTATTTCTCTATACCCAAGA
295	CIR081	AAAGAACCCATGAGAAGA	GCTGTCTATGTTGGTGG
296	CIR133	TAGCCATTCTCACCCA	AGGCAGTCAGAGTCAAAG

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
297	CIR167	CGCTCGGTTATTTAGTTT	AAATTCCAGCTCATGGT
298	CIR183	CCAGATTAGAACCTATGAAAC	TAGCCCATTTCTTACCAC
299	CIR202	TGAAAGTTGAAAGTGTGG	ACGCTTTAGTTGCAGAG
300	CIR272	AGACAAGTGGAAGAGGG	TATCTGTTGTTGGGTGG
301	CIR293	CCGCTTTATCACATCTCT	GGTTGTCTTTCAGTTTGG
302	CIR362	GAGAGAAAGTGGAGGAAA	CTCCCACCGCTAAAA
303	DPL0039	CCGTCATATCAGTGTACATACAGGT	AGTCGCTACAACCTTCTTCCCTTC
304	DPL0139	AGGGATTTGCTGGCAGTAGTT	CACCAAGTCAATTGAGTGATACTAGC
305	DPL0443	ACGATGACGTCAAGGATGGTAT	CGGATCCTCCTCTTCCTCC
306	DPL0742	GAAAGATCGAGTCAATGACATCAC	AGACACATCTCCCAAATCAACAC
307	DPL0743	GCTTAGGGTTATCTCAAGTTGGAA	GTCGAAACGATGATGATGAAGA
308	MUSB1035	TCATGATAGCAACGAGTGGTGC	GTCGAGTTGTATTAGTGTGCCCCG
309	TMB 1735	GATGTGATGTGCCTAGCAT	TGTATCCAGATAATTGCACGTC
CHROMOSOME 13			
310	BNL1421	TGAAGATTTGGAGGCAATTG	GAAATCAAGCCTCAATTCCG
311	BNL1495	TGAAGATTTGGAGGCAATTG	ATAAATGGCATCAGCCCAA
312	BNL3254	CACACAGTGTCTTTGGGTG	AGCCTCAAAGGCCAAAAGTT
313	BNL3281	GGCGCCATAATTTCCACA	CATGTGCAGCGTATGCTCTC
314	BNL3479	AGTGGGTTGGACTTTCATGC	CACGGGCTTTTTTTTTTTCA
315	BNL3623	TTAATAGAGGGACCAAAAGTGATAT	TTAGCGTTAATATTGTATGTTCAACTC
316	BNL 4061	TAGTAGGTGTCCCCTGTGCC	TGAAGCACCAGATGAAAACA
317	CIR020	ATGCTGGGAAGCTGTA	TTCTTGTGGTGGATTTG
318	CIR027	CGTTAGAATACCAAGCTG	AGGAGGATTTGTAAAGG
319	CIR054	TTTCCCTGGTATGCTG	CAATTTCTTCTCTCGTT

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
320	CIR057	TTTCGTTCCATTGCTT	GTGTCTTTGATTTCGGTTT
321	CIR079	TCCTCGTAGCTCGGT	GCTGAGCTGAACCATT
322	CIR135	AAGCAAAGCAAACAAAG	GCTTGCCAGTATGATGT
323	CIR342	CTGGGTTTCTTTGGTG	TGCTGGGAAGATGTAAG
324	CIR380	CTATCTTTCCACGTCCATA	CTTCTTCATTTTCCCTTTT
325	CIR406	CAAAGCTGATAATGATGCAC	AGCTCAATTATTCAACACACAC
326	GH 0646	GTCTCGATTCAATACAACTCGAGC	TTCTGCTCAGTTTCCTCCTCTTCA
327	GH 0681	ACCCGGCCAAATTTAAGCAAAGAAG	CTTGCCACGTTGGATGTACACAG
328	MUSB 0059	GGATTTTCCCGCTTCTCC	TCACCGTTTGGAAGAAAGG
329	MUSB 0685	CCTTCTTCTCTTCTTCCTCGCTAT	CCCGTTCCTCTTCAGGTAAAC
330	MUSB 1188	AGCACAGATGGCACAACCTC	CACAAACCACCCACCAACC
331	MUSB1263	GGTTAGACAAAGGCATACTCTGGCA	GCGAACCTCCATTTATTGGGACATG
332	MUSS203	TACTCACGCTTTCGTTTCCC	ACTGGGGAAGGAAGATTTGC
333	TMB 0312	AGCTTTTCCATTCCAGAGCA	GGTTGTTGCAAGAGTTCACG
334	TMB 1638	AAAACCAAGAATCGAGGAAAAA	TGCAATCCTCGAAGGTCTTT
CHROMOSOME 14			
335	BNL1059	CCTTCTCTGACACTCTGCCC	TGTATTCTCTTCTTTTCCTTATACTTTT
336	BNL2443	TTTATTGGTCGGTCTTTGCC	TTAGGGTGTTCCTTTGGGCAC
337	BNL3034	AAAGGAAATGGTCATTGGCA	AGTACCCGCCATTTCAAGTG
338	BNL3099	GCCCATGTTCAAATCAATCA	CCCCGACCTGAATCTAACCT
339	BNL3145	AACGAGGGAAAACGGAGAGT	CAAAACGACGCCATTTAGGT
340	BNL3259	TTTTGAAATTCCAGCGAAGG	GTCAATACCTGCTTCTCCACG
341	BNL3267	GTCAAACAGCAACAGGCAAA	CCAAATGTCCACCCTTTAGC
342	BNL3482	ATTTGCCCCAGGTTTTTTTTT	GCAACACCTTTTCCTCCCTA

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
343	BNL3545	AGTCAGTTTTTTGTAGCAATATGC	AACCATTAATTCCCTATTTAACCG
344	BNL3644	GTGCTGTTTGGGCCTTACAT	TAAGCGCATTGACACACACA
345	CIR047	ATTCTACCAAACCTCTACC	CCCGTGTGAGTGAAA
346	CIR058	CCATCTTCCTTTCATACC	AGCTGAAGAACTATAACCCA
347	CIR097	ACTGGATGATGAAGCC	GACTTTCCCTTTACCTCA
348	CIR175	TGCAACAAACTTCAACTC	TCCAAAGAAGAATATGGTC
349	CIR181	AAACCTAGACAGCATGTAAA	TCTTGAAGGGAAACGA
350	CIR202	TGAAAGTTGAAAGTGTGG	ACGCTTTAGTTGCAGAG
351	CIR210	CCTGATAGTGAGTTTCTTCTT	TGAAATGTGAGTGTTTGTG
352	CIR228	TCCAGGTAAACTCAACAA	TCATCAGTTCAATCACAAG
353	CIR239	CCATTTAACCTTGCTTG	GTTCTGTTGGATAGCATTT
354	CIR246	TTAGGGTTTAGTTGAATGG	ATGAACACACGCACG
355	CIR288	GTGGGTCTTGCCTTG	TGGAGATGGTGGTAGTG
356	CIR292	CTTCTTCTTCGTCTTCGT	TCAGCCGCACATTAG
357	CIR295	ATCACGCCAAAGAAAC	TGTGGAGGCGTAAACT
358	CM 0167	CGAGATTTTAAGATTGTG	TGATGGCAAAGCACC
359	DPL0354	TAGTGGTGGTTAAGAAGAAGGTGG	CCGCTTCAGTCTTTGCTTTAACTA
360	JESPR 0147	GCTTAGATCTGGACTACCGAATCCT	CCAAATCAACATCCTCCATTACCC
361	JESPR0231	GCTGGTGGGATTCTCTG	CTATGAACTGCTGGCTATGG
362	MUSB1035	TCATGATAGCAACGAGTGGTGC	GTCGAGTTGTATTAGTGTGCCCCG
363	NAU1070	CCCTCCATAACCAAAAGTTG	ACCAACAATGGTGACCTCTT
364	NAU3189	AAAATCAAACGCCTGAAAAC	AAGCTTCGTTTTGAAGAAGG
365	NAU3439	CTGCCAAAATAACCCAAAG	TTCAGAAAAGGAATGGAAGG
366	NAU3485	GTTCAAAGTCGGGTATTGG	AGTGCAACGGCTTAGGATAC
367	TMB 1268	CAGGTACCATTGATGCCAAA	CTCGAAACCTAGTGCCCTGT

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
CHROMOSOME 15			
368	BNL 0786	CTTTCACGTGTAATTTGTTGATA	GATCTTAACTCTTGCTCTCTCTCTCTC
369	BNL1693	CCCTTGGAATAGCAGGTG	CATGTGTCTCCGTGTGTGTGTG
370	BNL3090	GAAATCATTGGAAGACATATACTACA	TTGCTCCGTATTTTCCAGCT
371	BNL3345	CGAAGCGCGATTAAGAGAAC	AAAGCGAAGCCAACAGTCTC
372	CIR105	GTCTCTTGTCTTTCTTTCTTAC	AACCAAACCTGAACCCA
373	CIR110	GCTTTCTTCTTCGGTTT	CAGTGATGCTTGAGTTTC
374	CIR143	AAGAAAGAAGAACTTCCC	GCCATTAAGAAGGACAAA
375	CIR158	TGTTGCTCCTTAATTGG	GGGAGATTGTTGGAGTT
376	CIR199	CAGAATTTGACCGTTTC	GCCATGATATTTCCGT
377	CIR234	AGCACTCATCCATCACA	GCACCCTTTAGAAACAAG
378	CIR270	CGGAGTTTCAGACATTT	GAGGTGTTACATTTAGTGGT
379	CIR311	CCTTGTGAAGAGAGGGT	GGTGCTAGATTTGTCAGTC
380	CIR370	CTTTTCCCCTTTACACC	GGACATTGGCATTTCATA
381	CIR398	ATACATACACACACACACA	GAGGGAGAAACAGAAGAG
382	CIR411	AGGTGAAGTGTAGAAGTAG	AGTTATCTATGTGTGTGTG
383	DPL0264	GGGCAGTGAAAGACTACCCTTTAG	TGATAGAGGCGATGAAACTGTATG
384	DPL0300	GAAATATTGCTTGTCTGCTTCAGG	GGGTCAAACCACGACTTTATTAGA
385	DPL0322	AAACCTCGTAGTCATAGGCTCAAA	AACTATGCACACAGATTTGGTACG
386	DLP 0504	CCTACACCCAATGTGAAATAGGA	ACTAAAGCCAGAGCCATAGGAACT
387	JESPR 297	GAGAACTCGTTAAAGCACAATG	GTTAATAGAGTTGGGTTTCTCATG
388	MUSB 0537	TCACCAAGCAGCAATTTAGC	CAAAGCTCCACAATTTTCAGG
389	MUSS161	AGAGGAATCGGACAATGACG	CCCAAGAATCTGAAGCATCC
390	MUSS422	TGGTTTTGCCCATCTTTACG	GAAAGGGAAGATGAGGAGGG
391	NAU2419	TCAAAACATTGGCATTGAAC	CACCAAATTCAGGTTACAA

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
392	NAU3433	GCACTGTGTTCAAGCTTCTG	AGCTTGTCTCCTTTTGGCTA
393	NAU4073	CCCACCCTTTTCTTCTTTTT	GCTGCCAAATTTTCATCTCTT
394	NAU5100	ATCATTGGCTTCAAAGGACT	GTCACAAACCCCAAAAACCTC
CHROMOSOME 16			
395	BNL 0580	CTATGTTTGGCCTTGGCATT	TAGTGACAGATATCCCCGGC
396	BNL 1604	AGAGGGAGTAAAGATTTGGGG	TCCAGTTCTTTTTGCCTTGG
397	BNL2986	TAGAGCCAAGTGGTGATCCC	AAAGGGGGGAATGATTATGC
398	BNL3065	CAAACGGGAGACCAAAAAA	CGAACTGGCGAGTTAGTGCT
399	BNL3793	TGTTTGGTTCCCGTTCCTAC	ACATGTCTGCAAATGGTGGA
400	CIR100	AATCACTATCCTCCTCCC	TGGATTGCTTCTTCTTCT
401	CIR107	AATCACTATCCTCCTCCC	TGGATTGCTTCTTCTTCT
402	CIR175	TGCAACAACTTCAACTC	TCCAAAGAAGAATATGGTC
403	CM 0066	GGATACGTAGGCCTCCACATATTC	GCTGCCTGCTGTTGAATGCTG
404	DPL0139	AGGGATTTGCTGGCAGTAGTT	CACCAAGTCAATTGAGTGATACTAGC
405	DPL0168	AGTAGCCTCGCCTAAACCTAGACT	GACGAAAGGTAGAGAATGGAGAAA
406	DPL0342	AAAGGACAACCTCGACAGATACAT	TGGTGGAAGATGACTATGACGATA
407	DPL0443	ACGATGACGTCAAGGATGGTAT	CGGATCCTCCTCTTCCTCC
408	DPL0501	CAGCATCTTAGTTGTTGCTTCACT	CTTGAGTGCTTGAGCAACCTTT
409	DPL0507	TTATTTGAGACTGGTACCCTGGTT	CGACCCTCTAGGTATTAGGGCTAT
410	JESPR 292	GCTTGCAATCTCCTACACC	GAATATGTTTCATAGAATGGC
411	NAU2186	CAAAACGCTTTCGAATACAA	GATTACACCGCAGAGTCCTT
412	NAU2887	CACCATGAGCCACTAATTCA	ACACATTTTTCCCTTTTTGG
413	NAU3911	GCGGAGAATAAAAGCATGAC	CCAATTCACACGTATTTGGA
414	NAU5152	TCCTTTCTACCCATGCCTAC	GTCACGAGAAGCAGAGGACT

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
CHROMOSOME 17			
415	BNL1061	GCTTGTCATCTCCATTGCTG	TAGCCCGGTTTCATGTTCTTC
416	BNL2443	TTTATTGGTCGGTCTTTGCC	TTAGGGTGTTCCTTTGGGCAC
417	BNL3241	GTATTAAAATAATAAGAGTCT	GACCATGGACCGAGTTGAGT
418	BNL3408	ATCCAAACCATTGCACCACT	GTGTACGTTGAGAAGTCATCTGC
419	BNL3955	AGAGATGCAATGGGATCGAC	ATGTGATAATGCGGGGAATG
420	CIR038	AGAGCTTCAGGTAAGACAA	TGAACTAGCAAATCAGACA
421	CIR180	TTGAAGAACGTAGGTGG	TCCGACCTGTTCAAAT
422	CIR185	GCATTTGTATTTCCCTGT	GATCAAGTCCAGAGTCCA
423	CIR251	ACCCATCTTCTGGTGA	CAAAGAGAAACAAGTAGCA
424	CIR261	GCTGTAATCAAATAAGCTC	GGAGAGTCGCATCAA
425	CIR347	CTCTCTCTTACCTGAATCTGT	AACGCTACTTGTGCTATTT
426	CIR375	CCAAAATTAGGTGCGTGT	TAAAAGTTGAACATCCTACG
427	CIR406	CAAAGCTGATAATGATGCAC	AGCTCAATTATTCAACACACAC
428	DPL0045	GCCCATGGAACCATATAGTAGTGT	CTGGTATAACATCTGTCCTTGCTG
429	DPL0058	ATATTGAGCCCTTCTTCATTGTCC	ATCCTCTATGGAGGCTCTTTGTTT
430	MUSB0641	GAGCTGGTCCAAAAGTGTGC	GGCAAGTCACGAGAAACTCC
431	NAU1167	CTGACTTGGACCGAGAACTT	AAGAGCCCTGGACAATGATA
432	NAU2994	GGCGATTTGGTAAGGAGTAA	CTGAAATTACAACAAAGACG
433	NAU3016	TATGGTCGAGATGAAAAGCA	GCTTGCCATGTTCATACAGA
434	NAU3639	TGCAAAATCTGCCTTCAATA	CCAGTCACCAAGACAAATGA
435	NAU3875	ATTTTCCACTCCCTCCAATC	TGATGGAAGAGCCTCTCATT
CHROMOSOME 18			
436	BNL1421	TGAAGATTTGGAGGCAATTG	GAAATCAAGCCTCAATTCGG
437	BNL1690	TTTGTCTTTCTGTTACCAAATGG	CCAGGAAATTTGAGGTGGAA

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
438	BNL1721	TGTCGGAATCTTAAGACCGG	GCGCAGATCCTCTTACCAAA
439	BNL2544	GCCGAAACTAAAACGTCCAA	TCCTTACTCACTAAGCAGCCG
440	BNL3479	AGTGGGTTGGACTTTCATGC	CACGGGCTTTTTTTTTTTTCA
441	CIR020	ATGCTGGGAAGCTGTA	TTCTTGTGGTGGATTTG
442	CIR040	CCCACCAAGAGCATT	TTCTTATATTTGCTACCCAC
443	CIR096	ACCCATCACCGTATCTT	GATCTCATATTTGGCTCTG
444	CIR099	ATGATTCAAGTCGCGT	TTCAAGGCTGAGTCAAA
445	CIR216	ATCTGAACCATCATCCTC	TTCTGATTGGCACTTTC
446	CIR277	TGAGTTGGGAAGTAAATG	CCTGTTGCTTGGATG
447	CIR301	ACCTTTAGTTTCTGGTCTTT	TTTACCGTTTAGTCCATTC
448	DPL0049	CTTGGTATTGGTGAATGAGTTAAGC	GAGGAAGTGACATTATACCCAACC
449	DPL0229	GAGTGGTTTAGTTGTAAAGACCCATGT	TATTACTTGCACAGCCTCTTAGGG
450	MUSS203	TACTCACGCTTTCGTTTCCC	ACTGGGGAAGGAAGATTTGC
CHROMOSOME 19			
451	BNL1690	TTTGTCTTTCTGTTACCAAATGG	CCAGGAAATTTGAGGTGGAA
452	BNL2448	TAACTTTATCCGCGGAATCG	TAGTTTGATCAGTTTGATGATTTAGC
453	BNL3452	TGTAAGTGAAGCAGCCGTACG	GCCAAAGCAGAGTGAGATCC
454	BNL3482	ATTTGCCCCAGGTTTTTTTTT	GCAACACCTTTTCCTCCCTA
455	BNL3569	GCCAATCACCGAGAACAATT	CGCTTATTGCCTTGATTGGT
456	CIR024	TGTAGACAGTCATGTCCTTAT	TGAGTCGGATACATTGC
457	CIR165	ATAAGTGGAGACAGGCA	GACCAGCACAGGAAAC
458	CIR139	AAACAAATGGAGAGGGT	ACCTGTGGTCTGCAAT
459	CIR168	GGATGAAAGGATTCAAA	ATCCTGGCTGAAGAAC
460	CIR176	TTTACCTCACAAGACTCTCA	ATTTGAGCAATGAACACTAC

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
461	CIR179	ATGGGTCCAAAGTAAGAG	GATTTGGGAAGCAGAA
462	CIR212	ATGAACGCTACTGGGA	ACAAGCAAACAACCTGA
463	CIR219	TTGCCTTGGTCTTTGT	CGAAACCATTAACTTCCT
464	CIR222	TCATCAACAATCCTTCC	TACTGTCCCTCTTGCAT
465	CIR224	AGGTTTGCTGTTTCTACC	AACAGAGGGTGACAGTTT
466	CIR229	AATAACTGGACTCAACGAC	ACCTGTGTTCTTATCCTAAA
467	CIR240	CTTCCGATACCCTCG	TGAAGGAGGCTGTTATG
468	CIR242	GCATACAAACATAGGAACA	GTGGCAATTACACTTCAC
469	CIR255	TGCATTCAACCCAAA	AAGGAGAAAGAGTGTAAGG
470	CIR344	GACTTGTCTTCCAGCTAC	TTTCTTCTCTTTTATCTCC
471	CIR398	ATACATACACACACACACA	GAGGGAGAAACAGAAGAG
472	CIR413	TTAAAGCTCACACACACA	CAACAGTAACGAAGAACAAT
473	CIR415	ATGTTCTTGACATTTCCAT	TATATGTGTGTGTGTGTG
474	DPL0071	GCAAACACCATCCTACCACAA	GGTTCTATGATCAAGGCTTGGTTT
475	DPL0140	TATAGTTAGAAGCCAATGCCAAGG	GAGAACCACCTTTCTTCAGCATC
476	DPL0163	TTCTATTCCAATGCTCTTGCCT	AATAGAGAAAGTGAGTGGAGGACG
477	DPL0169	TACTTCGACCAATCCACAGTACAA	GAGTAGAATCGACTTCCATCAGGT
478	DPL0247	AATTAACCAACAAAGGGACCGT	AATAGGAAAGCGCGGTTGTT
479	DPL0309	AGACAGTCCCAACATCCTACTCTC	CGTTGTCATTCGTCTCATTGAC
480	DPL0444	GGCACGAATTCCTTCAAGATT	ATATATCTCTGCACACACGCTGAA
481	DPL0594	TTCATGGAAGTGCTGGTATTCA	TACGCTATTCTTTCAACCAACACC
482	DPL0898	CAGGTAGTTTCTAAAGGCATTC	TCCCTGTGTCATCAAGTGTC
483	JESPR 204	CTCCAGGTTCAATGGTCTG	GCCATGTTGGACAAGTAGTC
484	MUCS585	GCAGAGACACAAGAAATCAATCC	TGCTGACGACGAGTATGAGG

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
485	MUSB0641	GAGCTGGTCCAAAAGTGTGC	GGCAAGTCACGAGAAACTCC
486	NAU2741	AGTCCACGTCCACAGACTTT	GGCACCTTGGAATACATCTC
487	NAU5347	AAAGAAGTTCCGTTCAAGG	ACTGCATACTGTTTGCTCCA
488	TMB 0835	TCCCATTTTGATTCCCAGAG	CGATCTTTGGGAAGGGTTCT
CHROMOSOME 20			
489	BNL3099	GCCCATGTTCAAATCAATCA	CCCCGACCTGAATCTAACCT
490	BNL3482	ATTTGCCCCAGGTTTTTTTT	GCAACACCTTTTCCTCCCTA
491	CIR43	CAGGGCTTCTTTATTATGT	GGTGAAGTGGTTTCTCTC
492	CIR63	CACTATAAACCCAAGCAGT	GTGTGTTGTTGTTGAGGA
493	CIR080	TGAAACAAACAGAGCC	CATGGAAGAAAGATTGA
494	CIR094	ATACCTCCTTTGGCATC	ATTCAGCAACTTCACACA
495	CIR121	GGTGAATCCGACAAAC	AATTGTAAGAGCCGAAA
496	CIR166	CTACTCTTTCTTCTTTGTGG	ACTTGTGGAACTATTCTTG
497	CIR171	GAAATCCAAATCCAACC	AACCACCCGACTCTTT
498	CIR187	TGGTTCTTCTTGATTGG	TTGGGAAACTTGTAGGA
499	CIR305	TTTCCAGCAAAAGAAGT	GAATTTTGAAGTGTCTG
500	CIR340	TGATGCCTTTATTCTGACTT	CCCCACCACAATGATAC
501	DPL0026	CAGAAATCCCTAAATCCAAGAACC	ATGCTACTTCTTCAGCTTCTGCTT
502	DPL0135	GCCTCTGAACATGTAGAAATGAATG	AGCATGCGAACTACAGAATAGTGA
503	DPL0225	TAAAGTGGATACAATGACGACGAC	CTTCAGCCATACATGCTGTTTATC
504	DPL0442	TTACGGTGGCTAATGTAATATCCC	ATTCTTGAGAGTTCACCAGGAAAG
505	JESPR153	GATTACCTTCATAGGCCACTG	GAAAACATGAGCATCCTGTG
506	MUSS096	TCTGATAAACAGCGACAAAAGG	AAGAAATGAACTCTCACATGGC
507	NAU922	GGAGTTTGGGAAACCCTATC	CCATGACTTGAAGCAGATGA

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
CHROMOSOME 21			
508	BNL1053	AGGGTCTGTCATGGTTGGAG	CATGCATGCGTACGTGTGTA
509	BNL1231	TAATAAAAGGGAAAGGAAAGAGTT	TATGGCTCTAGAATATTCCCTCG
510	BNL2805	AGTTTGGAATTACAATAAATGTACTCG	CCAAGGTCGGTCGGTTACTA
511	CIR013	TCATTGCCATTTGACC	TCCACCTTCCACACC
512	CIR061	TTAGTCCTCTACATACCGAA	TCATAATAAAGGCGTGG
513	CIR068	TAGCCATCCAAATCATC	TGTACCTTGGTTAATTCCT
514	CIR069	GTCACTGCTATACACTTTCC	TATTGGGCTTTGATTG
515	CIR070	AACCACCAACCATTCA	TGGGACTCGGTCATC
516	CIR077	TGCCTTGGGATGACT	AATGGATGTTTCGGG
517	CIR112	ACAGTTTCTTGATGGCTAC	ATGTCTTCTGGGCTCTT
518	CIR156	CATTGCCCAAGGAGA	GTAACCAATGAATCCCAG
519	CIR254	CTCATCACCATCAAGAAA	CTCTCACCACCACCC
520	CIR316	TTACAGGCACTACCACC	CCTTTCTGGCGACTT
521	CIR408	TTTTCACACACACACAC	GATCATACATGCACAAA
522	CIR410	TATATGTGTGTGTGTGTG	GTTCTTGACATTTCCATC
523	DPL0062	AGTAATGGA ACTCAGACCCAATGT	CTACAACCCTTGAAGCAAATTACC
524	DPL0215	GAATCTACATCAAAGGGTGCTTGT	CCACTTCTCAAGAAACGATAATGG
525	DPL0228	TTCAGTGCTGATACAATGACTGTG	CTCAAGCCTTGCAGTCTAGCTT
526	DPL0475	CATGCAGGTTGT TAAAGAAGGAAG	CGAAATTAAGCATGGTAGAAGGAC
CHROMOSOME 22			
527	BNL1061	GCTTGTCATCTCCATTGCTG	TAGCCCGGTTTCATGTTCTTC
528	BNL3955	AGAGATGCAATGGGATCGAC	ATGTGATAATGCGGGGAATG
529	CIR036	GTGAGACTTGAACCCAA	GACTCACAACCTGATTCTAC

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
530	CIR122	AATGTGGGCTGATACG	CAGACACAATCCACAAAG
531	CIR172	GGTCCATTCCTTCTTGT	CCGAAATCCTCTTCTTC
532	CIR183	CCAGATTAGAACCTATGAAAC	TAGCCCATTCTTACCAC
533	CIR218	GCGAAGCAAAGGAAG	CTCCAACATCGTCTCAA
534	CIR224	AGGTTTGCTGTTTCTACC	AACAGAGGGTGACAGTTT
535	CIR253	CCAACCAAGAAACCAG	GTAAGCATGGGCATTT
536	DPL0489	ACTCCTCCTTGCTCATGTTGAATA	CATGGATGACTCTTCTGCTTCATA
537	NAU2235	AGCTCACACAGATGAGTTTGT	CCATGGGTATGGATTCTTC
CHROMOSOME 23			
538	BNL686	ATTTTTCCTTGGTGGTCCT	ACATGATAGAAATATAAACCAAACACG
539	BNL1161	CATCTCCTCTGGAAAGAGCG	ATGAAGCAGCACATTCCATG
540	BNL1414	AAAAACCCCTTTCCATCCAT	GGGTGTCCTTCCCAAAAATT
541	BNL2590	GAAAAACCAAAAAGGAAAATCG	CTCCCTCTCTCTAACCGGCT
542	BNL2961	TCGAAAGGGTGTTTCTTCTT	GGGGATGCTTGTCACATCTT
543	BNL3031	AGGCTGACCCTTTAAGGAGC	AACCAACTTTTCCAACACCG
544	BNL3140	CACCATTGTGGCAACTGAGT	GGAAAAGGGAAAGCCATTGT
545	BNL3145	AACGAGGGAAAACGGAGAGT	CAAAACGACGCCATTTAGGT
546	BNL3383	GTGTTGTCATCGGCACTGAC	TGCAATGGTTCAGTGGTGAT
547	CIR060	CTTGCTTCCTCACCC	GAATGCTACTTTCATCCTAC
548	CIR194	ATTGTCTTGGACTTTGGT	TCAGTTGAAAGTATTCCCT
549	CIR200	CCAGGATTGAGTTAGTTT	TTCTTGAACACATTTGG
550	CIR283	AATGTCTGATTAGTTGTTGG	CTTCTCTTTCTTTCCCTCT
551	CIR286	TCTGCCCAAATAACAAA	CAGGGTAAGGGTGGA
552	CIR383	ATTTCAATTTGCGATTTC	CAACTTACATTTTATACACAC

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
553	CIR388	TTAAGCATCCAACAAGG	TCCAACTTTTGGTCTATGT
554	CIR413	TTAAAGCTCACACACACA	CAACAGTAACGAAGAACAAT
555	DPL0012	AATCTCTCACTCTCTTCGTCTCCA	CTTCTCCTTGCATCATTGTTGTAG
556	DPL0079	GTAAAGATGAGACTGTGAGGGCTT	TCATTCCAAGAAGCAGAAGACTAAC
557	DPL0262	TTCTCCATCTCTATCGACTTCCTC	TGTCCGTCTTCAAGTTGTCACTAA
558	DPL0307	CCTCTCTTAATTAATGCTCCTCCA	AAGACAACAGAAGTTGTTATCGGC
559	DPL0378	AGGTTGATGATCCTATGGTTGAAG	ATCTTATGTCCGTGTCTAGCCAAT
560	MUSB1040	AAAAGCGGTATTGCACCGAATCA	GCAGAAACCTTGGAGCCTAACC
561	NAU2967	CCTTTTATTACCCCCCTTCT	GCCAATTCAGCTGTTCTCTT
562	NAU3100	GCAATCAGCTCATCTTGCTT	TGACGAAAATTTGTTGGATG
CHROMOSOME 24			
563	BNL252	TGAAGAGCTCGTTGTTGCAC	CGAAAGAGACAAGCAATGCA
564	BNL2961	TCGAAAGGGTGTTTCTTCTT	GGGGATGCTTGTACACATCTT
565	BNL3627	TATGGGCCTGTCCACCTAAG	CAAAGCAACATGCACACACA
566	CIR061	TTAGTCCTCTACATACCGAA	TCATAATAAAGGCGTGG
567	CIR070	AACCACCAACCATTCA	TGGGACTCGGTCATC
568	CIR119	GGACCATGCAAAGAAG	AAAGGCTGTTTCTACCC
569	CIR278	TCCTCCAAGAACCCTC	GGCACCTTCATAACCTC
570	CIR343	CCAACAAGACCGACA	GAGGGTGAAAGAGAGAGA
571	CIR354	CACAATCCTCAGCCA	AGAGAAGGAAAGAGGAAA
572	CIR388	TTAAGCATCCAACAAGG	TCCAACTTTTGGTCTATGT
573	DPL0191	ACTGTTAACGGAATTCCAAAGACC	AAAGCATCCTCAGTAGGAGAAGG
574	DPL0461	CCCAACCTCTGATCACCTCTATAC	CTTTCCCACTCGTAACAAGGTAAG
575	NAU1197	AGCAAATATCTCTCCCCACA	CATGTTCCACGTCATTTCAT

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
576	NAU1336	TCGCTAATTCTACCTCCTTATT	GCGGGTAATTGTAGTACATGC
577	NAU1505	TATTGCTACGCACAACCACT	GATACCGTCTGGCAGAACTT
578	NAU2439	GGCAACACAACAAAGGACTA	CACTTGCTGCAGTTTACCAC
579	NAU2619	ACTCTTTTCTATGGATTGACCA	TCCACATTTCCAATTTTCCT
580	NAU3072	TGCTCCTCCTGAAGTACACA	TTTAGACCCCAAACCTTCAGG
CHROMOSOME 25			
581	BNL1440	CCGAAATATACTTGTCATCTAAACG	CCCCCGGACTAATTTTTCAA
582	BNL3103	ACTTTGAGATATTGTTATTCTACCCG	TCGAACAATTACGAATCAAATG
583	BNL3436	AACATAGCCTACCATTGCCG	TTGTTTGCCAAATTTGAAGC
584	BNL3806	GACAGGCCAGACCAGAACAT	TCAAACAAAGCACATATATAATACACA
585	CIR109	GAGGAAATCTTCAATTAGGT	ATCCACAAGAACTGAAAC
586	CIR150	TTTACAACCTCAATCCCATC	TCCCTTCTTTCACTTCC
587	CIR267	GCAAGTTTGAATGGTTG	CTTGGTTCTGCTTGGA
588	CIR298	TCTACAATGAACCCAACA	TCCTTGCTCCCATT
589	CIR299	AACAAGCACACATCTCTTAT	GGTAGACCTTGAAATCGT
590	CIR338	TATGCCAATGAAGAAAC	ATTAGCAAGAGATTAGGC
591	CIR407	GCACAGAACATCCATACA	TCTCTCTCTCTTTCACACAC
592	DPL0067	CTGGTGTCATTGCCAAGAGATA	ACTCCATTAATTAGGACCTTTGCC
593	DPL0239	GGAAACTATTGCTGCTAGTGAGGT	TCTTCAACTCCCCTGACCTATTT
594	DPL0323	AAGGACTTTGTCCAGTGTGAGAA	TATCCCAGCCATAAGATACCAAG
595	DPL0365	GAATCTCGCATCTGCATTGAA	GCACGTTTACTTATGGAATTCTCC
596	DPL0377	ACACTTAGAGAGCATCTCCGAATC	TGTTGCTTCAACCCTAATGGAT
597	DPL0519	ACGACCTGAATATGAATAGCCG	GTAATTGCTCCGTAAGTTTGTTC
598	NAU905	TGGCTGAACTTTGCAATTTA	AAGCAAGGGAGGTAATCCTT

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
599	NAU2002	GCCCTTTTTGGTAGATGAAC	ATCACTTCAGCTGGGGTTT
600	NAU2238	TTTTTCATGGCTGAACTTTG	ATTTCATTGCTCGCTTTAC
601	NAU2580	CCTTCTCCTTCTCCTCCTTC	CACAGACGCTTACCTCACAC
602	NAU3677	TGATACAATCAGCCAAACACA	GGCATTTGCAGGTTTTATTT
603	NAU3900	AATGGAAGATGTGGAGATGG	TGCTAACCTTTGGAAGATCC
CHROMOSOME 26			
604	BNL1064	TTTGCGGGTAATCCTATTGC	TGTCTATGGGACATTTTCGCA
605	BNL1227	CATCAAGATCTATCTCTCTATACCG	TTTACCCTCCGATCTCAACG
606	BNL3482	ATTTGCCCCAGGTTTTTTTTT	GCAACACCTTTTCCTCCCTA
607	CIR032	CAAGTTTCCTTGTAAGTTC	GATCTGCTTCTTTAGCTC
608	CIR039	GGAGCAGAAACAACCA	TTCCCATCTTCACTTCTC
609	CIR078	TGCATGATGAAGTTAGA	ACATAAATCCCAAGAAC
610	CIR085	ATTCCGATGTCTCCCT	TTTAGCCTGATAAGTTCGT
611	CIR143	AAGAAAGAAGAACTTCCC	GCCATTAAGAAGGACAAA
612	CIR167	CGCTCGGTATTATAGTTT	AAATTCCAGCTCATGGT
613	CIR170	TCGGTAAAGATGGGTG	ATTGGTGCTGGTTGAG
614	CIR233	AGGCAGTAGCATTTATCAG	GTGTTGGTTGTTTATGGTT
615	CIR235	GCTAGTGCCTGACGAC	CCCACACCCGTATTT
616	CIR272	AGACAAGTGGAAGAGGG	TATCTGTTGTTGGGTGG
617	CIR391	GTTGAAATCTGCCGTAA	CACACACACACACTCT
618	DPL0665	GCAGAAACCCACCTAATTTAAGAAG	GTAGAGGTTGGAGCACTTGTCATT
619	DPL0890	ACAGCATTAGCAGGCACCTT	TATGAACGATGTGCTAGCCG
620	NAU2881	CAGCACCACCAGTAACAAGA	TCTTCTTCCAAAACCCAAAG
621	NAU3189	AAAATCAAACGCCTGAAAAC	AAGCTTCGTTTTGAAGAAGG

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
NO RECORD FOUND			
622	BNL 0243	GCCGAAACTAAAACGTCCAA	TCCTTACTCACTAAGCAGCCG
623	BNL 0341	ACCTGGGGTACTTGTCCACA	CCATCCCATTGTGTGATACCC
624	BNL0542	TCGATCACATTTATAAGAACTATTGG	TTCATTTTGAACATTCGCCA
625	BNL1030	TTTGGAGCCATTTACATGCA	AAACCACTTCTGCATCTGGA
626	BNL1034	TTGCTTTCAATGGAAAACCC	CGTCGCAAAGTTGAGAATCA
627	BNL1317	AAAAATCAGCCAAATTGGGA	CGTCAACAATTGTCCCAAGA
628	BNL1531	CTGCAACAAGAGCCTGTGTC	ATGGAGATTGGCTGAGATGG
629	BNL2569	CAGAGAGCCATTGTGAACGA	ATAATGCTAGGGCATGTGGC
630	BNL2570	TTCTACAAAAAAAGAAAAAATGGG	AAATACGGATGGGACCAACC
631	BNL 2572	GTCCTATTACTAAAATTGTTAATTTAGCC	CGATGTAAATCAATCAGGTCA
632	BNL2652	TTCATCATTCTAGCCTGAGTCC	GCGATAATCCTTCCAGGGAT
633	BNL2691	TAAGATGATCGTCCCCCGTA	TGGGAAGATATTTGGTGGGA
634	BNL2715	AGGAATTTGGTTAGACCATGG	GTTCGCTCTGTAAAATTAGCTACG
635	BNL 2895	CGATTTTACTGCTTCAGACTTG	TACCATCTCACGGATCCACA
636	BNL2920	TTCTTGCATTGAATAATACTGGC	CTTAATTCTAAAAATCAATAAATTTAGCC
637	BNL2921	CGAGAGATTTTAAAGGGAAACA	GGGAGTGGTCTGATGGAAAA
638	BNL 3085	TGGACATCCTTCTGGAAACC	TGTGGAGTCATCAATATGTTGC
639	BNL 3147	ATGGCTCTCTCTGAGCGTGT	CGGTTCAAGAGGCTTTGTTGT
640	BNL3282	ACTAAAACAAATGTAGCGTGTGG	TTTAGGTTTGGGTAAGTAGAGGC
641	BNL 3400	CAATTTTTCATAAACAGAGATCCG	GTCTTATGCTTGTCAATTCTGGG
642	BNL3424	TGTGCCGTCTCAAAATGAAG	AAGACCAATCTGTTGCCAGC
643	BNL 3592	GTTCTAGTCTCTTTCTTTTATGGGC	TTGATTGAGATGCCAATGGA
644	BNL 3601	TTCCGTTGATGGAAATTGAA	ACAAGAATGCGTGTGTCTGC

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
NO RECORD FOUND			
645	BNL 3649	GCAAAAACGAGTTGACCCAT	CCTGGTTTTCAAGCCTGTTC
646	BNL3650	TCGATTTTCCTTATTTGATTTCTG	AATTTGTCCAGATTCATTCTTCA
647	BNL3874	CATGTTCTAATCATATATATATGTATATATATGTGT	AAAATAACAAAAGCCATGGAATAA
648	BNL 3902	GAGTTTGGGGGCTGTGTATG	GGGGTGCTTATGTCAGACGT
649	BNL3932	TCGGGATTTTTTATGGCAAAG	GAACACTCAACAAGGGGGAA
650	BNL3948	GTAATGTTCAACACTTTGCTATTCC	GTTGGTTGGGTGAGCAGAAT
651	BNL3972	AGGACAGCGATGTGTTGTTG	CACCATACTTGTTAATAATTCAGC
652	BNL 3994	TTGAGGGCATCCAAATCCAT	CCTCCACCATACACGTGCTA
653	BNL4030	CCTCCCTCACTTAAGGTGCA	ATGTTGTAAGGGTGCAAGGC
654	BNL4034	GAGGAAGGATGGCTAACTGGTATAA	GTCAAACACATATCACACACAC
655	CM 029	TTCCAAGTTCCAATTTCTTC	ATCAACCACTTTGACAATGTT
656	CIR 307	GACTTGAAAAGATTACACAC	GAATTTGCTGGCTCT
657	DPL0009	CACTGATAAAGCTCAGGATTTCTACTC	GTGACCAAGATTGGAAGAAGAGTT
658	DPL0019	ATTCACGAATCTCGTGGTGTATC	GTTATGATCAAGTCGGGTGGTTAT
659	DPL0035	CATGGTTGTACCGGTTAGTATGTG	CAGCAATGAGACCATTGTATACCC
660	DPL0051	CACCACAGGTTAGAGAAAGGAAAG	CAAGTTCTGTTTCCACCCTATTTG
661	DPL0055	CATGGCTACCTATCCACTCAACTT	GAAGTTTGAGTTTAGGCCTTAGGGT
662	DPL0068	GTTCAACAGGTCTGTACCAGTTCC	GCAAATGATCTCTGCCCTGTAA
663	DPL0069	GCCAGTAACTTTTATGCTTGGAGA	CTACTTACAGGCACTCTCCACCTC
664	DPL0073	TTTCCATGTATGTATGTGAGAGGTG	GCTCCCACATAATTGAGCTTAGGT
665	DPL0075	GAGGTCATTTCAGTCCAACCTTTT	AGAGACCGGAAGAATTTTCGAGTAT
666	DPL0080	GAACCAGAGGGATGATAATGACAC	GTCCAATCCAATATCAGTCCTTTC
667	DPL0085	AGCTTAAAGGCTTATACACCACGA	TATTCGTTACGAGTACGGAGAG

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
NO RECORD FOUND			
668	DPL0088	GATTGCGGATTTCAATGCAG	ATGCAGGATATCTGTCCCTAAATG
669	DPL0100	TATATGCTTGTGGGAGTAATGGTG	CTTATGGCTCATCTATTAGGGCTTT
670	DPL0112	TACACTGGAGTAAAGGAGAGGCA	ACATGAACTCAATTTAGGAGGCAG
671	DPL0113	AAGTTAGTAGCAGCAAATTCTGGC	GCTTCAAATTTCTGACGAACCTC
672	DPL0139	GCCTCTGAACATGTAGAAATGAATG	AGCATGCGAACTACAGAATAGTGA
673	DPL0146	ATATGTTGGAAGTTGGAAGTCTG	AGAATTTGCCAAAGGTACAGAGAG
674	DPL0177	CAATTATTCAGAAGCCACCTAACC	GAGAGAAAGATGCACCACATTCTT
675	DPL0183	TTATTTCTTCCCTTGCGTTCTG	AGAGGTGGCAATGGAGTTCTT
676	DPL0193	TTAGGTCTGCTACCTTTGAAGCAT	CATCACCATCCTTCTTCTTCACTT
677	DPL0202	GGTTTCGTAGAAAGAGACCCAAC	TACACTGTCTTAAATGCACCCTTG
678	DPL0212	TGATAATGCTGATGTCATAGACGC	AGAAGTGGATGAAGAACTGATGAC
679	DPL0218	ACCTTTGAACCGTCGATCTCTA	ACTTTACCCTCCTCTTCATCCTTC
680	DPL0223	AGTCTCAAGAGGTGGTCATTATGC	GCATACCTAGAGGAATTAGCAGCA
681	DPL0234	CACACATCAAGGAGATGGATTTCT	ACTTCCAACCAGAACCGTATGTAT
682	DPL0241	CACTTGGAATTGGGATGTTCTT	AGACATTCCCTCCTCCCAAAGTAGT
683	DPL0242	CTTCAGAATTTGGTTCCTGTCTCT	AATATAAGGATGTAGCTGATGCCG
684	DPL0249	ACAGAGCTATGGGAAATCATGGTA	TGTAAGTCAAATTGCTGCTAAGAC
685	DPL0253	TCACTATCTCAAGACCACCTTCAA	AGTTCAAAGGACTCACCTGATGAT
686	DPL0278	CAGTGGAGTTTGGTGTAGTGGTAG	CAGAAGGACTTTACCCAACCTATG
687	DPL0279	CCCATCTATAACATGGAAGCAAAC	GTTTGAGGACGTGTGAGAAATCAT
688	DPL0283	AGAAACAGATATGACACCTGCTGA	CCTTCTGTTCTTTCTCTGCCTTTA
689	DPL0317	GCTGCATATACTTGCATTCACTTC	GCAAGAGATTGAACAATTGGGT
690	DPL0318	TAGCAAGGACCTTTGGTAGATCAG	TACATGTGCGTTATGGAATCAGAC

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
NO RECORD FOUND			
691	DPL0348	AGAATGGTTGAAGTGATGGGTTAG	CCCATTCTGTCCTTTCATCAAT
692	DPL0353	GACCTTGATTGATCAGTGCTACC	ATTAATTTGTGGAGCAACCACC
693	DPL0370	TAAGTTGCTGATCATCATGGTAGG	CTGCTATCGCTATGATTGAAACAC
694	DPL0405	GAGATCCATGCTAACGTCTTACAAA	ATGGGAGGAGGGAGTGGA
695	DPL0417	ATAAGCACTTGTCTTTGAGGGAT	AAGACCGACACCGATTTAAGG
696	DPL0448	CTGTTTCTTAGTCTGCTTATTGTCCTC	TTCGTCATAATGTACCTGACAAGG
697	DPL0457	CACCTTATTCGTTTCCACCTTTAG	GCTTGTTCTCTTAGCGTCAAA
698	DPL0469	AAAGGTTCTGGAGAGTTATGGACA	AGTTCGTAGGGTGACTCGAATTT
699	DPL0473	CGTTACAGGCGTAACTAAAGAGGT	ATGTATATGACATTGAGTGGCTGC
700	DPL0486	CTTGATGCCTCTACTTATGCAACA	AATGGTGATAAGACCAGAAGGTGT
701	DPL0495	CGTGTTCTCTTGTAATGAACTTGC	ATCCATCTTATTGGTGCATACCAG
702	DPL0511	TACATGCAGTGCTACAGAAGAACA	CTTGTATGCCATCATTAACCCTTC
703	DPL0520	GATTCTCCCAGCAATTAAAGACC	AGACGAAAGTGAGATTCTCTGAGG
704	DPL0528	ATGCCTCTAAACAGGCAAATCA	TAAACCTTCAGCTGGTTCTCCTC
705	DPL0529	ACTCTCAGGATCTGAGTACAACCC	GTAAAGGATCCTAGTGCTCATGG
706	DPL0538	CTGAAGAAGACTCTAGGCTGAAGG	CCAGTTTGTTGGTAGATATTGGT
707	DPL0580	TAGGTAAGTTTGGTGGGTGATGAT	TCTCATCTCATCTAATGCCAACG
708	DPL0608	ACTACAAAGACACCCAATGGTAGG	GTGTTAGTGCGCTTCTGTGATTT
709	DPL0646	GGATTCTTGGATCATAAAGGTCAG	GAAAGAAGAAAGTCCACCATGAAC
710	DPL0670	AGGAATTTTCGGCTAACCTTTGT	AAGAGAGACTAGAAGCAACCGTGT
711	DPL0699	ATTAACCGCGAATATCCCAAC	CTGTGTCTATATCCATGGCTTTCAT
712	DPL0715	AAATCCAACGGCTCTTATACTGTG	GAGGAGTAACCTTACAGCGCATAC
713	DPL0717	CTCCATGATTTCTGAAACACAGGT	TTGTACTAACATACCTCCGGGTCT

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
NO RECORD FOUND			
714	DPL0728	ATCCAAGATCCTTATTATGGCCTC	TGAGAGTGTAGCCATTGTTGTTGT
715	DPL0734	AAAGGCACCAGCATTGGTT	CACAGAGGCAGAGACTTAAAGACA
716	DPL0800	CTCCCTCTCCCTCTTACTCAAAC	CATTCTAATTATCAGTTGGCCCTG
717	DPL0835	CAAATTGTGGGATCATCGAA	CACTGAAGCCCTGATGGAGT
718	GH 0039	CCAGTTTATAATAAGAATCATAGTTTGGTGG	CACATTCACTTCAAAGTCCATCAC
719	GH 0058	GACTTTGAGAGGGATTTTACAGTG	CACCCAATTTAAGCAGAAATTG
720	GH0083	GGTTTGATCAGTTTGATGATTTAGC	CCGCGGAATCGTCAAC
721	GH0107	CATATGTGACTTAACATTCATCGTC	CTCACCCATGTTTGTTCTGA
722	GH0129	ACACAAGCGATCAACAAGG	GAAATGATGTGAGCTCTTGTTTC
723	GH 132	TCATGGAACACCAAAGTTGGA	ACATGATAGATTATTCAGCAATGCA
724	GH 0211	GATTGATAAAGATAGGGTTGTGTCAC	CATTATGTGCCTTCAAATTCCTGGC
725	GH 0247	CTTCTTCCGCCACGTAAGTCC	CAGCCTAACCAAGAACCCAATCG
726	GH 0288	CTATTCCACAAGCTTCATTCTGCAG	GGAGCACAAATGAGGAAGTATACTG
727	GH 0470	ACATCAACTTTCAAACCGTTCAACC	CTGGAAGCTAAATATACAGAGCAAG
728	GH 0501	CACAAATTGAAAGATACCCAGATCTTC	TTCTTCATTCCCGTTTCGATTCAG
729	GH 0548	CCATCATTATTTTACCTTTGCCTCTC	GGTGGTTTTTGCACCATCGTTTAAG
730	GH 0645	TCAACACTTCAAGCCTGTCTCAC	AGGTTTTTGGTTAGGGGAATATCATG
731	GH 0662	TATCCTCATATTCATTGTCAAACACGAG	GTCCAAGGATATGATATTCCAAAGACC
732	JESPR 29	CACCGTTTCCAAGTAAGATT	GGTTAATCTTAGTTGAGGTC
733	JESPR0046	GCTGTTGACTAACACATAAATAC	ATTGTAAATGTTACTGTATGATGCC
734	JESPR0056	CCAGTTAGCACCAATTTAGG	CCACAATAACACACTGGAATC
735	JESPR 065	CCACCCAATTTAAGAAGAAATTG	GGTTAGTTGTATTAGGGTCGTTG
736	JESPR 0066	CTGGACTAACTATTTGGTATCCCTC	GATCTGGACTACCGCTAATCAC

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
NO RECORD FOUND			
737	JESPR 0119	CTCAGGGA ACTATTTGTAGTAGC	GATCCACAAGAACTGAACTAG
738	JESPR 127	GATTTGGGTAACATTGGCTC	CTGCAGTGTTGTGTTGGGTAGA
739	JESPR 154	GTTCCCTCAGTTGCTCAGAAG	GGAGGAGTTGGCAGAAAATAGC
740	JESPR 208	CGCAACCAAACATATACTTCACAC	CCCTTTCCATCCATAGAACG
741	JESPR 211	CATCATTTTTTCCAAGTTCCAATTTC	CAAACCGTTAAGGCTCCAGC
742	JESPR 0223	TGGTCCAAAGCTCAAAG	CGTTACGGATTATTGGACATG
743	JESPR 0291	CATTCCCCACTTTGCTCTTAC	CATGTTTCTTTGCCCATC
744	JESPR307	CTTGGCCATGTATTCCTTCA	GAAAGACACTAAGCTGAGGC
745	MUCS557	GGCATCTAGTTGAGGGAAGG	TGGAACATGCACTTTAATCACC
746	MUSB 0073	CTTCCAAAACCAACATGAAGC	GTGAGGGAGGAAGGGAACC
747	MUSB 0078	CCCTCGAGACACCTAAGACC	GTGATGGTGGTAGTCATTTGG
748	MUSB 0155	TCACAAGGCCTAGATTGATGC	TGCATGTGACATAAACTGAAGG
749	MUSB 0264	AAACATCAGGGTGCCAAGC	GGTCCCCAAACCTTTCTTAGG
750	MUSB 0859	GCGGAAGCATTAAGTAGGCATAAGC	GGACATGGCATCGGCCTAG
751	MUSB 1048	CCCTTGTCCTTCACCTCTGAAGC	AGGGCAATTGATTCTCTGGTGG
752	MUSB 1050	ATCTTTGAAAGGTAGGTCCGAGTGT	TGCTGACAAATTCAGAAGCTTGCT
753	MUSB 1316	GCCTCAGACTTGACCATTGAGG	CCCGAAAACCTTTGCCCAAACC
754	TMB0471	AAGAATTAGCGGAAGTGGTCA	TTTGACAAAACATGGATGGA
755	TMB0836	CATTGCTTTCAACCCAATCA	TGGCATGGTCCAATTGTCTA
756	TMB1296	TCACTTGCATTGCTCTTTG	TCTCAGCTTCAGTCCCGTTT
757	TMB 1356	GTGTACATTGCGCTTTGAG	TCCAAAATTTCAAGCCAACC
758	TMB1421	TGCATATAATGCAAGAATTCCA	AGCAATTGGTATTAGAACTAGG
759	TMB1427	TGTTTTTGGGTACAGTTTTGACA	TTCTCTTCAAAGGGGAGTGTTT

Sl. No.	Name of the primer	Primer sequence information (5' to 3')	
		Forward	Reverse
NO RECORD FOUND			
760	TMB 1496	GGCGGTAGCAGTGAGAGAAG	AAACAAAGCCGGACGTAATG
761	TMB 1578	CCAAGTCTCCTCTCCCTCGT	GGCCTACTGTTGCTGCAAAT
762	TMB 1648	GCTACAAGCAGCATTAACAAGA	TTTGGGGATGTCTAATGCAA
763	TMB1738	TTGTTAGCAATATGCAATATGAAC	GGGTTTAGTTGAATGGGACC
764	TMB 1740	CACTCCAAACTCATCGCTCA	TGATTCATGATTCCCCCATT
765	TMB1806	TCCATGAAGAAAGAATGGAAA	TTCAGTGAAACAAAGGGAACC
766	TMB 1980	ATTGAAGGGAAACCGAATGA	AGAAGACGGTCGAATCGAGA
767	TMB 2295	TGAGTTCATGTTCCCCACTG	CTAAACATACTCTGTCAAACAC
768	TMB 2386	GAAGAGTCGAAATAAAAATACCACAA	ACGGTGCAAACAGGTGAAGT
769	TMB 2762	TCCCATTCAAATAAAAAGAAAAGAA	TCGGTTCTAGCTGTCCAAAAA
770	TMB 2826	TGGAAAATCGAGGAAAATGG	CTAAGCCCAAAATCGAGCTG
771	TMB 2958	AATTGTTTAGTTTAGTTTTGC	AGTAACAATAATAATCAAAATAA
772	NAU0874	AAATGGCGTGCTTGAATAAC	TGTGATGAAGAACCCTCTCA
773	NAU 923	GGAATTCAAGGTTGAAGGAG	CCTCTTCTTTGGCTCTGAAA
774	NAU1037	CACCTTCACCTAACCATCAA	GAAGAATTGCGAGAAGAGGA
775	NAU1200	CAACAGCAACAACCACAA	CTGCCTCGAGGACAAATAGT
776	NAU1233	TTCGGGAAAGTTAGAGGAGA	TCCTCAGAGCTCGGAATAGT
777	NAU1298	TCCACCTAGGAATCAGTGAAG	CTTCCCACACCTCTGTAACC
778	NAU 1369	TGGCAGAGATGAATGTAAGC	GGTAACGGATGGAAAATCAC
779	NAU2035	CGAGAAACTTCACTGGACCT	GAAAAGGTAGGCTTGTTGGA
780	NAU 2631	CGATACACAAAAGCAGCAAC	ACAGGCTATTTCAGCACTCC
781	NAU3260	TTTTGCAGATGTTTGTAGGG	TTTCTTCAACAGGGGGCTAAG
782	NAU3588	CCCCATAGGGCATACTTCTA	GCCAACAAGAACAACAACAC

Reference: as per the published reports of Cotton Marker Database

(CMD) (http://www.cottonmarker.org/cgi-bin/cmd_search_marker.cgi)

Publications

Research Article

Combining ability analysis in intraspecific F₁ diallel cross of upland cotton (*Gossypium hirsutum* L.)

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Abstract

Diallel analysis was carried out by involving nine parents and their 72 cross combinations in upland cotton for assessing their combining ability for yield and its component characters. Variance due to parents and hybrids showed significant differences between all the characters studied except number of bolls, boll weight, single plant yield, lint index and seed index. Significance of variance in parents versus hybrids interaction provides adequacy for comparing the heterotic expression for all the characters except boll weight, ginning per cent, lint index and seed index. The GCA variances were larger than those of SCA for all the traits except number of bolls per plant, indicating the preponderance of additive action. The parents MCU 5 and MCU 7 were proved to be good general combiners for single plant yield and other economic traits and hence need to be included in the yield improvement programmes. The hybrid combinations viz., MCU 5 x MCU 7, Khandwa 2 x Suraj, KC 2 x MCU 5, Anjali x MCU 7 and Anjali x Suraj recorded superior *per se* performance for number of bolls, boll weight and single plant yield and other characters. Among these crosses KC 2 x MCU 5, Anjali x Suraj and Anjali x MCU 7 exhibited additive type gene action with one good general combining ability parent for number of bolls, boll weight and lint index respectively. Hence, selection can be made in these crosses in early generation itself.

Keywords:

Cotton, interspecific, combining ability, diallel

Introduction:

Cotton is an important fibre crop and it plays a vital role as a cash crop in commerce of many countries. Cotton production, processing and doing trade in cotton goods provide employment to about 60 million people in India. It provides fibre for textile industry, cellulose from its lint, oil and protein rich meal from its seed (Kumar *et al.*, 2014). The development of new variety with high yield and fibre quality is the primary objective of all cotton breeders. In any breeding programme, the choice of parents is an important aspect for the process of the crop improvement. Diallel analysis provides a systematic approach for detection of appropriate parents and crosses in terms of investigated traits. Among the several biometrical methods developed to identify superior parents for heterosis breeding, the diallel analysis has received considerable attention (Khan *et al.*, 2009). An investigation was taken up in cotton to study the general and specific combining ability and the gene action determining the yield and its yield components using 9 x 9 F₁ diallel design.

Material and methods

Breeding material and field procedure: The research work pertaining to study the genetic potential of genotypes and combining ability in F₁ hybrids of cotton (*Gossypium hirsutum* L.) was conducted during 2012-14 at the Department of Cotton, Tamil Nadu Agricultural University, Coimbatore. Nine diverse genotypes (Suraj, Surabhi, Khandwa 2, Anjali, KC 2, KC 3, MCU 5, MCU 7 and G.Cot 16) of upland cotton were raised during

winter 2012-2013 and were crossed in a complete diallel fashion. During winter 2013-14, the parents and 72 F₁s were raised in a Randomized Block Design with two replications. The package of practices recommended for the cotton cultivation in Tamil Nadu was followed throughout the crop growing period. The diallel analysis was performed as based on the model 1 and method 1 suggested by Griffing (1956).

Traits measurement and statistical analyses: The data were recorded on five randomly selected plants per replication for nine characters namely, days to first boll bursting, plant height at maturity, number of sympodia per plant, number of bolls per plant, boll weight, single plant yield, ginning per cent, lint index and seed index. Statistical analysis was carried out by using the mean values over five sample plants through INDOSTAT package.

Results and Discussion

Analysis of variance: Analysis of variance showed highly significant differences due to genotypes for all the traits indicating the presence of sufficient variability in the experimental materials (Table 1). Significance of variance in parents versus hybrids interaction provides adequacy for comparing the heterotic expression for all the characters except boll weight, ginning per cent, lint index and seed index. Parents and hybrids showed significant differences between all the characters studied except number of bolls, boll weight, single plant yield, lint index and seed index. It was also confirmed by the results reported in earlier studies

of Jatoi *et al.* (2010) for boll weight and Kumar *et al.* (2014) for single plant yield. GCA and SCA variances are significant for all the characters studied except number of bolls per plant for GCA and number of sympodia per plant and boll weight for SCA. Reciprocals were significantly dissimilar all the traits (Table 2).

Effects of gene action: The higher SCA than GCA of a character indicates the preponderance of non-additive gene action. Additive gene action provides fixable effects, and the non-additive gene action results are non-fixable. If GCA variance was greater than SCA for the particular character, it indicates preponderance of additive gene action. The current study, analysis of combining ability revealed that variances for GCA were larger than those of SCA for all the traits except number of bolls per plant, indicating the preponderance of additive action, which could be exploited for the improvement of these traits by mass selection. Similar findings were reported by Jatoi *et al.* (2010) in upland cotton. Preponderance of additive type of gene effects suggested directional selection for isolating better homozygous lines from segregating population for these traits. These observations are in conformity with findings obtained by Yuan *et al.* (2002), Khan *et al.* (2005) and Aguiar *et al.* (2007) in upland cotton. In this present study, additive gene action was determined for all the characters studied except number of bolls per plant. Additive gene action for kapas yield, lint index, seed index and boll weight was reported in earlier studies of Iyanar *et al.* (2005), and non-additive gene action for number of bolls per plant was reported by Imran *et al.* (2012), and have been confirmed by our results.

Choice of parents: The nine parents and their resultant 72 F₁ hybrids varies significantly each other in its yield components. Information on the *per se* performance and nature of general combining ability (*gca*) of characters is necessary for selection of suitable parents for developing hybrids. Therefore, the present study was aimed for their *per se* performance and *gca* effects. The *per se* performance of parents for yield and its component characters are presented in Table 3 and compared with grand mean. Based on *per se*, parent MCU 5 recorded higher mean for single plant yield (87.34 g/plant), boll weight (4.55 g/boll), number of sympodial branches per plant (20.09), number of bolls per plant (24.50) and ginning per cent (34.68%) followed by Anjali which recorded high *per se* for single plant yield, boll weight, number of sympodial branches and number of bolls per plant. The parent KC 3 recorded high *per se* for number of bolls, ginning per cent, lint index and seed index. The parent MCU 7 recorded high *per se* for single plant yield and number of sympodial branches. G.Cot 16 registered higher mean for lint index and seed

index. The parent Suraj recorded high *per se* for boll weight and ginning per cent. High mean values remain as a selection index in choice of parents and the parents possessing high *per se* performance will result in superior hybrids. Therefore, these parents can be exploited in hybridization for improving this character through pedigree breeding (Hassan *et al.*, 2000).

The estimates of *gca* effect (Tables 4 to 12) showed that, parent MCU 5 had recorded positive and significant *gca* effect for plant height, number of sympodial branches and single plant yield. The parent Suraj was a good combiner for boll weight, ginning per cent and lint index, while MCU 7 was a good combiner for single plant yield and ginning per cent. Good general combiners for boll weight and seed index were Anjali and G.Cot 16, respectively. KC 3 exhibited positive and significant *gca* effects for ginning per cent. Similar results were reported by Kumar *et al.* (2014) and high *gca* effect in desirable direction for a particular character indicates the presence of additive genes for that character in the parent, it could be expected that when the parents possessing high *gca* effects were combined; larger proportion of progenies would have high *per se* value for the character concerned facilitating easy selection for the character. Based on the high *per se* performance and high *gca* effect, the parent MCU 5 was considered as best general combiner as it had significantly higher values for plant height, sympodial branches and single plant yield. The parent Suraj had recorded high *per se* performance and *gca* effects for boll weight and ginning per cent. The parent Anjali for boll weight, KC 3 and G.Cot 16 for ginning per cent and seed index, respectively, showed better expression for high *per se* and *gca* effects.

In general, identification of parents for breeding programme based on either *per se* performance or *gca* effects alone was misleading in the selection programme. In the present study, considering *gca* effects and *per se* performance together, the parents MCU 5, Anjali, KC 3, MCU 7, Suraj and G.Cot 16 were selected as the best, since these were having high mean values for six, five, four, two, two and two traits respectively and also good combining ability for three, two, one, three, three and one yield component traits, respectively. None of the parents was found to be excellent general combiner for all the traits. Hence, it would be desirable to have multiple crosses and subject them to selection in segregating generations to detect superior genotypes with higher yield.

Choice of crosses: The specific combining ability (*sca*) effect alone may not be the appropriate choice for exploitation of heterosis because the hybrid with low mean value may also possess high *sca* effect. Hence, the cross combinations were to

be identified based on two criterias viz., *per se* performance and the gene action involved in the crosses for further exploitation. In the present investigation, hybrids MCU 5 x MCU 7, Khandwa 2 x Suraj and KC 2 x MCU 5 recorded high *per se* for number of sympodial branches, number of bolls per plant and single plant yield. Hybrid Anjali x MCU 7 recorded high *per se* effects for single plant yield, ginning per cent and lint index. The hybrid Anjali x Suraj recorded high *per se* for boll weight, single plant yield and lint index. The hybrid KC 3 X G.Cot 16 had shown high *per se* for seed index. Hence based on yield and component characters, the crosses MCU 5 x MCU 7, Khandwa 2 x Suraj, KC 2 x MCU 5, Anjali x MCU 7 and Anjali x Suraj were considered as desirable crosses.

In addition to superior *per se* performance, the nature of gene action is an important criterion to select the crosses for pedigree breeding (Tables 4 to 12). Crosses with additive type of gene action are desirable as this facilitates early generation selection. None of the crosses was found desirable simultaneously for all the characters. Based on *sca* effects, MCU 7 x KC 3 recorded significant *sca* effects for number of bolls per plant, boll weight, single plant yield and lint index. Hybrid MCU 7 x KC 3 for boll weight and single plant yield, with high x low *gca* resulted in non-additive gene interactions in these crosses. In this situation, we could go for recombination breeding, whereas the parents with positive *gca* effects and parents with low negative significant *gca* effects. Similar findings were reported by Muthu *et al.* (2005) and Ahuja and Dhayal (2007). Parents with positive significant *gca* effects involved additive type of gene action that would be easily fixable. For yield contributing characters such as number of bolls per plant, hybrids MCU 5 x MCU 7 and Suraj x Khandwa 2 had possessed significant positive *sca* effects. In case of other three high yielding crosses viz., KC 2 x MCU 5, Anjali x Suraj and Anjali x MCU 7 non significant *sca* was observed for number of bolls, boll weight and lint index, respectively and also for its other component characters. It indicated the presence of additive gene action and hence selection can be effective in these crosses in early generation itself. Additive genetic effects were also observed for most of the yield related traits with enough genetic variability and effective selection (Lukonge *et al.*, 2008).

From the above discussion, it might be concluded that the parent MCU 5 had superior *per se* performance for more number of traits studied. Based on high *per se* performance and high *gca* effect, the parents MCU 5, Anjali, KC 3, MCU 7, Suraj and G.Cot 16 were considered as best general combiners as they had significantly higher values for single plant yield, number of sympodial branches and number of bolls. Most of

the high yielding crosses, exhibiting desirable *sca* effects, involved parents with high and low *gca* effects, indicating the influence of non-additive gene interactions in these crosses. Among the hybrids, MCU 5 x MCU 7, Khandwa 2 x Suraj, KC 2 x MCU 5, Anjali x MCU 7 and Anjali x Suraj exhibited superior *per se* performance and one of the parents with good general combining ability and additive type of gene action. Hence, selection can be made in early generation itself in these crosses. Based on *sca* effects, MCU 7 x KC 3, MCU 5 x MCU 7 recorded significant *sca* effects for number of bolls per plant and single plant yield. An increase in the seed cotton yield along with other traits will be a valuable addition to cotton cultivars.

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Table 1. Analysis of variance showing means square for yield and its component characters in a 9 x 9 F₁ diallel cross of upland cotton

Source	d.f	Days to first boll bursting	Plant height (cm)	Number of sympodial branches per plant	Number of bolls per plant	Boll weight (g)	Single plant yield (g)	Ginning per cent (%)	Lint index	Seed index
Replications	1	0.357	15.223	4.590	13.387	0.072	13.629	0.026	0.243	1.993
Genotypes	80	6.721 **	358.857 **	6.747 **	14.823 **	0.255 **	277.862 **	23.179 **	0.644 **	2.368 **
Parents	8	2.735 **	156.155 **	11.733 **	6.476	0.186	47.231	3.712 **	0.391	1.928
Hybrids	71	7174 **	374.639 **	6.023 *	14.205 **	0.266 **	296.090 **	25.690 **	0.682 **	2.414 **
Parents V _s Hybrids	1	6.435 **	859.956 **	18.257 *	125.434 **	0.015	828.759 **	0.672	0.002	2.660
F ₁ 's	35	2.880 **	320.599 **	6.306 *	14.577 **	0.330 **	350.116 **	23.748 **	0.561 **	2.126 *
Reciprocals	35	11.499 **	405.372 **	5.893 *	14.043 *	0.207	248.219 **	28.337 **	0.798 **	2.711 **
F ₁ V _s reciprocals	1	6.126 **	1190.365 **	0.703	6.860	0.093	80.655	1.015	0.853	2.052
Error	80	0.631	14.072	3.554	7.565	0.140	41.255	0.629	0.243	1.151
Total	161	3.655	185.401	5.147	11.207	0.197	158.652	11.830	0.442	1.761

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

Table 2. Analysis of variance and genetic contribution of parents, hybrids and reciprocals in a 9 x 9 F₁ diallel cross of upland cotton

Source	d.f	Days to first boll bursting	Plant height (cm)	Number of sympodial branches per plant	Number of bolls per plant	Boll weight (g)	Single plant yield (g)	Ginning per cent (%)	Lint index	Seed index
GCA	8	6.181 **	272.977 **	7.875 **	5.153	0.390 **	243.812 **	13.932 **	0.370 **	1.790 **
SCA	36	2.009 **	145.663 **	2.066	6.023 *	0.071	92.759 **	7.234 ***	0.314 **	1.035 *
Reciprocal	36	4.085 **	192.406 **	3.681 **	9.302 **	0.125 *	161.797 **	15.424 **	0.320 **	1.198 **
Error	80	0.315	7.036	1.777	3.782	0.070	20.628	0.314	0.121	0.576

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

Table 3. Per se performance of parents for yield and its component characters in a 9 x 9 F₁ diallel cross of upland cotton

Parents	Days to first boll bursting	Plant height (cm)	Number of sympodial branches per plant	Number of bolls per plant	Boll Weight (g)	Single plant yield (g)	Ginning per cent (%)	Lint index	Seed index
Suraj	102.63	95.03	12.50	20.00	4.51	76.60	34.50	5.35	10.14
Surabhi	102.33	103.80	15.50	20.10	4.29	80.06	33.85	4.87	9.46
Khandwa 2	101.90	96.10	12.10	18.50	3.91	75.14	30.76	4.14	9.32
Anjali	105.20	110.53	15.00	22.00	4.47	85.09	34.04	5.26	7.74
KC 2	103.00	93.70	15.63	19.50	4.34	78.70	33.03	5.17	10.47
KC 3	101.40	99.40	14.70	22.40	3.87	81.06	35.31	5.48	10.04
MCU 5	101.20	114.90	20.09	24.50	4.55	87.34	34.68	5.11	9.63
MCU 7	102.20	101.88	17.00	21.60	3.75	84.90	32.49	5.11	10.61
G.Cot 16	102.53	86.07	13.67	20.80	4.01	73.10	33.80	5.70	11.15
Grand mean	102.49	100.16	15.13	21.06	4.19	80.22	33.61	5.13	9.84
CD (P = 0.05)	0.55	2.59	2.39	4.31	0.45	3.62	1.69	1.51	3.45

Table 4. General and specific combining ability effects for days to first boll bursting, plant height, number of symbodial branches per plant, number of bolls per plant and boll weight (g)

	Suraj	Surabhi	Khandwa 2	Anjali	KC 2	KC 3	MCU 5	MCU 7	G.Cot 16
Days to first boll bursting									
Suraj	-0.227	-0.453	0.915*	0.422	0.131	-0.548	-0.132	0.116	-0.489
Surabhi	0.313	-0.184	0.072	0.328	1.488**	1.159**	-0.175	-0.777*	-1.282**
Khandwa 2	0.400	0.300	-0.640**	-1.398**	0.493	0.195	0.606	-0.034	-0.977**
Anjali	-2.550**	2.500**	-0.283	1.404**	-1.950**	0.504	1.388**	-0.415	1.780**
KC 2	1.350**	-1.250**	2.000**	-0.600	-0.406**	0.331	-0.348	-0.205	-0.698
KC 3	-0.500	0.250	-0.370	-2.517**	0.000	-0.277*	0.768*	-0.472	-0.839*
MCU 5	0.350	0.650	1.225**	-4.100**	-0.255	1.500**	0.157	-0.218	0.277
MCU 7	0.500	-0.050	0.137	-0.400	0.000	0.238	1.150**	0.059	2.975**
G.Cot 16	-0.250	-0.500	0.350	-3.850**	-0.512	0.150	-0.100	-2.700**	0.114
Plant height (cm)									
Suraj	-1.770**	3.748*	1.319	-2.304	7.695**	-18.713**	6.596**	-9.758**	6.480**
Surabhi	0.510	4.143**	0.506	-7.979**	2.900	1.424	4.670**	0.479	-7.623**
Khandwa 2	-1.500	-5.000**	-1.788**	-6.740**	-2.466	-5.007**	-0.449	-7.428**	14.226**
Anjali	-20.923**	13.210**	3.497	0.657	-5.687**	19.880**	-3.944*	-1.611	-7.187**
KC 2	-12.280**	-4.533*	4.000*	-17.225**	0.316	11.901**	-3.773*	4.316*	-14.316**
KC 3	1.400	1.950	-7.012**	-8.980**	-15.000**	0.044	-17.968**	2.053	0.756
MCU 5	14.650**	-8.963**	3.313	13.673**	4.767*	-5.500**	6.886**	3.194	4.185*
MCU 7	3.400	1.750	-2.587	-16.375**	-9.260**	4.275*	-15.143**	-1.611**	-2.702
G.Cot 16	15.873**	-1.482	-13.000**	-12.132**	-0.087	-12.262**	-6.478**	5.950**	-6.877**
Number of sympodial branches									
Suraj	-0.742*	0.428	0.110	-0.542	1.080	-1.126	0.549	1.265	0.334
Surabhi	1.950*	0.183	1.735*	0.258	-0.645	0.649	0.374	-1.210	-0.641
Khandwa 2	-1.400	-0.850	-0.349	-0.035	-0.014	-0.015	0.055	0.208	1.240
Anjali	-2.400*	1.475	1.400	0.503	-0.515	1.328	-0.014	0.869	0.738
KC 2	-0.800	-2.000	-0.100	1.250	-0.119	2.000*	-0.505	-0.759	-0.427
KC 3	-0.450	2.950**	0.855	-1.550	-1.000	0.137	-1.081	0.597	-0.696
MCU 5	1.500	-1.750	2.300*	0.717	2.030*	-1.050	1.112*	-1.040	-0.121
MCU 7	-0.750	-0.800	-0.212	-0.700	0.950	1.038	1.000	0.347	-0.155
G.Cot 16	-0.500	2.350*	-0.400	-0.550	-0.638	0.650	-1.500	-0.500	-1.073**

Table 4. Contd..

	Suraj	Surabhi	Khandwa 2	Anjali	KC 2	KC 3	MCU 5	MCU 7	G.Cot 16
Number of bolls per plant									
Suraj	-0.104	-0.602	3.941**	-1.293	0.258	-0.158	2.143	-1.382	0.418
Surabhi	-1.063	0.236	2.151	2.175	1.769	0.553	-1.297	0.628	-1.472
Khandwa 2	-2.950*	0.400	-0.020	0.555	0.974	-1.349	-1.209	-0.654	0.584
Anjali	-2.950*	1.407	2.882*	0.414	-1.710	1.675	-0.043	1.300	-0.300
KC 2	-3.600*	-0.050	-3.500*	0.150	-0.587	1.826	-0.236	-1.349	1.326
KC 3	1.500	1.050	-1.208	-1.250	-0.600	0.128	-1.090	0.148	-0.215
MCU 5	-0.800	0.800	-1.532	3.868**	3.563*	2.900*	0.728	2.836*	-0.614
MCU 7	0.600	0.850	-1.688	-2.500	0.050	3.438*	0.850	0.253	0.911
G.Cot 16	1.000	1.550	-1.750	-1.600	-2.725	1.900	-2.900*	-3.950**	-1.047*
Boll weight (g)									
Suraj	0.231**	-0.109	-0.056	0.258	0.210	-0.082	-0.039	-0.183	0.172
Surabhi	0.440*	-0.021	-0.077	-0.151	0.082	-0.030	0.087	0.197	-0.116
Khandwa 2	-0.108	-0.165	-0.166**	-0.108	-0.008	0.005	0.015	0.152	0.054
Anjali	-0.033	0.023	-0.170	0.154*	0.309	-0.246	0.002	-0.141	0.136
KC 2	0.000	-0.390*	-0.110	0.117	0.119*	-0.193	-0.386*	0.126	-0.027
KC 3	-0.410*	0.400*	-0.055	-0.275	0.297	-0.214**	0.050	0.149	0.259
MCU 5	-0.210	-0.050	-0.208	-0.230	-0.207	-0.055	-0.051	0.224	-0.391*
MCU 7	0.308	0.085	0.150	-0.278	0.485*	0.410*	-0.023	0.020	-0.020
G.Cot 16	0.365	-0.105	-0.005	-0.092	0.030	-0.517**	-0.320	-0.007	-0.072

**Significant at 1 % level, *Significant at 5 % level; diagonal values indicate the *gca* effects.

Table 5. General and specific combining ability effects for single plant yield, ginning percentage, lint index and seed index

	Suraj	Surabhi	Khandwa 2	Anjali	KC 2	KC 3	MCU 5	MCU 7	G.Cot 16
Single plant yield (g)									
Suraj	1.924	0.757	12.357**	3.662	4.541	-8.446**	3.076	-2.684	0.605
Surabhi	13.498**	-1.521	5.147	3.042	-0.141	1.265	-7.523*	-2.654	3.621
Khandwa 2	-1.980	-3.770	-0.709	-10.328**	-3.439	0.149	-0.701	-2.206	9.080**
Anjali	-10.768**	12.343**	7.800*	1.669	-9.034**	3.519	7.224*	9.291**	-2.512
KC 2	-2.035	-13.347**	-3.603	1.510	0.237	9.013**	5.148	6.568*	-4.266
KC 3	1.735	12.500**	-13.683**	-15.880**	-5.252	-5.036**	-10.259**	-2.894	3.137
MCU 5	2.523	-5.613	3.032	6.785*	11.608**	0.262	6.020**	11.655**	2.702
MCU 7	-5.313	9.138**	-9.662**	-0.243	-0.957	16.202**	7.877*	2.835**	-9.688**
G.Cot 16	12.442**	3.697	-11.490**	-8.940**	-5.010	-7.670*	-8.360*	-16.320**	-5.419**

Table 5. Contd..

	Suraj	Surabhi	Khandwa 2	Anjali	KC 2	KC 3	MCU 5	MCU 7	G.Cot 16
Ginning percentage (%)									
Suraj	1.041**	-0.296	-0.256	1.937**	-0.170	0.104	0.165	0.976**	-1.456**
Surabhi	-1.485**	-1.307**	0.020	-1.225**	-0.277	0.177	1.010**	-2.559**	0.112
Khandwa 2	-1.525**	-2.682**	-0.377**	3.365**	-1.197**	-2.153**	1.175**	0.274	0.685
Anjali	-0.547	0.208	-0.608	0.418**	-4.599**	0.217	-2.522**	2.291**	0.760*
KC 2	0.280	5.875**	-3.935**	2.038**	-0.968**	2.908**	-2.427**	3.397**	0.826*
KC 3	-2.455**	-0.290	3.515**	-3.930**	3.010**	0.673**	2.508**	-0.866*	-3.438**
MCU 5	-0.052	2.265**	-1.600**	-1.052**	0.847*	0.073	0.250*	-0.899*	0.238
MCU 7	3.135**	3.137**	-2.005**	0.647	-1.452**	2.045**	-3.620**	1.027**	0.376
G.Cot 16	1.977**	2.818**	-2.615**	-2.870**	0.180	-5.928**	6.610**	-3.030**	-0.759**
Lint index									
Suraj	0.243**	-0.174	-0.043	0.288	0.071	-0.070	0.183	0.001	0.007
Surabhi	0.058	-0.158*	0.108	-0.319	-0.033	0.189	0.793**	-0.393	-0.230
Khandwa 2	-0.130	-0.515*	-0.161*	0.459*	-0.500*	-0.696**	0.502*	0.742**	0.086
Anjali	-0.482	-0.105	-0.065	0.061	-0.407	0.040	-0.282	0.266	-0.063
KC 2	0.057	0.457	-0.617*	0.307	-0.167*	0.528*	-0.604**	-0.101	0.663**
KC 3	-0.322	-0.045	0.392	-0.825**	-0.115	0.133	0.307	0.171	-0.563**
MCU 5	-0.350	0.090	-0.450	-0.082	0.007	-0.245	0.014	-0.619**	-0.241
MCU 7	0.495*	0.630*	-0.062	-0.013	-0.148	0.565*	0.065	-0.030	-0.110
G.Cot 16	-0.025	0.187	-0.500*	-0.517*	0.070	-0.550*	0.822**	-0.810**	0.064
seed index									
Suraj	0.026	-0.225	0.064	-0.124	0.125	-0.224	0.215	-0.457	0.740
Surabhi	0.810	0.318	0.172	0.163	0.252	0.213	1.125*	0.210	-0.528
Khandwa 2	0.430	0.195	-0.181	-0.262	-0.591	-0.452	0.419	1.357**	-0.188
Anjali	-0.595	-0.275	0.090	-0.318	1.635**	0.122	0.825	-0.224	-0.309
KC 2	-0.017	-1.947**	0.335	-0.405	0.181	-0.270	-0.288	-1.635**	0.865
KC 3	0.483	0.043	-0.722	0.185	-1.513**	-0.015	-0.570	0.621	0.691
MCU 5	-0.623	-0.985	-0.125	0.330	-0.385	-0.462	-0.054	-0.683	-0.575
MCU 7	-0.390	-0.090	0.848	-0.285	0.263	0.143	1.575**	-0.490**	-0.577
G.Cot 16	-1.070*	-0.960	0.195	0.288	0.045	1.910**	-1.350*	-0.262	0.533**

**Significant at 1 % level, *Significant at 5 % level; diagonal values indicate the *gca* effect

Estimation of Heterosis for Yield and Yield Attributing Traits in Diallel Crosses of Upland Cotton (*Gossypium hirsutum* L.)

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ABSTRACT

Diallel analysis was carried out by involving nine parents and their seventy two cross combinations in upland cotton to identify the best heterotic crosses for seed cotton yield and its attributing traits. Analysis of variance showed highly significant differences due to genotypes for all the traits indicating the presence of sufficient variability in the experimental materials. Variance due to parents and hybrids showed significant differences between all the characters studied except number of bolls, boll weight, single plant yield, lint index and seed index. Significance of variance in parents versus hybrids interaction provides adequacy for comparing the heterotic expression for all the characters except boll weight, ginning percent, lint index and seed index. Heterosis was worked out over mid parent, better parent and standard check variety. Based on study of relative heterosis and heterobeltiosis, it was found that number of sympodia per plant, number of bolls per plant and boll weight were main contributors towards increase in heterotic effects for single plant yield. Three crosses viz., MCU 5 x MCU 7 (27.40%), KC 2 x MCU 5 (22.18%) and Anjali x MCU 5 (20.72%) were best heterotic crosses over standard check for single plant yield and could be exploited.

Key words Heterosis, Diallel cross, Upland cotton, Yield attributing traits

Cotton (*Gossypium spp.*), popularly known as “King of fibre” and “White Gold”, is one of the most important commercial cash crops and plays a key role in economic, political and social affairs of the world. Cotton enjoys a pre-eminent status among all the cash crops in the country, being the principal material for flourishing textile industries. The predominant species cultivated in India is *G. hirsutum* which cover about 90% of the total area. The development of new variety with high yield and fibre quality is the primary objective of all cotton breeders. Heterosis breeding is useful to identify the cross combinations which are promising in conventional breeding programme. Cotton is highly amenable for both heterosis and recombination breeding. Heterosis has substantially remained as one of the significant developments in cotton breeding programs (Ganapathy and

Nadarajan, 2008; Khan *et al.*, 2010). India is pioneer in commercialization of heterosis in cotton and noticeable heterosis is also reported in cotton by many workers (Wu *et al.*, 2004; Tuteja *et al.*, 2005). The estimates of heterosis provided useful information with regard to the possibilities and extent of improvement in the yield characters of breeding material through selection. Therefore, the present studies were undertaken to estimate the heterosis effects in cotton through 9 x 9 diallel analysis.

MATERIALS AND METHODS

Genetic material and field procedure:

The research work pertaining to study the yield and its contributing characters in F_1 hybrids of cotton (*Gossypium hirsutum* L.) was conducted during 2012-14 at the Department of Cotton, Tamil Nadu Agricultural University, Coimbatore. Nine diverse genotypes (*Suraj*, *Surabhi*, *Khandwa 2*, *Anjali*, KC 2, KC 3, MCU 5, MCU 7 and G.Cot 16) of upland cotton were raised during winter 2012-2013 and also they were crossed in a complete diallel fashion. During winter 2013-14, the parents and seventy two F_1 s were raised along with standard check (MCU 13) in a RBD design with two replications. The package of practices recommended for the cotton cultivation in Tamil Nadu was followed throughout the crop growing period.

Traits measurement and statistical analyses:

In each genotypes and their cross combinations, data were recorded on five randomly selected plants per replication for eight characters namely, plant height (cm), number of sympodia per plant, number of bolls per plant, boll weight (g), single plant yield (g), ginning percent, lint index and seed index. The means were computed for statistical analysis using the analysis of variance technique to determine significant differences among genotypes for the traits.

Heterosis is the amount by which a hybrid exceeds its mid parent value (relative heterosis - d_i) or its better parent (heterobeltiosis - d_{ii}) or standard check variety (useful/standard heterosis - d_{iii}). The term heterobeltiosis coined by Fonseca (1965), was also estimated in terms of

Table 1. Analysis of variance showing means square for yield and its attributing traits

Source	d.f	Plant height (cm)	Number of sympodial branches per plant	Number of bolls per plant	Boll weight (g)	Single plant yield (g)	Ginning percent (%)	Lint index	Seed index
Replications	1	15.223	4.590	13.387	0.072	13.629	0.026	0.243	1.993
Genotypes	80	358.857 **	6.747 **	14.823 **	0.255 **	277.862 **	23.179 **	0.644 **	2.368 **
Parents	8	156.155 **	11.733 **	6.476	0.186	47.231	3.712 **	0.391	1.928
Hybrids	71	374.639 **	6.023 *	14.205 **	0.266 **	296.090 **	25.690 **	0.682 **	2.414 **
Parents $\times$ Hybrids	1	859.956 **	18.257 *	125.434 **	0.015	828.759 **	0.672	0.002	2.660
F ₁ 's	35	320.599 **	6.306 *	14.577 **	0.330 **	350.116 **	23.748 **	0.561 **	2.126 *
Reciprocals	35	405.372 **	5.893 *	14.043 *	0.207	248.219 **	28.337 **	0.798 **	2.711 **
F ₁ $\times$ reciprocals	1	1190.365 **	0.703	6.860	0.093	80.655	1.015	0.853	2.052
Error	80	14.072	3.554	7.565	0.140	41.255	0.629	0.243	1.151
Total	161	185.401	5.147	11.207	0.197	158.652	11.830	0.442	1.761

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

percent increase or decrease of the F₁ hybrid over its better parent. In the present study relative heterosis, heterobeltiosis and standard heterosis were determined as percent increase (+) or decrease (-) of F₁ over mid parent ($F_1 - \overline{MP} / \times 100$) parent, over better ($F_1 - / \times 100$) parent and over best or highest ($F_1 - / \times 100$) parent respectively. The statistical significance of heterosis was assessed by 't' test according to Wynne *et al.* (1970) as under.

$$T = F_{ij} - MP_{ij} / \sqrt{3/8 \text{ EMS}}$$

Where F_{ij} = The F₁ hybrid value of ith and jth parents

MP_{ij} = Mid parent value of ith and jth parents

EMS = Error mean square for the respective traits

RESULTS AND DISCUSSION

Analysis of variance:

Analysis of variance showed highly significant differences due to genotypes for all the traits indicating the presence of sufficient variability in the experimental materials (Table 1). Significance of variance in parents versus hybrids interaction provides adequacy for comparing the heterotic expression for all the characters except boll weight, ginning percent, lint index and seed index. Parents and hybrids showed significant differences between all the characters studied except number of bolls, boll weight, single plant yield, lint index and seed index. It was also confirmed by the results reported in earlier studies of Jatoi *et al.*, (2010) in boll weight and Kumar *et al.*, (2014) in single plant yield.

Expression of heterosis for yield attributing traits:

Estimation of heterotic effects is necessary to identify the new cross combinations that are suitable for direct exploitation. Therefore, heterosis over mid parent, better parent and standard parent was estimated in the entire cross combinations under study (Tables 2 and 3).

Plant height:

The magnitude of heterosis over mid parent ranged from -32.56% (Suraj $\times$ Anjali) to 25.48% (KC 3 $\times$ KC 2). Out of seventy two hybrids, twelve hybrids recorded significantly positive heterosis while thirty six hybrids recorded significantly negative heterosis (Table 2). Heterobeltiosis ranged from -38.65% (Anjali $\times$ G.Cot 16) to 22.12% (KC 3 $\times$ KC 2) and it was found to be positively significant in five hybrids. These findings are supported by previous researchers like Kumar, 2007 and Abro, *et al.*, 2014 who also reported heterosis and heterobeltiosis for plant height. None of the hybrids recorded positive and significant standard heterosis over the check MCU 13.

Number of sympodial branches per plant:

The hybrid MCU 5 $\times$ KC 2 and Khardwa 2 $\times$ Surabhi showed minimum (-18.38%) and maximum (34.55%) relative heterosis respectively (Table 2). Significantly positive relative heterosis was exhibited by eleven hybrids. The range of heterobeltiosis was from -27.50% in MCU 5 $\times$ G.Cot 16 to 32.00% in Khardwa 2 $\times$ Suraj and a total of only three hybrids recorded significantly positive heterosis over better

Table 2. Expression of heterosis in hybrids (%) for plant height, no. of sympodial branches, no. of bolls and boll weight

SI No.	Hybrids	1. Plant height			2. No. of sympodial branches			3. Number of bolls			4. Boll weight		
		d _i	d _{ii}	d _{iii}	d _i	d _{ii}	d _{iii}	d _i	d _{ii}	d _{iii}	d _i	d _{ii}	d _{iii}
1	Suraj X Surabi	0.88	-3.40	-13.34**	30.18 *	15.48	26.23	9.73	9.45	3.48	2.37	-4.90	19.00*
2	Suraj X Khardwa 2	-5.91	-6.45	-22.30**	13.69	13.22	-3.39	26.75 *	22.00	14.77	-7.58	-17.70 *	2.75
3	Suraj X Anjali	-32.56 **	-37.30 **	-40.10**	-4.44	-14.00	-9.03	-6.67	-10.91	-7.81	1.95	-3.50	20.50*
4	Suraj X KC 2	-7.15 *	-7.79	-24.29**	12.20	-0.83	9.31	-1.27	-2.50	-8.28	2.25	-4.50	19.25*
5	Suraj X KC 3	-23.25 **	-24.95 **	-35.52**	4.12	-5.44	-1.97	17.45	11.16	17.12	-15.72 *	-25.20 **	-6.50
6	Suraj X MCU 5	14.34 **	4.44	3.72	15.30	-7.91	30.47*	14.61	4.08	19.94	-13.19	-17.10 *	3.50
7	Suraj X MCU 7	-14.77 **	-17.64 **	-27.48**	11.72	-4.71	14.25	10.10	6.02	7.71	4.91	-8.20	14.75
8	Suraj X G.cot 16	18.57 **	12.99 **	-7.22*	9.88	3.18	-0.56	16.67	14.42	11.95	9.05	-1.80	22.75*
9	Surabi X Suraj	-0.27	-4.57	-14.22**	-1.75	-12.50	-1.27	20.63	20.63	13.50	-8.88	-13.98	-3.00
10	Surabi X Khardwa 2	-8.55 *	-12.02 **	-20.92**	19.57	5.00	18.48	36.62 **	31.50 *	23.71	-4.24	-5.38	-5.50
11	Surabi X Anjali	-3.35	-6.20	-10.40**	19.35	15.63	30.47*	32.21 **	26.20 *	30.57*	-0.30	-5.49	5.50
12	Surabi X KC 2	-2.41	-7.25 *	-16.63**	-14.64	-15.63	-4.80	26.08 *	24.50	17.12	-3.96	-7.72	0.25
13	Surabi X KC 3	-0.49	-2.69	-12.53**	30.29 **	25.00 *	41.04**	20.28	13.84	19.94	10.48	8.75	8.75
14	Surabi X MCU 5	-8.29 **	-12.64 **	-13.24**	-11.33	-20.36 *	12.83	7.87	-2.04	12.89	-2.22	-8.13	4.50
15	Surabi X MCU 7	-4.41	-5.38	-14.95**	-11.52	-14.12	2.96	22.60	18.06	19.94	16.00	12.37	12.25
16	Surabi X G.cot 16	-13.92 **	-21.35 **	-29.30**	13.94	5.62	19.18	11.76	9.62	7.24	-2.56	-2.62	-2.50
17	Khardwa 2 X Suraj	-2.74	-3.23	-19.71**	34.69 *	32.00 *	16.36	59.47 **	51.50 **	42.52**	1.82	-3.88	8.25
18	Khardwa 2 X Surabi	1.60	-2.22	-12.27**	34.55 **	19.35	30.47*	33.86 **	26.87	19.94	-0.72	-4.08	3.00
19	Khardwa 2 X Anjali	-13.56 **	-19.24 **	-22.85**	30.37 *	17.33	24.12	36.82 **	24.39	28.69*	-7.27	-12.09	-1.75
20	Khardwa 2 X KC 2	-1.21	-2.40	-19.01**	12.20	-0.83	9.31	8.80	4.62	-4.05	-2.88	-6.68	1.25
21	Khardwa 2 X KC 3	-18.24 **	-19.64 **	-30.96**	25.17 *	13.67	17.84	4.38	-5.87	-0.85	-3.87	-5.37	-5.25
22	Khardwa 2 X MCU 5	-3.65	-11.58 **	-12.19**	19.66	-4.43	35.40*	1.18	-12.24	1.13	-10.99	-16.37 *	-5.00
23	Khardwa 2 X MCU 7	-18.91 **	-21.25 **	-30.67**	10.86	-5.44	13.40	8.21	-0.81	0.75	12.77	9.25	9.25
24	Khardwa 2 X G.cot 16	-5.31	-10.21 *	-25.50**	20.79	13.43	9.31	9.79	2.40	0.19	0.56	0.50	0.75
25	Anjali X Suraj	7.89 *	0.13	-3.93	28.73 *	18.00	24.82	21.43	15.91	19.94	14.99	8.55	22.25*
26	Anjali X Surabi	-28.07 **	-30.41 **	-33.23**	1.97	0.32	9.66	18.53	13.41	17.36	0.72	-2.68	4.50
27	Anjali X Khardwa 2	-20.55 **	-25.88 **	-28.89**	9.23	-1.33	4.37	6.67	-1.82	1.60	7.91	6.62	6.50
28	Anjali X KC 2	-29.95 **	-35.41 **	-38.03**	12.31	10.04	21.30	5.06	-0.91	2.54	17.87 *	13.25	22.75*
29	Anjali X KC 3	0.04	-5.19	-9.04**	11.11	10.00	16.36	10.36	9.37	15.24	-7.68	-9.13	-9.25
30	Anjali X MCU 5	-1.81	-3.47	-4.14	4.87	-8.41	29.76*	22.58 *	16.33	34.05**	-4.33	-10.11	2.25
31	Anjali X MCU 7	-29.82 **	-32.70 **	-35.44**	6.87	0.59	20.59	5.50	4.55	8.18	2.45	-0.75	-0.75
32	Anjali X G.cot 16	-30.89 **	-38.65 **	-41.14**	9.54	4.67	10.72	-1.87	-4.55	-1.22	8.43	8.36	8.50
33	KC 2 X Suraj	18.67 **	18.02 **	-3.06	20.00	6.88	20.59	33.50 **	33.50 *	25.59*	12.29	5.99	19.50*
34	KC 2 X Surabi	6.70 *	1.67	-8.79*	11.11	9.38	23.41	24.69 *	24.38	17.59	15.44	11.54	19.50*
35	KC 2 X Khardwa 2	-9.84 **	-10.82 **	-25.93**	11.74	-1.88	10.72	42.34 **	37.00 **	28.88*	8.03	6.75	6.75
36	KC 2 X Anjali	3.80	-3.96	-8.25*	-5.16	-8.12	3.67	2.38	-2.27	1.13	10.57	4.82	17.00
37	KC 2 X KC 3	-6.00	-8.55 *	-21.43**	11.40	6.87	20.59	14.62	8.48	14.30	7.30	5.62	5.50
38	KC 2 X MCU 5	-2.50	-11.37 **	-11.99**	3.08	-7.42	31.17*	21.35 *	10.20	27.00*	-13.68	-18.90 *	-7.75
39	KC 2 X MCU 7	-10.76 **	-14.21 **	-24.46**	0.00	-2.94	16.36	5.29	1.39	3.01	28.13 **	24.13 *	24.25*
40	KC 2 X G.cot 16	-19.28 **	-22.69 **	-37.18**	-6.79	-13.59	-2.54	0.49	-1.44	-3.57	6.56	6.49	6.50
41	KC 3 X Suraj	-25.99 **	-27.47 **	-37.94**	7.64	-1.33	4.37	4.29	-0.45	3.01	7.23	1.22	14.00
42	KC 3 X Surabi	-4.04	-6.26	-15.90**	-7.54	-9.03	-0.56	11.16	6.36	10.07	-14.35	-17.25	-11.25
43	KC 3 X Khardwa 2	-3.74	-5.15	-18.84**	10.70	0.00	5.78	16.05	6.82	10.54	-1.45	-2.63	-2.75
44	KC 3 X Anjali	17.60 **	11.47 **	6.48	30.67 **	30.67 *	38.22**	22.73 *	22.73	27.00*	-1.12	-6.27	4.50

SI No.	Hybrids	1. Plant height			2. No. of sympodial branches			3. Number of bolls			4. Boll weight		
		d _i	d _{ii}	d _{iii}	d _i	d _{ii}	d _{iii}	d _i	d _{ii}	d _{iii}	d _i	d _{ii}	d _{iii}
45	KC 3 X KC 2	25.48 **	22.12**	4.49	24.71 *	22.20	34.70*	22.89 *	15.91	19.94	-12.95	-16.36	-9.25
46	KC 3 X MCU 5	-27.91 **	-32.90 **	-33.36**	-13.37	-24.34 *	7.19	12.69	6.94	23.24	-7.72	-13.30	-1.25
47	KC 3 X MCU 7	-2.03	-3.41	-14.95**	13.75	7.06	28.35*	26.15 *	25.00 *	29.35*	18.19 *	14.50	14.50
48	KC 3 X G.cot 16	-18.62 **	-23.94 **	-34.92**	5.35	0.67	6.49	13.55	10.45	14.30	-8.31	-8.36	-8.25
49	MCU 5 X <i>Suraj</i>	-13.63 **	-21.13 **	-21.61**	-4.62	-22.50 *	9.31	23.18 *	12.92	27.47*	-3.95	-8.70	14.25
50	MCU 5 X <i>Surabi</i>	8.14 **	2.87	2.25	9.86	-2.50	37.52**	1.59	-6.67	5.36	-7.86	-14.40	7.00
51	MCU 5 X <i>Khardwa</i> 2	-10.02 **	-17.41 **	-17.92**	-9.03	-27.00 **	2.96	15.60	2.35	15.52	-5.22	-15.60 *	5.50
52	MCU 5 X <i>Anjali</i>	-25.89 **	-27.33 **	-27.77**	-3.06	-15.18	19.68	-9.72	-13.48	-2.35	-3.86	-9.00	13.75
53	MCU 5 X KC 2	-11.55 **	-19.74 **	-20.22**	-18.38 *	-27.30 **	2.54	-8.62	-17.19	-6.49	-12.10	-17.90 *	2.75
54	MCU 5 X KC 3	-17.82 **	-23.39 **	-23.85**	-0.29	-13.50	22.00	-12.07	-15.00	-4.05	-8.62	-18.90 *	1.50
55	MCU 5 X MCU 7	-19.80 **	-24.38 **	-24.84**	-5.41	-12.50	23.41	23.68 *	17.50	32.64*	0.23	-12.30	9.75
56	MCU 5 X G.cot 16	-9.13 **	-20.56 **	-21.05**	-13.86	-27.50 **	2.26	-12.05	-17.92	-7.34	-24.93 **	-32.40 **	-15.50
57	MCU 7 X <i>Suraj</i>	-21.74 **	-24.41 **	-33.36**	20.00	4.12	24.82	3.33	-1.36	2.07	-6.53	-11.76	-0.75
58	MCU 7 X <i>Surabi</i>	-7.77 *	-8.57 *	-17.98**	-0.31	-4.71	14.25	13.06	8.18	11.95	4.34	0.82	8.00
59	MCU 7 X <i>Khardwa</i> 2	-13.78 **	-16.27 **	-26.19**	13.40	-2.94	16.36	22.47	12.73	16.65	2.97	1.75	1.75
60	MCU 7 X <i>Anjali</i>	1.12	-2.78	-7.13**	15.63	8.82	30.47*	27.27 *	27.27 *	31.70*	6.91	1.34	13.25
61	MCU 7 X KC 2	8.25 *	3.84	-8.45**	-10.51	-14.12	2.96	5.06	-0.91	2.54	-4.20	-7.95	-0.25
62	MCU 7 X KC 3	-10.77 **	-11.91 **	-22.34**	1.74	-5.15	13.75	-7.09	-7.92	-2.96	-4.51	-6.00	-6.00
63	MCU 7 X MCU 5	8.11 **	2.05	1.34	-16.42	-22.85 *	9.31	13.98	8.16	24.65	3.63	-2.64	10.75
64	MCU 7 X G.cot 16	-5.99	-13.33 **	-23.60**	-4.13	-13.53	3.67	-7.94	-10.45	-7.34	3.31	3.25	3.50
65	G.cot 16 X <i>Suraj</i>	-16.48 **	-20.45 **	-34.66**	13.96	7.86	6.49	6.34	3.81	2.54	-1.70	-7.21	4.50
66	G.cot 16 X <i>Surabi</i>	-10.68 **	-18.34 **	-26.74**	-17.29	-21.29	-13.96	-4.14	-6.19	-7.34	-0.84	-4.20	2.75
67	G.cot 16 X <i>Khardwa</i> 2	23.23 **	16.75 **	-3.03	24.90 *	16.43	14.95	25.57 *	18.10	16.65	2.09	0.87	0.75
68	G.cot 16 X <i>Anjali</i>	-6.00	-16.43 **	-20.17**	15.86	12.00	18.48	12.56	10.00	13.83	6.91	1.34	13.00
69	G.cot 16 X KC 2	-18.92 **	-22.25 **	-37.04**	1.92	-3.39	6.49	28.15 *	23.57	22.06	0.84	-3.11	5.00
70	G.cot 16 X KC 3	7.69 *	0.43	-13.73**	-3.83	-6.12	-2.68	-5.53	-8.48	-3.57	19.49 *	17.62	17.50
71	G.cot 16 X MCU 5	3.84	-9.22 **	-9.84**	2.67	-12.89	23.41	12.09	4.08	19.94	-5.96	-11.65	0.50
72	G.cot 16 X MCU 7	-18.56 **	-24.91 **	-33.88**	1.29	-7.65	10.72	29.58 **	27.78 *	29.82*	7.10	3.75	3.75

parent. The range of standard heterosis was from -13.96% in G.Cot 16 x *Surabhi* to 41.04% in *Surabi* x KC 3. Similar findings were also reported by Tuteja, *et al.*, 2005, Verma, *et al.*, 2006, Abro, *et al.*, 2009 and Geddam, *et al.*, 2011 for this trait. Twelve hybrids recorded positive and significant standard heterosis for this trait. None of the hybrids exhibited significantly negative standard heterosis over the check MCU 13.

Number of bolls per plant:

In cotton, the number of bolls per plant and boll weight are two important yield attributing components which are mostly positively associated with seed cotton yield. The hybrid *Khardwa* 2 x *Suraj* recorded highest positively significant relative heterosis (59.47%), heterobeltiosis (51.50%) and standard heterosis (42.52%) followed by *Anjali* x MCU 5 with positive significant values of standard heterosis (34.05%), for MCU 5 x MCU 7 (32.64%) and for KC 2 x MCU 5 (27.00%). Out of seventy two hybrids, twenty one hybrids recorded significantly

positive relative heterosis, eight hybrids for heterobeltiosis and thirteen hybrids recorded significantly positive standard heterosis over the check MCU 13. None of the hybrids exhibited significantly negative heterosis (Table 2). Such high heterotic response would be useful for obtaining more number of bolls per plant which ultimately results in higher seed cotton yield (Bhatade, *et al.*, 1994).

Boll Weight:

The hybrid KC 2 x MCU 7 recorded highest relative heterosis (28.13%) and heterobeltiosis (24.13%), while the hybrids *Suraj* x G.Cot 16 and *Anjali* x KC 2 registered the highest value of standard heterosis (22.75%). The hybrid MCU 5 x G.Cot 16 recorded lowest negatively significant relative heterosis (-24.93%), heterobeltiosis (-32.40%) and lowest negative standard heterosis (-15.50%). None of the hybrids exhibited significantly negative standard heterosis over the check MCU 13. Among seventy two hybrids, five hybrids recorded positive and significant relative heterosis, one hybrid showed positive significant heterobeltiosis and

Table 3. Expression of heterosis in hybrids (%) for single plant yield, ginning percentage, lint index and seed index

SI No.	Hybrids	5. Single plant yield			6. Ginning percentage			7. Lint index			8. Seed index		
		d _i	d _{ii}	d _{iii}	d _i	d _{ii}	d _{iii}	d _i	d _{ii}	d _{iii}	d _i	d _{ii}	d _{iii}
1	Suraj X Surabi	28.96 **	26.50 **	12.52	-8.85 **	-10.34 **	-8.89**	3.19	1.80	-11.79	14.42	11.30	1.27
2	Suraj X Khardwa 2	29.10 **	27.55 **	9.45	-1.73	-7.69 **	-6.18**	10.07	0.60	-12.82	9.11	5.40	-4.09
3	Suraj X Anjali	2.54	-2.33	-7.19	5.08 *	3.64	5.34*	1.95	-0.57	-9.36	3.61	-8.10	-16.38
4	Suraj X KC 2	17.26 *	15.99	1.74	-1.19	-3.97	-2.41	4.72	3.00	-7.80	2.74	0.43	-4.28
5	Suraj X KC 3	-2.83	-5.26	-14.03	-6.73 **	-7.15 **	-4.79*	-2.58	-6.84	-11.44	4.49	4.28	-4.73
6	Suraj X MCU 5	21.90 **	14.68 *	11.62	-0.03	-0.49	1.13	3.07	1.96	-9.71	-0.48	-2.35	-11.19
7	Suraj X MCU 7	3.00	-1.79	-6.88	17.37 **	13.16 **	14.98**	15.39	14.20	1.04	-13.73	-16.21	-19.11*
8	Suraj X G.cot 16	28.14 **	24.90 **	7.18	-0.50	-2.20	-0.61	1.12	-5.09	-6.24	-1.37	-6.46	-5.10
9	Surabi X Suraj	-5.13	-7.15	-16.75*	0.28	-0.45	-0.26	-3.82	-6.92	-13.86	-0.63	-6.21	-13.47
10	Surabi X Khardwa 2	10.56	7.21	-4.42	-10.19 **	-14.47 **	-15.56**	-3.83	-12.10	-23.92**	16.87	14.86	-2.64
11	Surabi X Anjali	23.75 **	20.05 **	13.47	-7.35 **	-7.40 **	-8.48**	-10.33	-12.55	-20.28*	20.55	12.11	-8.19
12	Surabi X KC 2	-9.46	-10.19	-19.93**	9.65 **	8.09 **	6.71**	2.65	0.97	-9.53	-7.50	-13.99	-18.02
13	Surabi X KC 3	16.51 *	15.75	4.43	-5.71 **	-7.46 **	-5.11*	0.00	-4.38	-9.19	13.03	7.17	-2.09
14	Surabi X MCU 5	-6.80	-10.71	-13.09	3.80	2.78	3.51	15.92	14.68	1.56	13.88	10.18	-3.55
15	Surabi X MCU 7	14.51 *	11.21	5.09	1.44	-0.81	-2.09	2.33	1.27	-10.40	3.52	-4.34	-7.64
16	Surabi X G.cot 16	13.64	8.74	-3.05	1.14	0.85	-0.44	-6.82	-12.54	-13.69	-5.06	-14.22	-12.92
17	Khardwa 2 X Suraj	34.79 **	33.39 **	13.49	7.96 **	2.48	2.67	13.22	-1.03	-8.32	1.15	-4.54	-11.92
18	Khardwa 2 X Surabi	20.35 **	16.54 *	3.99	6.23 **	1.76	0.00	22.39 *	11.51	-5.89	11.79	9.10	-6.10
19	Khardwa 2 X Anjali	6.25	-0.05	-5.07	11.39 **	6.42 **	5.17*	16.95	2.95	-6.24	13.86	5.89	-13.28
20	Khardwa 2 X KC 2	2.93	0.51	-11.85	-15.82 **	-18.41 **	-21.75**	-19.85 *	-28.92 **	-36.22**	2.16	-5.01	-9.55
21	Khardwa 2 X KC 3	-13.70	-16.93 *	-24.28**	5.81 **	-0.65	1.86	1.05	-12.59	-16.98*	-7.25	-12.05	-19.65*
22	Khardwa 2 X MCU 5	16.13 *	7.93	5.05	0.11	-5.20 *	-4.53	10.32	-1.66	-13.00	10.17	6.60	-6.64
23	Khardwa 2 X MCU 7	-3.85	-9.45	-13.93	1.89	-0.45	-6.07*	23.23 *	9.89	-2.77	19.68 *	10.60	6.82
24	Khardwa 2 X G.cot 16	5.44	4.11	-12.98	-6.30 **	-10.19 **	-11.85**	-4.95	-19.12 *	-20.10*	4.81	-5.29	-3.91
25	Anjali X Suraj	29.51 **	23.11 **	16.17*	9.10 **	8.30 **	8.51**	19.77 *	15.90	7.28	14.44	2.37	-5.55
26	Anjali X Surabi	-6.14	-8.86	-13.67	-8.31 **	-8.51 **	-9.70**	-2.48	-3.80	-16.64*	21.91 *	12.53	-3.18
27	Anjali X Khardwa 2	-13.26	-18.29 *	-21.99**	15.63 **	10.12 **	8.71**	21.33 *	10.90	-3.81	7.97	0.32	-14.92
28	Anjali X KC 2	-1.04	-4.71	-9.73	-9.55 **	-10.84 **	-11.96**	-3.34	-4.93	-14.90	22.31 *	7.88	2.82
29	Anjali X KC 3	-14.62 *	-16.60 *	-20.43**	-11.12 **	-12.77 **	-10.54**	-13.55	-17.34	-21.49**	12.80	1.34	-7.37
30	Anjali X MCU 5	25.70 **	24.02 **	20.72**	-11.12 **	-12.00 **	-11.38**	-4.45	-5.48	-16.29*	24.65 *	14.13	-0.09
31	Anjali X MCU 7	17.92 **	17.85 *	11.32	13.73 **	11.21 **	9.79**	6.98	5.88	-6.41	-4.51	-16.26	-19.11*
32	Anjali X G.cot 16	-9.66	-15.98 *	-20.41**	-8.64 **	-8.90 **	-10.05**	-12.80	-18.16 *	-19.24*	8.56	-6.77	-5.37
33	KC 2 X Suraj	22.57 **	20.70 *	6.09	-2.08	-4.22	-4.04	0.72	-2.53	-9.71	4.77	4.04	-4.00
34	KC 2 X Surabi	23.90 **	23.08 **	9.82	-25.21 **	-26.14 **	-27.41**	-12.72	-13.90	-25.30**	32.61 **	29.00**	17.38
35	KC 2 X Khardwa 2	11.99	9.25	-3.71	9.22 **	5.52 *	1.10	7.44	-1.80	-14.90	-3.99	-7.25	-15.65
36	KC 2 X Anjali	-4.95	-8.36	-13.09	-21.72 **	-22.91 **	-23.81**	-16.18	-18.25	-25.48**	36.47 **	21.05	10.10
37	KC 2 X KC 3	6.93	5.58	-4.50	14.32 **	10.58 **	13.39**	4.96	0.36	-4.68	-14.32	-14.49	-21.84*
38	KC 2 X MCU 5	31.82 **	25.53 **	22.18**	-8.01 **	-10.24 **	-9.61**	-13.55	-14.48	-24.26**	-1.61	-3.45	-12.19
39	KC 2 X MCU 7	16.29 *	12.25	6.04	8.20 **	7.36 **	2.87	-7.47	-8.42	-18.89*	-17.32	-19.70	-22.47*
40	KC 2 X G.cot 16	-5.12	-8.66	-19.58*	-2.09	-3.25	-5.02*	7.48	0.88	-0.35	11.82	6.05	7.64
41	KC 3 X Suraj	-6.95	-9.48	-17.79*	8.48 **	7.71 **	9.47**	11.16	7.58	-0.35	-5.61	-6.26	-13.47
42	KC 3 X Surabi	-14.53 *	-15.03	-23.30**	-3.38	-4.97 *	-3.43	8.06	6.60	-7.63	9.74	6.75	-2.91
43	KC 3 X Khardwa 2	21.31 **	16.92 *	5.40	-14.67 **	-19.84 **	-18.52**	-12.36	-19.90 *	-30.50**	6.37	2.75	-6.55
44	KC 3 X Anjali	23.61 **	20.64 **	14.40	12.01 **	10.47 **	12.28**	20.47 *	17.49	7.11	10.54	-1.95	-10.74

SI No.	Hybrids	5. Single plant yield			6. Ginning percentage			7. Lint index			8. Seed index		
		d _i	d _{ii}	d _{iii}	d _i	d _{ii}	d _{iii}	d _i	d _{ii}	d _{iii}	d _i	d _{ii}	d _{iii}
45	KC 3 X KC 2	20.33 **	18.62 *	6.88	-2.90	-5.63 *	-4.09	12.68	10.83	-0.69	13.43	10.89	5.64
46	KC 3 X MCU 5	-7.80	-11.14	-13.52	6.00 **	5.51 *	7.23**	5.44	4.31	-7.63	-7.26	-9.00	-17.20
47	KC 3 X MCU 7	17.81 **	15.11 *	8.66	7.59 **	3.73	5.43*	17.96 *	16.75	3.29	1.50	-1.41	-4.82
48	KC 3 X G.cot 16	-7.03	-11.57	-20.17**	-30.31 **	-31.50 **	-30.37**	-21.40 **	-26.23 **	-27.21**	25.96 **	19.46 *	21.20*
49	MCU 5 X Suraj	16.28 *	9.33	5.83	0.53	-0.19	1.42	14.26	10.57	2.43	9.33	8.58	0.18
50	MCU 5 X Surabi	6.79	2.53	-0.58	-9.62 **	-11.10 **	-9.67**	15.15	13.60	-1.56	29.27 **	25.75 *	14.47
51	MCU 5 X Khardwa 2	8.79	1.37	-1.67	9.72 **	3.07	4.76*	29.65 **	18.50	2.77	8.80	5.10	-4.37
52	MCU 5 X Anjali	10.11	8.90	5.58	-5.49 **	-6.79 **	-5.26*	-2.63	-5.04	-13.52	16.40	3.25	-6.10
53	MCU 5 X KC 2	4.30	-0.67	-3.59	-13.46 **	-15.90 **	-14.52**	-14.36	-15.76	-24.44**	1.86	-0.43	-5.19
54	MCU 5 X KC 3	-8.27	-11.40	-14.10	4.63 *	4.16	6.79**	11.07	6.20	0.87	0.05	-0.15	-8.83
55	MCU 5 X MCU 7	33.80 **	32.19 **	27.40**	-10.55 **	-13.76 **	-12.37**	-9.95	-10.87	-21.14*	2.38	-0.57	-4.00
56	MCU 5 X G.cot 16	1.89	-6.25	-9.11	15.59 **	13.61 **	15.45**	8.04	1.40	0.17	-17.21	-21.48 *	-20.29*
57	MCU 7 X Suraj	16.35 *	10.59	4.63	0.25	-3.39	-3.22	-6.43	-9.45	-16.12	-8.51	-12.09	-12.01
58	MCU 7 X Surabi	-7.74	-10.42	-15.15*	-16.63 **	-18.91 **	-20.30**	-20.73 *	-21.80 *	-32.24**	1.00	-6.09	-6.01
59	MCU 7 X Khardwa 2	20.14 **	13.18	7.02	15.85 **	13.61 **	5.55*	25.49 **	14.70	-0.69	-1.18	-8.73	-8.64
60	MCU 7 X Anjali	18.35 **	18.29 *	12.17	10.58 **	7.27 **	6.01*	5.85	3.23	-5.89	0.91	-14.05	-14.01
61	MCU 7 X KC 2	18.77 **	14.37	8.11	17.90 **	16.06 **	11.30**	-2.26	-3.87	-13.86	-25.52 **	-27.32**	-27.30**
62	MCU 7 X KC 3	-21.33 **	-23.15 **	-27.20**	-4.29 *	-8.78 **	-6.45**	-7.82	-11.86	-16.29*	-3.28	-7.50	-7.46
63	MCU 7 X MCU 5	15.18 *	13.64	10.32	12.25 **	7.92 **	8.65**	-12.56	-13.50	-23.40**	-28.24 **	-32.73**	-32.67**
64	MCU 7 X G.cot 16	-26.60 **	-31.74 **	-35.33**	-5.66 **	-8.18 **	-9.87**	-20.84 *	-25.70 **	-26.69**	-15.08	-15.65	-14.38
65	G.cot 16 X Suraj	-4.70	-6.93	-19.99**	-11.61 **	-12.26 **	-12.08**	-3.75	-9.00	-5.37	18.92 *	14.27	14.38
66	G.cot 16 X Surabi	4.01	-0.57	-11.29	-15.53 **	-15.72 **	-16.81**	-15.14	-23.17 **	-20.10*	12.30	4.41	4.46
67	G.cot 16 X Khardwa 2	36.44 **	34.50 **	12.28	9.91 **	4.68 *	3.34	10.65	-6.50	-2.77	0.10	-7.55	-7.46
68	G.cot 16 X Anjali	12.97	4.94	-0.49	7.92 **	7.86 **	6.62**	1.24	-5.00	-1.21	4.80	-10.73	-10.65
69	G.cot 16 X KC 2	8.34	4.42	-8.19	-3.49	-4.87 *	-6.07*	0.45	-6.50	-2.77	9.32	6.68	6.82
70	G.cot 16 X KC 3	12.90	7.29	-3.08	3.38	1.46	4.04	-7.58	-11.58	-7.97	-9.70	-13.64	-13.56
71	G.cot 16 X MCU 5	22.59 **	12.53	9.27	-22.70 **	-23.46 **	-22.91**	-25.56 **	-31.08 **	-28.25**	11.08	4.14	4.19
72	G.cot 16 X MCU 7	14.84 *	6.79	1.05	11.60 **	9.12 **	7.72**	5.45	-2.42	1.56	-8.10	-9.73	-9.65

nine hybrids showed positive significant standard heterosis (Table 2). Similar findings were also reported by Solanki *et al.* (2014) for this trait.

Single plant yield:

Among seventy two hybrids, thirty three hybrids recorded positive and significant relative heterosis, twenty hybrids showed positive significant heterobeltiosis and five hybrids showed positive significant standard heterosis (Table 3). The hybrid MCU 5 x MCU 7 recorded maximum positive significant relative heterosis (33.80%), heterobeltiosis (32.19%) and standard heterosis (27.40%) followed by KC 2 x MCU 5 with positive significant values of relative heterosis (31.82%), heterobeltiosis (25.53%) and standard heterosis (22.18%). The hybrid Anjali x MCU 5 also recorded highest positively significant relative heterosis (25.70%), heterobeltiosis (24.02%) and standard heterosis (20.72%). The results reported in the present investigation are in agreement with earlier workers (Abro *et al.*, 2009; Jyotiba *et al.*, 2010; Basal *et al.*, 2011; Geddam, *et al.*,

2011; Patil, *et al.*, 2011).

Ginning outturn (%):

The hybrid MCU 7 x KC 2 recorded maximum positive significant relative heterosis (17.90%) and heterobeltiosis (16.06%) followed by MCU 5 x G.Cot 16 with positive significant values of relative heterosis (15.59%), heterobeltiosis (13.61%) and standard heterosis (15.45%). The hybrid KC 3 x G.Cot 16 recorded lowest negative significant relative heterosis (-30.31%), heterobeltiosis (-31.50%) and standard heterosis (-30.37%). Among seventy two hybrids, twenty seven hybrids recorded positive and significant relative heterosis, nineteen hybrids showed positive significant heterobeltiosis and twenty one hybrids showed positive significant standard heterosis (Table 3). Nirania *et al.*, 2004, Rauf, *et al.*, 2005, Preetha and Raveendran, 2008, Patel, *et al.*, 2009 and Geddam, *et al.*, 2011 also reported varying magnitude of heterosis for this character.

Lint index:

The magnitude of relative heterosis ranged from -25.56% in the hybrid G.Cot 16 x MCU 5 to 29.65% in MCU 5 x Khardwa 2, wherein eight hybrids exhibited significantly positive heterosis. Similar findings have also been reported by Nirania, *et al.*, 2004, Khosla, *et al.*, 2007, Pole, *et al.*, 2008 and Jyotiba, *et al.*, 2010. None of the hybrids exhibited significantly positive heterosis over the better parent. But nine hybrids exhibited significantly negative heterosis for heterobeltiosis. G.Cot 16 x MCU 5 recorded minimum negative significant heterobeltiosis. In heterosis over the standard check also, none of the hybrids exhibited significantly positive heterosis. Heterosis over the standard check was negatively significant for twenty three hybrids for this trait (Table 3).

Seed index:

The mid parent heterosis ranged from -28.24% in MCU 7 x MCU 5 to 36.47% in KC 2 x Anjali (Table 3). Nine hybrids exhibited significantly positive relative heterosis whereas negative expression over mid parent was observed in two hybrids. Positive and negative expression of heterobeltiosis was exhibited in three hybrids over the better parent. The lowest (-32.73%) and highest (29.00%) values of heterobeltiosis was recorded in MCU 7 x MCU 5 and KC 2 x *Surabhi*, respectively. The range of standard heterosis varied from -32.67% in MCU 7 x MCU 5 to 21.20% in KC 3 x G.Cot 16 for seed index. Only one hybrid recorded significantly positive heterosis and eight hybrids exhibited significantly negative heterosis over the check. Pole, *et al.*, 2008 and Jyotiba, *et al.*, 2010 reported high heterosis for seed index.

Seed cotton yield in cotton is one of the most important economic characters and is the final product of the multiplicative interaction of contributing traits. It is imperative to know the causes of heterosis for seed cotton yield. Whitehouse *et al.*, 1958 and Grafius, 1959 suggested that there may not be any gene system for yield *per se* as yield is an end product of the multiplicative interaction between the yield components. This would indicate that the heterosis for yield should be through heterosis for the individual yield components or alternatively due to the multiplicative effects of partial dominance of component characters. William and Gilbert, 1960 reported that even simple dominance in respect of yield components may lead to expression of heterosis for yield.

The results of the present study suggested that number of sympodia per plant, number of bolls per plant and boll weight were the main contributors toward increased in heterotic effects for single plant yield. While ginning percentage, seed index and lint index were secondary contributors towards increased heterotic effects

for single plant yield in specific cross combinations only. Similar findings have been reported by Khan *et al.*, 2009, Jyotiba, *et al.*, 2010, Kaushik and Shastry, 2011 and Patil, *et al.*, 2011.

Based on data of standard heterosis, it can be concluded that, three cross combinations namely MCU 5 x MCU 7, KC 2 x MCU 5 and *Anjali* x MCU 5 appeared to be the most heterotic crosses for single plant yield to exploit heterosis in cotton.

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Studies on Genetic Parameters in Okra [*Abelmoschus esculentus* (L.)]

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ABSTRACT

The present investigation “Studies on genetic variability, heritability and genetic advance in okra [*Abelmoschus esculentus* (L.) Moench]” was carried out during kharif season of 2012-2013 at the Vegetable Research Farm, Department of Horticulture, College of Agriculture, J.N.K.V.V., Jabalpur (M.P.). The experimental material for the present investigation was comprised of 30 genotypes of okra. These genotypes were sown in Randomized Complete Block Design with three replications, to estimate the genetic variability. The estimates of mean sum of square due to genotypes were highly significant for all the characters, indicating the presence of genetic diversity in the existing material. The variation was highest for fruit yield per plant, followed by fruit yield per hectare, plant height at 120 DAS, plant height at 90 DAS, plant height at 60 DAS and fruiting span. High heritability coupled with high genetic advance as percentage of mean for traits like fruit yield per plant and fruit yield per plot suggested that the preponderance of additive genes. It also indicated higher response for selection of high yielding genotypes as these characters are governed by additive gene actions.

Key words Variability, Heritability, Genetic advance, okra and *Abelmoschus esculentus*

Okra [*Abelmoschus esculentus* (L.)] has captured a prominent position among vegetables. It is choicest fruit vegetable grown extensively in the tropical, subtropical and warm area of the world like India, Africa, Turkey and other neighbouring countries. In India, okra is one of the most important vegetable crop grown for its tender green fruits during summer and rainy seasons. Okra is known by many local names in different parts of the world. It is called lady's finger in England, Gumbo in U.S.A. and Bhindi in India. In India, among fresh vegetables, 60 per cent share of export goes to okra. It is a hardy crop and can grow with considerable success on a wide range of soils and under variable environmental conditions. In India it is grown twice in a year for getting regular supply. In the country, a large number of okra varieties are grown, the variation occurs with regards to quantitative and qualitative traits. The plant height, number of primary branches per plant, number of fruits per plant, size of fruit i.e. length as well as weight of fruits are the yield contributing characters while, colour of fruit and fiber content determine the quality of fruit.

The foremost challenge to the existence of mankind has always been to produce adequate quantity of food from the available acreage to meet the requirements of ever expanding world population. The rate of yield gain in crop improvement programme must match the rate of population growth so, as to avoid malnutrition and hunger. Attempts have been made to determine the magnitude of heritable and non-heritable components and genetic parameters such as genotypic and phenotypic coefficient of variation, heritability and genetic advance as percentage of mean in some of the quantitative characters of okra.

In any crop improvement program, basic information with respect to variability present in the crop is essential. Yield being a complex trait, is collectively influenced by various component characters, which are polygenically inherited and highly influenced by environmental variations. Genetic variability, heritability and genetic advance are pre-requisite for improvement of any crop for the selection of superior genotypes and improvement of any traits. It is very difficult to judge whether observed variability is heritable or not heritable. Moreover, knowledge of heritability is essential for selection based improvement as it indicates the extent of transmissibility of a character in future generations. The present study was, therefore aimed to study variability, heritability and genetic advance among thirty genotypes of okra.

MATERIALS AND METHODS

An experiment was conducted at Horticulture complex, Department of Horticulture, J.N.K.V.V., Jabalpur (MP) during 2012-13 to study variability, heritability and genetic advance among thirty genotypes of okra. The soil of the experimental field was medium black, uniform texture with good drainage and medium NPK status. Jabalpur is situated on Kymore Plateau and Satpura hills agro-climatic zone of Madhya Pradesh at 23.91° North latitude, 79.5° East longitudes and on an altitude of 411.78 meters above the mean sea level. The tropic of cancer passes through the middle of the district. The climate of region is typically semi arid and sub tropical having extreme winter and summer.

Thirty genotypes of okra were grown in a randomized block design with three replications. Every genotype in each

Table 1. Estimates of genetic parameters in twenty characters of okra

Characters	Grand Mean	Range		Coefficient of variations		Heritability % (BS)	Genetic Advance	GA as % of mean
		Min.	Max.	Phe.	Gen.			
Plant height 30 DAS	15.52	12.63	19.07	13.30	8.47	40.58	1.72	11.10
Plant height 60 DAS	57.18	44.31	66.09	12.01	9.52	62.78	8.90	15.57
Plant height 90 DAS	98.49	86.28	124.69	8.96	7.50	70.18	12.69	12.89
Plant height 120 DAS	105.83	95.19	138.82	8.90	8.24	85.77	16.53	15.62
Leaves /plant 30 DAS	4.58	4.07	5.13	9.52	4.16	19.11	0.17	3.74
Leaves /plant 60 DAS	10.68	7.87	13.13	15.53	11.25	52.52	1.79	16.82
Leaves /plant 90 DAS	20.32	18.07	24.07	8.51	6.89	65.46	2.32	11.45
Leaves/plant 120 DAS	25.29	22.50	30.20	7.71	6.13	63.28	2.53	10.02
Branches/plant	1.93	0.93	2.73	26.82	20.31	57.35	0.61	31.80
Inter nodal length (cm)	3.93	3.41	4.57	8.62	6.54	57.59	0.40	10.19
Nodes to first flowering	5.00	4.40	5.73	12.12	6.49	28.72	0.35	7.15
Days to 50% flowering	48.23	45.00	52.00	4.07	3.15	59.86	2.42	5.02
Fruiting span	76.30	70.33	80.67	4.64	4.30	85.79	6.27	8.22
No. of fruits/ plant	20.28	16.90	25.27	10.72	8.54	63.51	2.83	13.99
Fruit length (cm)	16.21	15.16	17.59	4.48	2.94	43.09	0.64	3.97
Fruit diameter (mm)	18.18	16.81	19.19	3.93	2.98	57.44	0.84	4.66
Fruits weight(g)	14.72	8.67	18.83	18.51	15.46	69.72	3.93	26.70
Fruits yield/ plant (g)	462.18	347.17	570.08	14.58	12.67	75.47	104.88	22.69
Fruits yield/ plot (kg)	9.244	6.943	11.402	14.58	12.67	75.47	2.09	22.68
Fruits yield/ ha (q)	114.07	85.68	140.70	16.14	11.69	52.45	19.90	17.45

replication was grown in a plot of 3.6 m length and 3.0 m width with a spacing of 60 cm between rows and 30 cm between plants. Five plants from each replication were taken for recording observation on eighteen characters *viz.* plant height, leaves per plant, Branches per plant, Length of internodes (cm), Number of nodes to first flowering, Numbers of nodes were counted at the time of first flowering, Days taken to 50% flowering, Fruiting span, Number of fruits per plants, Fruit length (cm), Fruit diameter (cm), Number of ridges on fruit, Fruit weight (g) and Yield per plant (g) and their mean was obtained.

The data were statistically analyzed for computation of genetic coefficients of variation using appropriate statistical analysis. Heritability in broad sense was estimated as per the formula given by Allard, 1960. The expected genetic advance was calculated by using formula as suggested by Johnson, *et al.*, 1995.

RESULTS AND DISCUSSION

The estimates of mean sum of square due to genotypes were highly significant for all the characters indicating the presence of genetic diversity in the existing material. Five traits *viz.*, fruit yield per plant, fruit yield per hectare, plant

height at 120 DAS, plant height at 90 DAS and plant height at 60 DAS exhibited the value of higher magnitude. The findings of Verma, *et al.*, 2004., Mannivannan *et al.*, 2007, Jindal *et al.*, 2009 are similar to that of the present findings.

The estimates of variability, heritability and genetic advance among thirty genotypes in twenty characters of okra are presented in table 1. In the present findings phenotypic coefficient of variation were observed to be higher than the corresponding genotypic coefficient of variation for all the characters studied, however the differences were narrow which implied their relative resistance to environmental variation. It also described that genetic factors were predominantly responsible for expression of those attributes and selection could be made effectively on the basis of phenotypic performance. The finding of Bendale, *et al.*, 2003 and Senapati, *et al.*, 2011 were similar to that of the present findings.

The present study revealed that the phenotypic coefficient of variation was higher than the corresponding genotypic coefficient of variation for all the traits, which might be due to interaction of the genotypes with the environment to some degree or other explaining environmental factors influencing the expression of these

characters. High phenotypic and genotypic coefficient of variation was observed for number of branches per plant followed by fruit weight, fruit yield per plant, fruit yield per plot, fruit yield per hectare and number of leaves per plant at 60 DAS. The high values of GCV suggested greater phenotypic and genotypic variability among the genotypes and responsiveness of the attributes for making further improvement by selection. However, fruit length, fruit diameter, days to 50 per cent flowering, number of leaves per plant at 30 DAS, fruiting span, number of leaves per plant at 120 DAS, nodes to first flowering, internodal length and number of leaves per plant at 60 DAS showed low estimates of genotypic and phenotypic coefficient of variation, indicating the potential of heterosis breeding for their amelioration.

Heritability which denotes the proportion of genetically controlled variability expressed by a programme for a particular character or a set of character is very important biometrical tool for guiding plant breeders for adoption of appropriate breeding procedures. High heritability in broad sense is helpful in identifying appropriate character for selection and enables the breeder to select superior genotypes on the basis of phenotypic expression of quantitative characters. The estimated values of heritability in broad sense were classified as high (more than 70%), medium (50-70%) and low (less than 50%).

Result indicated that the heritability estimates were observed high for fruiting span, followed by plant height at 120 DAS, fruit yield per plant, fruit yield per plot and plant height at 90 DAS. The results were in close proximate to that of Chaukhande *et al.*, 2011, Nagre *et al.*, 2011 and Nagre *et al.*, 2011 for plant height, Suresh Babu *et al.*, 2004 and Nwangburuka *et al.*, 2012 for fruit yield per plant, fruit yield per plot and plant height, Senapati, 2011 for fruit yield per plant and fruiting span. High values of broad sense heritability for the above characters expressed that they were least influenced by environmental modification. It reflected that the phenotypes were the true representative of their genotypes and selection based on phenotypic performance would be reliable.

Low estimation of heritability was recorded for fruit length, plant height at 30 DAS, nodes to first flowering and number of leaves per plant at 30 DAS. This is indicative of the fact that these characters are rather more influenced by the environment and may not respond much to selection. While, it was moderate for fruit weight, number of leaves per plant at 90 DAS, number of fruits per plant, number of leaves per plant at 120 DAS, plant height at 60 DAS, days to 50 per cent flowering, internodal length, fruit diameter, number of branches per plant, number of leaves per plant at 60 DAS and fruit yield per hectare which indicated that selection based on phenotypic performance would be

rewarding. The results were in close proximate to that of Hazra and Basu, 2000 for number of branches per plant, number of leaves per plant, days to 50 per cent flowering and number of fruits per plant, Dhankar and Dhankar 2002 for number of fruits per plant and plant height.

Heritability however, indicates only the effectiveness with which selection of a genotype can be based on phenotypic performance, but fails to indicate the genetic progress. Heritability estimates along with genetic gains are more effective and reliable in predicting the improvement through selection Johnson *et al.*, 1955. Estimates of genetic advance helps to predict the extent of improvement that can be achieved for improving the different characters. The estimated values of genetic advance as percent of mean were classified as high (more than 20%), moderate (11-20%) and low (less than 11%).

Genetic advance as percentage of mean ranged between 3.74% for number of leaves per plant at 30 DAS to 31.80% for number of branches per plant. The highest estimate of genetic advance as percentage of mean was recorded for number of branches per plant, fruit weight, fruit yield per plant and fruit yield per plot. The results were in consonance with (4) and Nagre *et al.* (10) for fruit yield per plant, (11) for yield per plant and number of branches per plant.

According to assume scale for classification (as above), fruit yield per hectare, number of leaves per plant at 60 DAS, plant height at 120 DAS, plant height at 60 DAS, number of fruits per plant, plant height at 90 DAS, number of leaves per plant at 90 DAS and plant height at 30 DAS showed moderate value of genetic advance as percentage of mean. The findings were in agreement to the findings of Dhankar and Dhankar, 2002. for number of fruits per plant, plant height. Low estimates were observed for internodal length, number of leaves per plant at 120 DAS, fruiting span, nodes to first flowering, days to 50 per cent flowering, fruit diameter, fruit length and number of leaves per plant at 30 DAS. The findings were in agreement to Chaukhande, *et al.*, 2011 for fruit diameter

High heritability coupled with high genetic advance for traits like fruit yield per plant and fruit yield per plot. Suggested that the preponderance of additive genes. It also indicated higher response for selection of high yielding genotypes as these characters are governed by additive gene actions. The findings were in agreement to the findings of Singh and Singh, 2006 and Naidu *et al.*, 2007

High heritability supplemented with moderate genetic advances as percentage of mean were manifested by plant height at 120 DAS and plant height at 90 DAS which might be attributed to additive gene action conditioning their expression and phenotypic selection for their amenability

can be brought about. These findings corroborated the earlier findings of Kumar, *et al.*, 2011. High heritability coupled with low genetic advance as percentage of mean was observed for fruiting span. This revealed the predominance of non-additive gene action in the expression of these characters. Low estimates of heritability coupled with low genetic advances as percentage of mean were displayed by nodes to first flowering, fruit length and number of leaves per plant at 30 DAS that indicated that this character was highly influenced by environmental effects and consequently its selection would be ineffective.

On the basis of present investigation, it is concluded that the different characters have the influence of both additive and non additive gene action hence, the breeder should adopt suitable breeding methodology to utilize both additive and non additive gene effects simultaneously, since varietal and hybrid development will go a long way in the breeding programmes, especially in case of okra.

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Genetic Dissection of Fibre Quality Traits in Upland Cotton (*Gossypium hirsutum* L.)

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ABSTRACT

Nine upland cotton varieties were crossed in a complete diallel mating system to assess the genetics of 2.5% span length (SL), bundle strength (BS), micronaire value (MIC), Uniformity ratio (UR) and Elongation per cent (EP) utilizing Jinks numerical approach. Analysis of variance had showed highly significant differences due to genotypes for all the fibre traits. Additive component (D) was significant in all the traits and was lower in magnitude than dominant components (H_1 and H_2) of variation for 2.5% SL, BS, MIC and UR which was firmly supported by the value of $(H_1/D)^{1/2}$. Asymmetrical distribution of dominant and recessive genes in parents for 2.5% SL, BS, MIC and UR was confirmed, and soundly sustained by the value of $H_2/4H_1$. The h^2 value was significant for all the traits except UR. High narrow sense heritability (h^2_{ns}) was exhibited by MIC, while 2.5%SL, BS and EP possessed moderate heritability. The genes controlling EP were additive in nature and could be improved via selection while heterosis breeding might be fruitful for progress in 2.5% SL, BS, MIC and UR.

Key words Diallel cross, Gene action, Upland cotton, Fibre quality traits

Upland cotton (*Gossypium hirsutum* L.) is the most important fibre crop in the world, and it is the mainstay of the economy (Ali and Khan, 2007). Cotton is the main source of foreign exchange earnings and it brings about 65% of the total annual earnings from the export of raw cotton material and the finished products. The crop not only meets the needs of fibre requirements of local industry but also provides food in the form of edible oil (Ali and Awan, 2009). Fibre quality of a specific cotton genotype is a composite of various characteristics including 2.5% span length (SL), bundle strength (BS), micronaire value (MIC) and Elongation per cent (EP). These traits have their individual importance in spinning, weaving and dying units (Munro, 1987). Yarn strength is the processing result of greatest interest to yarn and textile manufacturers (Bradow, 1999). In addition to that fibre uniformity ratio (UR) is also of tremendous value in textile industry. It is highly correlated with efficient spinning and weaving processes which

converts the fibre into fabrics. But these traits are highly influenced by the environment with special reference to the fineness (Yuan *et al.*, 2005; Percy *et al.*, 2006). Therefore, it is the need of the day to improve fibre quality in the dominating *hirsutum* genotypes, to fulfill the requirements of growing textile industry, processing and end uses. Before embarking upon a plant improvement programme through selection and breeding, the breeders are required to collect informations about the existence of variation in different plant characters, the patterns of their inheritance and the extent to which the trait variability is transmitted to the next generation.

Several researchers (Ahmad and Azhar, 2000; Iqbal and Nadeem, 2003 and Nadeem and Azhar, 2005) had advocated the importance of genetic studies of the material before selecting the desirable plants. May and Green (1994) and Haq and Azhar (2004) reported that the additive type of gene action for fibre length, but non-additive gene effects for fibre strength and fibre fineness. Khan *et al.* (2001) and Shakeel *et al.* (2001) found that the non additive genes were involved in the inheritance of fibre uniformity while Hendawy *et al.* (1999) and Chen *et al.* (1999) provided dissimilar results. With this objective in mind, the present genetic experiment was conducted in the department by using 9 x 9 complete diallel cross techniques (Hayman, 1954; Jinks, 1954). The information derived from these investigations would be useful to the workers engaged in cotton fibre quality improvement program.

MATERIALS AND METHODS

This study was carried out to evaluate the fibre quality characters in F_1 hybrids of upland cotton that was conducted during 2012-14 at the Department of Cotton, Tamil Nadu Agricultural University, Coimbatore. Nine parental genotypes (Suraj, Surabhi, Khandwa 2, Anjali, KC 2, KC 3, MCU 5, MCU 7 and G.Cot 16) were raised during winter 2012-2013 and also they were crossed in a complete diallel fashion. During winter 2013-14, the parents and their seventy two F_1 s were raised in a RBD design with two replications. The package of practices recommended for the cotton

cultivation in Tamil Nadu was followed throughout the crop growing period.

Fibre quality characteristics were recorded using high volume instrument (HVI), Department of cotton, TNAU, Coimbatore. The computerised instrument recorded 2.5% span length (mm), bundle strength (g/tex), micronaire value ($\mu\text{g}/\text{inch}$), uniformity ratio (%) and elongation per cent (%) according to the international standards. The mean values of two replications were further tested for fitness to the additive dominance model for genetic analysis through INDOSTAT package.

RESULTS AND DISCUSSION

Analysis of variance

Analysis of variance had showed highly significant differences due to genotypes for all the fibre traits indicating the presence of sufficient variability in the experimental materials (Table 1). Significance of variance in parents V_s hybrids interaction provided adequacy for comparing the heterotic expression for all the characters. Parents and hybrids showed the significant differences between all the characters studied, it was also confirmed by the results reported in earlier studies of Kumar (2007).

Testing Validity of the hypothesis

The data were assessed for Additive-Dominance (AD) model by exploiting various adequacy parameters given in Table 2. Two broad tests were followed in order to test whether the diallel data conformed to the

hypothesis postulated by Hayman (1954) viz., t^2 test and estimation of regression co-efficient. The t^2 statistic, test the constancy of Vr-Wr over the arrays, a significant t^2 indicates heterogeneity of Vr-Wr, when one or more of the hypothesis are not satisfied for that particular character. The value of t^2 was not significant for 2.5% span length, bundle strength, micronaire value, uniformity ratio and elongation per cent. This test therefore indicates that for these five characters, the assumptions of the diallel were fulfilled.

In the second test, if all the assumptions of diallel hold true, the (Vr-Wr) regression co-efficient b, for each character is expected to be significantly different from zero, but not different from unity (Jinks and Hayman, 1953). The values of regression co-efficient were not significantly different from unity for the following four characters namely 2.5% span length, bundle strength, micronaire value and elongation per cent. Similar results were recorded by Ali *et al.* (2010). The characters such as 2.5% span length, bundle strength, micronaire value and elongation per cent were significantly different from zero. The characters 2.5% span length, bundle strength, micronaire value and elongation per cent satisfied both the assumptions.

The validity of hypothesis does not fulfilled uniformity ratio. In such cases, the estimates may not be reliable as they ought to be. Crumpacker and Allard (1962) explained that such partial failure of certain assumptions will not have much impact on genetic analysis. The results of the present study must be

Table 1. Anova for fibre quality traits in *Gossypium hirsutum* L.

Source of Variation	Degrees of freedom	2.5% span length (mm)	Bundle strength (g/tex)	Micronaire value ($\mu\text{g}/\text{inch}$)	Uniformity ratio (%)	Elongation per cent (%)
Genotypes	80	12.69**	3.82**	0.39**	5.20**	0.52**
Parents	8	22.64**	5.38**	0.36**	4.95**	0.98**
Hybrids	71	9.18**	3.32**	0.39**	5.27**	0.46**
Parents V_s Hybrids	1	182.81**	27.02**	0.19**	1.80*	0.87*
F_1 's	35	10.46**	2.61**	0.37**	5.09**	0.58**
Reciprocals	35	8.05**	3.85**	0.40**	5.28**	0.35*
F_1 vs reciprocals	1	3.95**	9.52**	0.99**	11.65**	0.14
Error	80	0.54	0.28	0.008	0.33	0.19
Total	161	6.616	2.050	0.197	2.771	0.35

**Significant at 1 per cent level

*Significant at 5 per cent level

considered in the light of these limitations (Hayman, 1954; Baker, 1978).

Genetic analysis of fibre quality traits

Genetics of fibre quality traits was evaluated by the calculation of genetic components of variation D, H_1 , H_2 and F (Table 2). All the fibre characters exhibited a significant additive variation (D) at $P < 0.05$ such as 2.5% SL, BS, MIC, UR and EP. This proved that the additive genetic effects are prominent in determination of these characters. Ahmad *et al.* (2003), Iqbal *et al.* (2003) and Haq and Azhar (2004) also investigated the significant value of additive component of variation (D) for these characters. Dominance components (H_1 and H_2) were significant for 2.5% SL, BS, MIC and UR, while EP demonstrated no significance value of both H_1 and H_2 (Table 2). These results showed that inheritance of EP was completely dominated by additive gene action whereas, the expression of 2.5% SL, BS, MIC and UR was determined by additive genetic effects with partial dominance (Ahmad *et al.*, 2003; Iqbal *et al.*, 2003; Basal and Turgut, 2005). The breeding value of line is a function of the additive gene action.

The additive genes are directly transported from the parents to the offspring, are responsible for the resemblance between relatives and it can be used to calculate inheritance (Falconer, 1989). Predominance of additive effects (D) in the genetic mechanism EP advocated that the genes for the characters are fixed

and the traits could be improved via selection by exploiting pedigree method right from F_2 generation. Similarly, higher values of H_1 and H_2 over D suggested the preponderance of dominant genes for 2.5% SL, BS, MIC and UR which revealed out that the variation in these parameters was controlled by genes having dominant effects at most of the loci and manipulation of the parents may be useful through exploitation of heterosis for improving these quality attributes.

(a). Average degree of dominance : $(H_1/D)^{1/2}$

The dominance additive ratio indicates the degree of dominance ($H_1/D^{1/2}$). The value of degree of dominance ($H_1/D^{1/2}$) for EP (0.40) was less than unity which confirmed the contribution of additive genes in the heritage of these characters (Table 2). However, the values of $H_1/D^{1/2}$ for 2.5% SL (1.18), BS (1.12), MIC (1.14) and UR (1.63) demonstrated the prevalence of dominant genes in the genetic control of these characters and this was well supported by higher values of dominant components over the additive ones for these quality characters. Dominance additive ratio of less than one refers to partial dominance, nearer to one indicates complete dominance and greater than one indicates over dominance (Falconer, 1989). Thus the degree of dominance for 2.5% SL, BS, MIC and UR was greater than one indicating the effect of over dominance in the genetics of these parameters (Ahmad *et al.*, 2003).

Table 2. Components of variations for quantitative traits in cotton

Components	2.5% span length	Bundle strength	Micronaire value	Uniformity ratio	Elongation per cent
t^2 value	0.03	1.28	0.59	0.72	1.68
b-0/SE	3.70**	4.08**	5.72**	1.31	9.17**
1-b/SE	0.65	-0.23	-0.17	2.54*	-0.83
V_0L_0	11.321	2.691	0.181	2.475	0.490
V_1L_1	4.361	1.132	0.091	1.363	0.131
W_0L_{01}	3.152	0.908	0.075	0.341	0.173
D	11.01±1.12*	2.54±0.28*	0.17±0.01*	2.29±0.52*	0.40±0.02*
H_1	15.30±2.46*	3.17±0.62*	0.23±0.03*	6.04±1.14*	0.06±0.04
H_2	11.35±2.12*	2.67±0.53*	0.18±0.02*	4.28±0.98*	0.06±0.03
F	9.56±2.61*	1.51±0.65*	0.05±0.03	3.29±1.21*	0.14±0.04*
h^2	35.99±1.42*	5.28±0.36*	0.04±0.02*	0.28±0.66	0.13±0.02*
E	0.31±0.35	0.15±0.09	0.004±0.005	0.19±0.16	0.09±0.01*
$(H_1/D)^{1/2}$	1.18	1.12	1.14	1.63	0.40
$H_2/4H_1$	0.19	0.21	0.20	0.18	0.25
K_D/K_r	2.17	1.73	1.31	2.60	2.64
h^2/H_2	3.17	1.98	0.20	0.07	2.12
h^2 ns	46.15	48.34	64.75	23.17	53.06

(b). Proportion of genes with positive and negative effects : $H_2/4H_1$

Asymmetrical distribution of dominant genes for all the traits was confirmed by unequal estimates of H_1 and H_2 which was soundly supported by the value of $H_2/4H_1$ for 2.5% SL (0.19), BS (1.12), MIC (1.14) and UR (1.63) (Ahmad *et al.*, 2003; Iqbal *et al.*, 2003; Basal and Turgut, 2005). Khan and Hassan (2011) and Raza *et al.* (2013) also reported similar results for 2.5% span length. The value of $H_2/4H_1$ was 0.25 for elongation per cent, this was due to the fact that dominant genes would be in equal proportions (Singh and Chaudary, 1985).

(c). Relative frequency of dominant to recessive alleles

The F value which is an estimate of the relative frequency of dominant to recessive alleles in the parental lines was positive for all the five fibre quality traits, revealing the excess of dominant alleles present in genetic material (e.g. Suraj, Surabhi, Khandwa 2, Anjali, KC 2, KC 3, MCU 5, MCU 7 and G.Cot 16) in which these characters were evaluated and the claim was strengthened by values of $\{K_D/K_r : (4DH_1)^{0.5} + F/(4DH_1)^{0.5} - F\}$ which was greater than one. Similar results was previously obtained by Khan and Hassan (2011).

(d). Heritability : h^2

The lack of significance for component h^2 for UR (0.28 ± 0.66) illustrated that dominance was not unidirectional except 2.5% SL (35.99 ± 1.42), BS (5.28 ± 0.36), MIC (0.04 ± 0.02) and EP (0.13 ± 0.02) which displayed significant h^2 value resulting in unidirectional type of dominance and suggesting that heterosis breeding could be rewarding for these traits (Iqbal *et al.*, 2003; Ahmad *et al.*, 2003). Significant environmental component (E) for EP (0.09 ± 0.01) indicated that this trait was highly affected by environmental conditions (Rahman *et al.*, 2007).

(e). Narrow sense heritability : h^2 n.s

Narrow sense heritability measures the extent of correspondence between breeding values and phenotypic values and expresses the magnitude of genotypic variance in the population, which is mainly responsible for changing the genetic composition of the population via selection (Falconer, 1989; Dabholkar, 1992). Estimates of narrow sense heritability showed a low heritability for UR (23.17) whereas, 2.5% SL (46.15), BS (48.34) and EP (53.06) showed a moderate heritability. Micronaire value exhibited the high heritability with 64.75%. High estimates of heritability in narrow sense represented fixable and additively

heritable variation, which indicated that selection response should be rapid for these characters. These results were in correspondence with those of Basal and Turgut (2005).

In the present study analysis of variance had showed highly significant differences due to genotypes for all the fibre traits indicating the presence of sufficient variability in the experimental materials which made the diallel analysis practical. Additive genes coupled with moderate narrow sense heritability were involved in the heritage of EP while the expression of 2.5% SL, BS, MIC and UR was determined by additive genetic effects with partial dominance. Full sib or half sib family selection, pedigree and progeny test would probably be necessary to achieve the genetic progress for EP, while heterosis breeding could be fruitful for improvement of 2.5% SL, BS, MIC and UR. The presence of additive genetic effects for traits may be helpful to cotton breeders. It reveals out a good index of heritability and it is transmitted from parents to offsprings.

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