STUDIES ON HETEROSIS, COMBINING ABILITY AND GENE ACTION FOR FIBRE CHARACTERS, YIELD AND ITS COMPONENTS IN INTRA AND INTERSPECIFIC HYBRIDS OF UPLAND COTTON (*Gossypium sp.*)

By

PATIL HANUMANT VAMANRAO
M.Sc. (Agri.)

DISSERTATION

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VASANTRAO NAIK MARATHWADA KRISHI
VIDYAPEETH, PARBHANI - 431 402 (M.S.) INDIA

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DECLARATION OF CANDIDATE

I hereby declare that this dissertation or part

thereof has not been previously

submitted by me to any other

University or Institution

for a degree or

diploma

Place : Parbhani

Date : 17/04/2015

(H.V. PATIL)

Dr. D.B. Deosarkar,
M.Sc. (Agri.), Ph.D.
Head,
Department of Agril. Botany,
Vasantrao Naik Marathwada Krishi Vidyapeeth,
Parbhani-431 402

CERTIFICATE - I

This is to certify that Shri. **PATIL HANUMANT VAMANRAO** has satisfactorily prosecuted his course and research for a period not less than four semesters and that the dissertation entitled **"STUDIES ON HETEROSIS, COMBINING ABILITY AND GENE ACTION FOR FIBRE CHARACTERS, YIELD AND ITS COMPONENTS IN INTRA AND INTERSPECIFIC HYBRIDS OF UPLAND COTTON (*Gossypium sp.*)"** submitted by him the result of original research work and is of sufficiently high standard to warrant is presentation to the examination.

I also certify that the dissertation or part there of has not been previously submitted by him for a degree of any University.

Place : Parbhani
Date : 17.4.15

(D.B. Deosarkar)
Research Guide

CERTIFICATE - II

This is to certify that the dissertation entitled "**STUDIES ON HETEROSIS, COMBINING ABILITY AND GENE ACTION FOR FIBRE CHARACTERS, YIELD AND ITS COMPONENTS IN INTRA AND INTERSPECIFIC HYBRIDS OF UPLAND COTTON (*Gossypium sp.*)**" submitted by **PATIL HANUMANT VAMANRAO** to the Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani in partial fulfillment of the requirements for the degree of **DOCTOR OF PHILOSOPHY (Agriculture)** in the subject of **AGRICULTURAL BOTANY (Genetics and Plant Breeding)** has been approved by the student's Advisory Committee after viva-voce examination in collaboration with the external examiner.

(R.S. Nandanwar)
External Examiner

(D.B. DEOSARKAR)
Research Guide

Advisory Committee Member

(B.D. BORADE)

(H.V. KALPANDE)

(S.P. MEHTRE)

(Md. ASMATUDDIN)

Associate Dean and Principal (P.G.)
College of Agriculture,
V.N.M.K.V., Parbhani 431 402

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LIST OF ABBREVIATIONS

%	:	Per cent
ANOVA	:	Analysis of variance
BC_1	:	Back cross generation of parent 1
BC_2	:	Back cross generation of parent 2
C.D.	:	Critical difference
cm	:	Centi meter
CMS	:	Cytoplasmic Male Sterile
Cov. (F.S)	:	Covariance of Full Sibs
Cov. (H.S)	:	Covariance of Half Sibs
d.f.	:	Degrees of Freedom
DRR	:	Directorate of Rice Research
et al.	:	and others
F_1	:	First filial generation
F_2	:	Second filial generation
Fig.	:	Figure
g	:	gram
GA	:	Genetic advance
gca	:	General combining ability
GCV	:	Genotypic coefficient of variation
h^2	:	Heritability in broad sense
ha	:	Hectare
K	:	Selection differential
kg	:	Kilo gram
L x T	:	Line x Tester
MS	:	Mean Sum of Square
No.	:	Number
P_1	:	Parent 1

P_2	:	Parent 2
PCV	:	Phenotypic coefficient of variation
RBD	:	Randomized Block Design
sca	:	Specific combining ability
SE	:	Standard Error
viz.,	:	namely
vs.	:	versus
X^2	:	Chi-square
σ^2e	:	Environmental variance
σ^2g	:	Genotypic variance
σ^2p	:	Phenotypic variance
σp	:	Phenotypic standard deviation

Introduction

CHAPTER-I

INTRODUCTION

Cotton (*Gossypium species*) is the world's most utilized natural textile fibre crop. This genus comprises about 50 diploid and tetraploid species (Fryxell *et al.,* 1984). Two tetraploid species *G. hirsutum* and *G. barbadense* accounts for 90 % and 5 %, respectively, of the world's cotton production (Wendel *et al.,* 1992). It is also one of the most important cash crop of India, which accounts for 60 % of total foreign exchange earnings through export of lint and value added cotton products. It provides raw material to domestic cotton industry comprising 503 textile mills, 1139 ginning factories and over 1000 oil expelling units. It plays a key role in the national economy in terms of contribution in industrial activities, employment and foreign exchange earnings in India.

Cotton is one of the principal commercial crop of India. World cotton production was estimated 116.7 million bales in 2013-14 which is 5 % less than the previous year 2012-13 as a result of 3.5 % decrease in the area and 2 % decrease in the productivity. India continued to maintain the largest area under cotton and second largest producer of cotton next to China. India reported 35.29 % area and 24 % of world production. China, India, USA and Pakistan are the major cotton producing countries in the world with the share of 75 % and 71 % of the world cotton production and area, respectively. India is the largest cotton growing country in the world (11.700 million ha) followed by China (5.050 million ha). India also sustained the position of being the second largest consumer and exporter of cotton and is expected to export 7.5 million bales and expected to consume 23 million bales in 2013-14. Among the major cotton growing countries, Australia ranks top in productivity level of 2151 kg lint/ha followed by Turky (1484 kg lint/ha), Brazil (1465 kg lint/ha) and China (1380 kg lint/ha) (Annual Report of AICCIP, 2013-14).

In India, there was decrease in area (3.5%) in 2013-14 as compared to previous year, but there was increase in cotton area in states like Gujarat, Karnataka and Punjab compared to previous year. As regards cotton production, the scintillating cotton production achieved in 2013-14 (112.80 lakh bales) by Gujarat with increase of 25% over last year. Cotton production increased in Maharashtra from 73.25 lakh bales (2012-13) to 75.25 lakh bales (2013-14) and in Marathwada from 20.23 lakh bales (2012-13) to 32.54 lakh bales (2013-14). The production in India increased from 365 lakh bales (2012-13) to 375 lakh bales (2013-14). The realized enhancement in the production level was possibly due to favorable late season rainfall due to which extra pickings were possible (Annual Report of AICCIP, 2013-14).

Cotton has its reputation as 'King of fibres' due to its inherent properties. It belongs to genus *Gossypium* under tribe *Gossypiene* of family *Malvaceae*. There are two diploid (2n = 26) cultivated species *viz*., *G. arboreum* and *G. herbaceum* indigenous to Asia and Africa and popularly known as desi cotton. Two cultivated tetraploid (2n = 52) species are *G.hirsutum* and *G.barbadense* initially introduced in India during the 17^{th} and 18^{th} centuries A.D (Simpson, 1954). It includes annuals and perennials. Cultivated cottons are annuals, bushy in habit growing to a height of 1-2 meters. The leaves are palmately lobed; flowers are funnel shaped. Petals are creamy white, yellow or red in colour. About 50 wild species of cotton are spread in five geographical regions *viz.*, America, Australia, Africa, Asia and Arabia.

In India, all these four species are under cultivation *G. hirsutum* covers about 80 % of the area followed by *G. arboreum* and *G. herbaceum* to a tune of 19 % area, however, the share of *G. barbadense* is comparatively negligible. Among the wild species, four species are tetraploids (*G. darwinii, G. tomentosum, G. lanceolatum,* and *G. mustelinum)* and rest are diploids. The wild species are grouped into seven diploid genomes i.e. A to G and polyploid genome designated as 'AD'. The first commercial hybrid in the cotton crop was developed in India at Surat by Dr. C. T. Patel (H4, intra *hirsutum* in 1971). More than 200 varieties and hybrids were evolved in the subsequent five decades. Hybrids occupy more than 80 % of cotton crop in India.

Genetic improvement has been hampered by the association of poor fibre properties with high yields and a lack of knowledge about genes that affect fibre properties. Generally, the female parental lines had higher additive effects for lint yield and lint percentage however, these females generally had lower additive effects for fibre strength. Significant effects widely existed among parents and F_2 populations for lint percentage, boll weight and fibre strength. Improvement in cotton fibre quality and lint yield remained challenging for cotton breeders. Many of the current high yielding, commercial upland cotton cultivars do not possess the fibre quality desired by the textile industry. One of the way to improve fibre quality of *G. hirsutum* is to transfer genes from *G. barbadense* (Mc Carty *et al.*, 2004).

Cotton production in the country has registered marked improvement in recent decades however, yield levels of hybrids appeared to have reached stagnation. One of the important reasons attributed to this is the lack of systematic efforts to improve parents for combining ability and develop new hybrids on such new high combiner lines. Among the interspecific (*G. hirsutum* x *G. barbadense*) and intraspecific (*G. hirsutum* x *G. hirsutum*) hybrids being cultivated in India; the interspecific hybrids assume special status owing to extra long staple of the fibre produced by them. Extra long staple cotton fetches high price in domestic and international market. The hybrids like DCH 32 and Varlakshmi have shown receding popularity because of their inherent susceptibility to biotic stresses and lack of ability to cope up with the changing needs of cotton growers. To overcome this decline in productivity in interspecific hybrids, it is necessary to develop and utilize potential *hirsutum* and *barbadense* lines. In the present study, it is decided to evaluate interspecific and intraspecific hybrid combinations based on *G. hirsutum* and *G. barbadense* lines.

In hybridization programme, development of new varieties/hybrids with high yield and better fibre properties is the primary objective of all cotton breeding projects. The first step in successful breeding programme is to select appropriate parents. Line x Tester analysis provides a systematic approach for detection of appropriate parents and crosses in terms of investigated traits. This method was applied to improve self and cross-pollinated plants (Kempthorne, 1957).

To mould the genetic base of a crop, estimation of gene action, relative magnitude of genetic variance and combining ability estimates are essential. Combining ability analysis helps in selection of parents and appropriate breeding strategy to achieve the objectives quickly in a reliable manner. Breeding strategy in turn depends on the gene action involved in that particular cross to get a desirable genotype. Generation mean analysis (Hayman, 1958) gives a comprehensive picture of gene action controlling the trait based on first degree statistics. Some researchers like Sandhu and Nittal (1988) studied two *G. arboreum* crosses and reported absence of non-allelic interaction in six parameter model while three parameter models predicted the presence of epistasis for seed cotton yield per plant.

Keeping in view the different points presented above, the present investigation was undertaken with the following objectives.

1. To estimate the magnitude of heterosis and combining ability of hybrids over parents for fibre quality and yield traits
2. To study the nature and magnitude of gene action involved in expression of fibre quality and yield characters by generation mean analysis
3. To study correlation and path analysis

Review of Literature

CHAPTER-II

REVIEW OF LITERATURE

Cotton is the world's most important cultivated fibre crop and second important edible oil source which has gained the status of an industry rather than a mere crop. Cotton crop belong to genus *Gossypium* that consists of 50 species. Out of these, four species are cultivated *viz., G. arboreum* L., *G. herbaceum* L., *G. hirsutum* L., and *G. barbadense* L. The former two diploid species are indigenous or Asiatic cottons and the other two are tetraploids, *G. hirsutum* is American cotton, while *G. barbadense* is Egyptian cotton. Though, the use of cotton fabrics was known as early as 3000 BC, cotton was relatively unimportant as a textile fibre until 16th century AD in major parts of world compared to linen, wool and silk. It was only after the industrial revolution in England during which cotton usage has spread faster. The cotton was introduced into India in mid 18th century and by 1950 the American cotton *Gossypium hirsutum* got acclimatized and established in about 20 % of the area. The economy of countries like India is trapped in improved yield, quality and production of cotton. So, the objective of a breeding programme is high seed cotton yield with better fiber proparties.

A brief review of the literature related to the present study is presented on the following heads.

2.1 Variability , heritability and genetic advance

2.2 Combining ability

2.3 Heterosis

2.4 Correlation

2.5 Path analysis

2.6 Generation mean analysis

2.1 Variability, heritability and genetic advance

2.1.1 Variability

The information on the nature and magnitude of variability of different quantitative and qualitative traits in any crop species plays a vital role while formulating the efficient breeding programmes. Superior genotypes can be isolated by selection if considerable genetic variation exists within the population. Besides genetic variability, heritability and genetic advance also play a vital role in the improvement of any character. The progress in breeding for the economic traits, which are mostly polygenically controlled and environmentally influenced, is determined by the nature and magnitude of their genotypic variability. Hence, it is essential to partition the overall variability into heritable and non-heritable components with the help of genetic parameters like genotypic and phenotypic coefficients of variation, heritability and genetic advance. The magnitude of heritability on one hand, and nature and extent of variability on the other hand gives an idea for effective genetic improvement through selection.

The available literature on variability studies in cotton is furnished in Table 1.

Table 1. Review of literature on genetic variability for different characters in cotton

Sr. No.	Character	Wider genetic variability	Narrow genetic variability
1	Days to 50 % flowering	Patil and Mathapati (1976)	Bavaji *et al.* (1989) Siddiqui (1996) Sumathi and Nadarajan (1996) Murthy (1997) Sangeetha (1998) Narisireddy and Ratnakumari (2004a) Kale *et al.* (2006) Preetha and Raveendran (2007) Sundas *et al.* (2010) Kancherla (2011) Kulkarni *et al.* (2011) Mendez-Natera *et al.* (2012)
2	Number of monopodia per plant	Singh *et al.* (1972) Singh (1993) Murthy (1997) Sangeetha (1998) Tuteja *et al.* (2004) Kumari and Chamundeshwari (2005) Kausik and Kapoor (2006) Sundas *et al.* (2010) Sabir *et al.* (2010) Patnaik and Sial (2010) Lal and Singh (2012)	Singh *et al.* (1978 a) Gite *et al.* (2007) Kulkarni *et al.* (2011) Kancherla (2011)

Table 1. Contd…

Sr. No.	Character	Wider genetic variability	Narrow genetic variability
3	Number of sympodia per plant	Singh *et al.* (1972) Singh *et al.* (1978 a) Reddy *et al.* (1991) Sumathi and Nadarajan (1996) Tuteja *et al.* (2004) Sundas *et al.* (2010) Mendez-Natera *et al.* (2012)	Naidu and Katarki (1968) Khorgade and Ekbote (1981) Murthy (1997) Sangeetha (1998) Rao and Reddy (2001) Kale *et al.* (2006) Gite *et al.* (2007) Singh *et al.* (2009) Soomro *et al.* (2010) Kulkarni *et al.* (2011) Kancherla (2011)
4	Plant height	Kale *et al.* (2006) Singh *et al.* (2009) Khan *et al.* (2009) Soomro *et al.* (2010) Sabir *et al.* (2010) Kulkarni *et al.* (2011)	Singh *et al.* (1987a)
5	Days to maturity	Pandey *et al.* (2002) Kale *et al.* (2006) Sundas *et al.* (2010)	
6	Boll weight	Dhanda *et al.* (1987) Boder *et al.* (1988) Krishnarao and Mary (1990) Rajarathinum *et al.* (1993) Singh *et al.* (1994) Sumathi and Nadarajan (1996) Jagtap and Mehetre (1998) Rao and Reddy (2001) Ahmad *et al.* (2003) Narisireddy and Ratnakumari (2004a) Kale *et al.* (2006) Preetha and Raveendran (2007) Khan *et al.* (2009) Singh *et al.* (2009) Patnaik and Sial (2009) Patnaik and Sial (2010) Soomro *et al.* (2010) Kancherla (2011) Lal and Singh (2012)	Murthy (1997) Pandey *et al.* (2002) Gite *et al.* (2007)

Table 1. Contd...

Sr. No.	Character	Wider genetic variability	Narrow genetic variability
7	Number of bolls per plant	Singh *et al.* (1987a) Boder *et al.* (1988) Krishnarao and Mary (1990) Singh *et al.* (1994) Murty *et al.* (1995) Sumathi and Nadarajan (1996) Murthy (1997) Jagtap and Mehetre (1998) Murty *et al.* (1999) Rao and Reddy (2001) Ahmad *et al.* (2003) Baloch (2004) Kausik and Kapoor(2006) Murty and Chamundeswari (2006) Preetha and Raveendran (2007) Singh *et al.* (2009) Sabir *et al.* (2010) Kancherla (2011) Kale *et al.* (2006) Sundas *et al.* (2010)	Khoragade and Ekbote (1981) Sethi and Singh (1984) Gite *et al.* (2007) Mendez-Natera *et al.* (2012)
8	Ginning percentage	Patil and Mathapati (1976)	Dhonda *et al.* (1987) Singh *et al.* (1987a) Bavaji *et al.* (1989) Krishnarao and Mary (1990) Sumathi and Nadarajan (1996) Murthy (1997) Jagtap and Mehetre (1998) Rao and Reddy (2001) Pandey *et al.* (2002) Ahmad *et al.* (2003) Kale *et al.* (2006) Preetha and Raveendran (2007) Kancherla (2011)

Table 1. Contd…

Sr. No.	Character	Wider genetic variability	Narrow genetic variability
9	Micronaire value	Dhanda *et al.* (1987) Avtar *et al.* (1993) Rao and Reddy (2001)	Krishnarao and Mary (1990) Nadarajan and Sreerangaswamy (1990) Rajarathinam *et al.* (1993) Sangeetha (1998) Kumar *et al.* (2000) Kancherla (2011)
10	Fibre length	Baloch (2004) Kale *et al.* (2006) Ali *et al.* (2009) Sabir *et al.* (2010)	Akhtar *et al.* (2008)
11	Uniformity ratio	Baloch (2004) Ali *et al.* (2009)	Preetha and Raveendran (2007) Kancherla (2011)
12	Fibre strength	Singh (1982) Avtar *et al.* (1993)	Rajarathinam *et al.* (1993) Sangeetha (1998) Kumar *et al.* (2000) Rao and Reddy (2001) Preetha and Raveendran (2007) Akhtar *et al.* (2008) Ali *et al.* (2009) Kulkarni *et al.* (2011) Kancherla (2011)
13	Seed cotton yield per plant	Singh *et al.* (1987a) Boder *et al.* (1988) Krishnarao and Mary (1990) Rajarathinam *et al.* (1993) Singh *et al.* (1994) Murty *et al.* (1995) Sumathi and Nadarajan (1996) Murthy (1997) Jagtap and Mehetre (1998) Ahuja and Tuteja (2000) Rao and Reddy (2001) Ahmad *et al.* (2003) Baloch (2004) Kumari and Chamundeshwari (2005) Murthy and Chamundeshwari (2005)	Gite *et al.* (2007)

Table 1. Contd...

Sr. No.	Character	Wider genetic variability	Narrow genetic variability
		Preetha and Raveendran (2007) Khan *et al.* (2009) Singh *et al.* (2009) Patnaik and Sial (2009) Patnaik and Sial (2010) Kancherla (2011) Lal and Singh (2012)	
14	Seed cotton yield qtl. / ha.	Patnaik and Sial (2009) Khan *et al.* (2009) Patnaik and Sial (2010)	

2.1.2 Heritability and Genetic advance as per cent of mean

Heritability is determined as the ratio of additive genetic component of variance to total phenotypic variance. Heritability measures the relative amount of the heritable portion of the variability, while the genetic advance helps to measure the amount of progress that could be expected with selection in a character. Estimates of heritability along with estimates of genetic advance are more useful in choice of selection method rather than heritability or genetic advance alone (Johnson *et al.*, 1955). High heritability is not always an indication of higher genetic gain (Swarup and Chaugale, 1962), whereas, high heritability coupled with high genetic advance indicates that the improvement could be made for a character by simple selection on phenotypic performance.

The available literature on heritability and genetic advance is presented in Table 2.

Table 2. Review of literature on heritability (h^2) and genetic advance (GA) for different characters in cotton

Sr. No	Character	High heritability and High genetic advance	High heritability and Low genetic advance	Low heritability and High genetic advance	Low heritability and Low genetic advance
1	Days to 50% flowering	Patil and Mathapati (1976) Singh and Singh (1981) Bindupriya (2008)	Patil and Chopde (1983) Jagtap and Kolhe (1987) Jagtap and Mehetre (1998) Sangeetha (1998) Preetha and Raveendran (2007) Kancherla (2011)		Sumathi and Nadarajan (1996) Kulkarni *et al.* (2011)
2	Number of monopodia per plant	Singh and Singh (1981) Sethi and Singh (1984) Murthy (1997) Tuteja *et al.* (2004) Kausik and Kapoor (2006) Patnaik and Sial (2010) Sundas *et al.* (2010) Lal and Singh (2012)		Kale *et al.* (2006)	Ahmed *et al.* (2006) Kancherla (2011)
3	Number of sympodia per plant	Sethi and Singh (1984) Sumathi and Nadarajan (1996) Sangeetha (1998) Valarmathi and Jehangir (1998a) Sundas *et al.* (2010)	Singh *et al.* (1978a) Doss and Kadambavanasundaram (1993) Ahmed *et al.* (2006) Kale *et al.* (2006) Kancherla (2011)		Rao and Reddy (2001) Kumari and Chamundeshwari (2005) Singh *et al.* (2009) Patnaik and Sial (2010) Kulkarni *et al.* (2010)
4	Plant height	Tuteja *et al.* (2004) Kulkarni *et al.* (2011)	Kausik and Kapoor (2006) Bindupriya (2008)		
5	Days to maturity		Bindupriya (2008) Kulkarni *et al.* (2011)		

Table 2. Contd…

Sr. No	Character	High heritability and High genetic advance	High heritability and Low genetic advance	Low heritability and High genetic advance	Low heritability and Low genetic advance
6	Boll weight	Singh *et al.* (1987a) Krishnarao and Mary (1990) Tiwari *et al.* (1992) Rajarathinam *et al.* (1993) Chhabra *et al.* (1995) Sumathi and Nadarajan (1996) Murthy (1997) Jagtap and Mehetre (1998) Sangeetha (1998) Valarmathi and Jehangir (1998a) Rao and Reddy (2001) Narisireddy and Ratnakumari (2004a) Kancherla (2011)	Singh and Singh (1981) Singh *et al.* (1994) Ahmed *et al.* (2006)		Ahmed *et al.* (2006)
7	Number of bolls per plant	Krishnarao and Mary (1990) Tiwari *et al.* (1992) Rajarathinam *et al.* (1993) Singh *et al.* (1994), Chhabra *et al.* (1995) Sumathi and Nadarajan (1996) Murthy (1997) Jagtap and Mehetre (1998) Valarmathi and Jehangir (1998a) Rao and Reddy (2001) Ahmed *et al.* (2006) Preetha and Raveendran (2007) Kumari *et al.* (2010), Kancherla (2011)	Doss and Kadambavanasundaram (1993)	Singh *et al.* (1987a)	

Table 2. Contd…

Sr. No	Character	High heritability and High genetic advance	High heritability and Low genetic advance	Low heritability and High genetic advance	Low heritability and Low genetic advance
8	Ginning percentage	Krishnarao and Mary (1990) Sangeetha (1998) Valarmathi and Jehangir (1998a)	Doss and Kadambavanasundaram (1993) Singh *et al.* (1994) Chhabra *et al.* (1995) Sumathi and Nadarajan (1996) Jagtap and Mehetre (1998) Sankarapandian *et al.* (1998) Rao and Reddy (2001) Kancherla (2011)		
9	Micronaire value	Krishnarao and Mary (1990) Nadarajan and Sreerangaswamy (1990) Avtar *et al.* (1993) Rajarathinam *et al.* (1993) Rao and Reddy (2001) Kancherla (2011)	Ahmed *et al.* (2006)		
10	Fibre length	Baloch *et al.* (2004)	Bindupriya (2008)		
11	Uniformity Ratio		Baloch (2004) Preetha and Raveendran (2007) Kancherla (2011)		
12	Fibre strength	Avtar *et al.* (1993) Valarmathi and Jehangir (1998a) Kancherla (2011)	Rajarathinam *et al.* (1993) Rao and Reddy (2001)		

Table 2. Contd...

Sr. No	Character	High heritability and High genetic advance	High heritability and Low genetic advance	Low heritability and High genetic advance	Low heritability and Low genetic advance
13	Seed cotton yield per plant	Krishnarao and Mary (1990) Doss and Kadambavanasundaram (1993) Singh *et al.* (1994) Murthy *et al.* (1995) Sumathi and Nadarajan (1996) Jagtap and Mehetre (1998) Sankarapandian *et al.* (1998) Ahuja and Tuteja (2000) Rao and Reddy (2001) Baloch (2004) Kumari and Chamundeshwari (2005) Ahmed *et al.* (2006) Kale *et al.* (2006) Preetha and Raveendran (2007) Kumari *et al.* (2010) Kancherla (2011)		Jain (1986)	Jain *et al.* (1984) Jain (1986)
14	Seed cotton yield qtl. / ha.	Patnaik and Sial (2009) Patnaik and Sial (2010)			

2.2 Combining ability

In any hybridization programme, identification and selection of superior parental lines is required to construct genetically diverse and potentially rewarding germplasm by gathering fixable gene effects more or less in a homozygous line. Combining ability describes the breeding value of parental lines to produce hybrids and it is also used for characterizing the nature and magnitude of gene action involved in the expression of quantitative traits.

The concept of combining ability has been proposed by Sprague and Tautum (1942) which measures the gene action. It was stated that general combining ability (GCA) effects is the average performance of a parent in combination with all other parents; whereas specific combining ability (SCA) effects are the deviation of the performance of two parents in a particular hybrid combination from that of expected from GCA effect of each parent. GCA effects reflect performance of parental line in combination with all other lines, so parent with the highest GCA effects should have greater impact on trait improvement. Specific combining ability effects identify the best hybrid combinations. The knowledge of various types of gene actions and their relative magnitude in controlling the trait is important in deciding proper breeding techniques (Miller *et al.,* 1980). Differences in general combining ability have been attributed to additive, additive x additive and higher order additive interactions, whereas, differences in specific combining ability have been attributed to non-additive genetic variance (Falconer, 1996).

Arunachalam (1974) emphasized that the combining ability analysis is operated with feasible and practical assumptions and hence more realistic. This model estimates the variance due to general combining ability and specific combining ability provides the diagnosis of predominant role of additive and non-additive gene action. The general combining ability and specific combining ability effects will help to locate the parents and crosses that are helpful in establishing a particular type of gene action.

Information concerning the different types of gene action, relative magnitude of genetic variance and combining ability estimates are significant structures to shape the genetic makeup of a crop. Biometrical estimation of genetic parameters governing yield and yield components in cotton revealed the importance of the both additive and dominant gene effects, their relative importance varying from character to character and material to material. Though, extensive studies have been made on the inheritance of yield and its components in cotton, knowledge on genetic basis of every breeding material is essential for devising suitable breeding programme. This information could prove important to the cotton breeders to develop a strategy in the screening of better parental combinations for further enhancement.

The review of literature on gene action governing the inheritance of fibre quality, yield and yield component characters is summarized and presented in Table 3.

Table 3. Review of literature on gene action governing different traits in cotton

Sr. No.	Character	Additive	Non-additive	Additive and Non-additive
1	Days to 50 % flowering	Bhandari (1980) Rao (1982) Jagtap and Kolhe (1993) Rao (1997) Kumaresan *et al.* (2000) Saravanan *et al.* (2003)	Jagtap and Kolhe (1987) Jagtap (1994) Narisireddy and Satyanarayana (2004) Muthu *et al.* (2005) Subramanian *et al.* (2005) Ahuja and Dhayal (2007) Preetha and Raveendran (2008) Kancherla (2011)	Patil and Chopde (1983) Bhatade *et al.* (1994) Shunmugavalli and Vijendradas (1995) Basha (1997) Murthy and Ranganathacharyulu (1998) Laxman and Ganesh (2003)
2	Number of monopodia per plant	Kalsy *et al.* (1981) Nirania *et al.* (1993) Gauder *et al.* (1996) Jagtap and Mehetre (1996) Murthy and Ranganathacharyulu (1998) Nimbalkar *et al.* (2004)	Bhandari (1980) Rao (1982) Laxman and Ganesh (2003) Narisireddy and Satyanarayana (2004) Ahuja and Dhayal (2007) Kancherla (2011)	Shunmugavalli and Vijendradas (1995) Basha (1997) Laxman and Ganesh (2003) Rauf *et al.* (2006)
3	Number of sympodia per plant	Bhandari (1980) Kalsy *et al.* (1981) Rao (1982) Nirania *et al.* (1993) Jagtap and Mehetre (1996)	Surana *et al.* (1996) Murthy and Ranganathacharyulu (1998) Valarmathi and Jehangir (1998b) Punitha *et al.* (1999b) Laxman and Ganesh (2003) Iqbal *et al.* (2003a) Narisireddy and Satyanarayana (2004) Ahuja and Dhayal (2007) Preethe and Raveendran (2008) Ravikumar *et al.* (2010) Kancherla (2011)	Bhatade *et al.* (1994) Basha (1997) Murthy and Ranganathacharyulu (1998) Rauf *et al.* (2006) Iqbal *et al.* (2007)

Table 3. Contd…

Sr. No.	Character	Additive	Non-additive	Additive and Non-additive
4	Plant height	Tomar and Singh (1992)	Nirania *et al.* (1992) Koodalingam and Ramligamm (1992) Krishnarao (1998) Gul- Hassan *et al.* (1999) Zia-Ul-Islam *et al.* (2001)	
5	Days to maturity		Ahuja and Dhayal (2007)	
6	Boll weight	Singh *et al.* (1978b) Kumar *et al.* (1984) Amalraj and Gawande (1985) Singh and Singh (1985) Bhatade and Sarsar (1993) Jagtap and Kolhe (1993) Jagtap (1994) Murthy *et al.* (1994) Jagtap and Mehetre (1996) Ahmed *et al.* (1997) Hassan *et al.* (1999) Islam *et al.* (2001) Saravanan *et al.* (2003) Rauf *et al.* (2006) Singh *et al.* (2010	Rao (1982) Duhoon *et al.* (1984) Jagtap and Kolhe (1987) Patil *et al.* (1990) Shanti and Selvaraj (1995) Tuteja *et al.* (1996) Murthy and Ranganathacharyulu (1998) Punitha *et al.* (1999b) Subhan *et al.* (2003) Muthu *et al.* (2005) Subramanian *et al.* (2005) Ahuja and Dhayal (2007) Ilyas *et al.* (2007) Ravikumar *et al.* (2010) Kancherla (2011)	Virk and Kalsy (1982) Jagtap and Kolhe (1986) Pavasia *et al.* (1989) Verma *et al.* (1991) Dagaonkar and Malkhandale (1993) Shunmugavalli and Vijendradas (1995) Rao(1997) Murthy and Ranganathacharyulu (1998) Pavasia *et al.* (1998) Valarmathi and Jehangir (1998b) Subhan *et al.* (2002) Laxman and Ganesh (2003) Narisireddy and Satyanarayana (2004) Iqbal *et al.* (2007)

Table 3. Contd...

Sr. No.	Character	Additive	Non-additive	Additive and Non-additive
7	Number of bolls per plant	Kumar *et al.* (1984) Amalraj and Gawande (1985) Bhatade and Sarsar (1993) Jagtap and Kolhe (1993) Nirania *et al.* (1993) Ahmed *et al.* (1997) Valarmathi and Jehangir (1998b) Murthy and Rao (1999) Kumaresan *et al.* (2000)	Singh *et al.* (1978b) Rao (1982) Duhoon *et al.* (1984) Singh and Singh (1985) Jagtap and Kolhe (1987) Patil *et al.* (1990) Verma *et al.* (1991) Jagtap (1994) Shanthi and Selvaraj (1995) Rathore *et al.* (1996) Hassan *et al.* (1999) Soomro *et al.* (2000) Iqbal *et al.* (2003a) Saravanan *et al.* (2003) Rauf *et al.* (2006) Ahuja and Dhayal (2007) Ravikumar *et al.* (2010) Kancherla (2011)	Singh *et al.* (1977) Kalsy *et al.* (1981) Virk and Kalsy (1982) Patil and Chopde (1983) Gupta and Singh (1986) Jagtap and Kolhe (1987) Dagaonkar and Malkhandale (1993) Bhatade *et al.* (1994) Tuteja *et al.* (1996) Rao (1997) Murthy and Ranganathacharyulu (1998) Subhan *et al.* (2002) Laxman and Ganesh (2003) Narisireddy and Satyanarayana (2004) Iqbal *et al.* (2007)

Table 3. Contd…

Sr. No.	Character	Additive	Non-additive	Additive and Non-additive
8	Ginning percentage	Patil and Chopde (1983) Kumar *et al.* (1984) Amalraj and Gawande (1985) Pavasia *et al.* (1989) Verma *et al.* (1991) Gururajan and Basu (1992) Bhatade and Sarsar (1993) Jagtap and Kolhe (1993) Bhatade *et al.* (1994) Pavasia and Shukla (1997) Murthy and Ranganathacharyulu (1998) Pavasia *et al.* (1999a) Islam *et al.* (2001) Iqbal *et al.* (2003a)	Rao (1982) Jagtap and Kolhe (1987) Singh *et al.* (1988) Kalsy *et al.* (1994) Tuteja *et al.* (1996) Valarmathi and Jehangir (1998b) Subramanian *et al.* (2005) Preetha and Raveendran (2008) Ravikumar *et al.* (2010) Singh *et al.* (2010) Kancherla (2011)	Gururajarao *et al.* (1977) Singh *et al.* (1978b) Desai *et al.* (1980) Virk and Kalsy (1982) Deshpande *et al.* (1984) Duhoon *et al.* (1984) Jagtap and Kolhe (1986) Jagtap and Kolhe (1987) Dagaonkar and Malkhandale (1993) Rathore *et al.* (1996) Rao (1997) Murthy and Ranganathacharyulu (1998) Laxman and Ganesh (2003) Neelima *et al.* (2004) Rauf *et al.* (2006) Iqbal *et al.* (2007)
9	Micronaire value	Nadarajan and Sreerangaswamy (1990) Surana *et al.* (1996) Pavasia and Shukla (1997) Mandloi *et al.* (1998) Pavasia *et al.* (1999a) Neelima *et al.* (2004) Subramanian *et al.* (2005) Rauf *et al.* (2006) De Aguiar *et al.* (2007) Karademir *et al.* (2007)	Cheatham *et al.* (2003) Pushpam and Raveendran (2005) Ahuja and Dhayal (2007) Ilyas *et al.* (2007) Basal *et al* .(2009) Singh *et al* .(2010) Saravanan *et al.* (2010) Ravikumar *et al.* (2010) Kancherla (2011)	Rao (1997)

Table 3. Contd…

Sr. No.	Character	Additive	Non-additive	Additive and Non-additive
10	Fibre length	Krishnarao (1998)	Mane and Bhatade (1992) Patel *et al.* (1997) Gul- Hassan *et al.* (1999)	
11	Uniformity ratio	Soomro *et al.* (2000) Neelima *et al.* (2004) De Aguiar *et al.* (2007)	Pushpam and Raveendran (2005) Ahuja and Dhayal (2007) Preetha and Raveendran (2008) Basal *et al.* (2009) Emine and Oktay (2010) Kancherla (2011)	Neelima *et al.* (2004)
12	Fiber strength	Cheatham *et al.* (2003) Iqbal *et al.* (2003a) Subramanian *et al.* (2005) Rauf *et al.* (2006) De Aguiar *et al.* (2007) Karademir *et al.* (2007) Basal *et al.* (2009)	Valarmathi and Jehangir (1998b) Pushpam and Raveendran (2005) Ahuja and Dhayal (2007) Ilyas *et al.* (2007) Emine and Oktay(2010) Ravikumar *et al.* (2010) Saravaran *et al.* (2010) Kancherla (2011)	Neelima *et al.* (2004)

Table 3. Contd…

Sr. No.	Character	Additive	Non-additive	Additive and Non-additive
13	Seed cotton yield per plant	Amalraj and Gawande (1985) Singh and Singh (1985) Gururajan and Basu (1992) Jagtap and Kolhe (1993) Nirania *et al.* (1993) Ahmed *et al.* (1997) Valarmathi and Jehangir (1998b) Murthy and Rao (1999) Ahuja and Dhayal (2007) De Aguiar *et al.* (2007) Karademir *et al* .(2007) Saifullah *et al.* (2009) Singh *et al.* (2010)	Deshpande *et al.* (1984) Jagtap and Kolhe (1987) Singh *et al.* (1988) Patil *et al.* (1990) Verma *et al.* (1991) Bhatade *et al.* (1992) Shanti and Selvaraj (1993) Jagtap (1994) Tuteja *et al.* (1996) Mandloi *et al.* (1998) Punitha *et al.* (1999b) Soomro *et al.* (2000) Islam *et al.* (2001) Subhan *et al.* (2003) Iqbal *et al.* (2003a) Muthu *et al.* (2005) Ahuja and Dhayal (2007) Saravaran *et al.* (2010) Ravikumar *et al.* (2010) Kancherla (2011)	Singh *et al.* (1978b) Kalsy *et al.* (1981) Rao (1982) Patil and Chopde (1983) Kumar *et al.* (1984) Jagtap and Kolhe (1986) Pavasia *et al.* (1989) Nadarajan and Sreerangaswamy (1990) Gururajan and Basu (1992) Dagaonkar and Malkhandale (1993) Kalsy *et al.* (1994) Shunmugavalli and Vijendradas (1995) Rathore *et al.* (1996). Rao (1997) Pavasia *et al.* (1998) Laxman and Ganesh (2003) Narisireddy and Satyanarayana (2004) Rauf *et al.* (2006) Iqbal *et al.* (2007)

2.3 HETEROSIS

Heterosis is the basic tool for the improvement of crops in the form of F_1 hybrids. Shull (1914) first coined the term heterosis and subsequently Whaley (1952) extended the term for increased vigour of the F_1 over the better parent which is now termed as heterobeltiosis. Heterosis refers to the superiority/inferiority of the F_1 hybrid over the mean parental value (mid parent heterosis) or the better parent (heterobeltiosis) or the best commercial hybrid/variety (standard heterosis). The pre-requisites for commercial exploitation of heterosis in cotton are identification of parents which shows good heterosis on crossing and production of hybrid seed with low cost. The magnitude of heterosis provides a basis for genetic diversity and a guide to the choice of desirable parents for developing superior F_1 hybrids; so as to exploit hybrid vigour or for building better gene pools to be employed in population improvement (Potdukhe, 2001).

The development and release of the first intra *hirsutum* hybrid, H_4 (Patel, 1971) and first interspecific (*G.hirsutum* x *G.barbadense*) hybrid, Varalaxmi (Katarki, 1972) revolutionized cotton production in India. In cotton, the earlier studies on heterosis have been mostly confined to yield and its components and relatively little work have been done on heterosis of fibre characters. Since, fibre quality is the ultimate character of economic importance, knowledge of fibre properties is very important. The available literature on heterosis, heterobeltiosis and standard heterosis in cotton is summarized and presented in Table 4.

Table 4. Review of litetature on heterosis over mid parent, better parent and standard checks for different characters in cotton

Sr. No.	Character	Heterosis over mid parent	Heterosis over better parent	Heterosis over Standard check
1	Days to 50 % flowering	Baker and Verhalen (1975) Sangwan and Yadava (1986) Siddiqui and Patil (1994) Basha (1997) Rajput *et al.* (1997) Kumaresan *et al.* (1999) Potdukhe (2002) Natera *et al.* (2007) Ganapathy and Nadarajan (2008) Deosarkar *et al.* (2009) Kancherla (2011)	Jagtap (1994) Vijendradas and Shunmugavalli (1996) Basha (1997) Potdukhe (2001) Natera *et al.* (2007) Siddiqui and Patil (1994) Rajput *et al.* (1997) Ganapathy and Nadarajan (2008) Deosarkar *et al.* (2009) Kancherla (2011)	Rajput *et al.* (1997) Muthu *et al.* (2005) Giri *et al.* (2006) Hemadia (2006) Deosarkar *et al.* (2009) Kancherla (2011)
2	Number of monopodia per plant	Singh and Singh (1982) Singh and Kalsy (1983) Gencer and Kaynak (1994) Basha (1997) Potdukhe (2001) Maisuria *et al.* (2006) Deosarkar *et al.* (2009) Kancherla (2011)	Singh and Singh (1982) Singh *et al.* (1995) Vijendradas and Shunmugavalli (1996) Basha (1997) Doss and Kadambavanasundaram (1997) Ahuja and Tuteja (2000) Potdukhe (2001) Deva *et al.* (2002) Kharde *et al.* (2004) Maisuria *et al.* (2006) Deosarkar *et al.* (2009) Kancherla (2011)	Tuteja *et al.* (1993) Muthu *et al.* (2005) Giri *et al.* (2006) Maisuria *et al.* (2006) Deosarkar *et al.* (2009) Tuteja *et al.* (2011) Kancherla (2011). Kumar *et al.* (2013)

Table 4. Contd...

Sr. No.	Character	Heterosis over mid parent	Heterosis over better parent	Heterosis over Standard check
3	Number of sympodia per plant	Duhoon *et al.* (1983) Rathinavelu and Premasekar (1990) Khadi *et al.* (1993) Gencer and Kaynak (1994) Basha (1997) Babar *et al.* (2001) Panhwar *et al.* (2002) Potdukhe (2002) Maisuria *et al.* (2006) Natera *et al.* (2007) Ganpathy and Nadarajan (2008) Deosarkar *et al.* (2009) Kancherla (2011)	Gencer and Káynak (1994) Singh *et al.* (1995) Basha (1997) Pavasia *et al.* (1999b) Ahuja and Tuteja (2000) Potdukhe (2001) Deva *et al.* (2002) Kharde *et al.* (2004) Maisuria *et al.* (2006) Natera *et al.* (2007) Ganapathy and Nadarjana (2008) Deosarkar *et al.* (2009) Kancherla (2011)	Tuteja *et al.* (1993) Babar *et al.* (2001) Muthu *et al.* (2005) Maisuria *et al.* (2006) Deosarkar *et al.* (2009 Kancherla (2011) Tuteja *et al.* (2013)
4	Plant height (cm)	Potdukhe (2002) Ganapathy and Nadarajan (2008)	Nirania *et al.* (1992) Pavasia *et al.* (1999) Ahuja and Tuteja (2000) Deva *et al.* (2002) Kharde *et al.* (2004) Ganapathy and Nadarajan (2008)	Tuteja *et al.* (1993) Bhatade and Rajeshwar (1994) Muthu *et al.* (2005) Giri *et al.* (2006) Kumar *et al.* (2013)
5	Days to maturity	Deosarkar *et al.* (2009)	Deosarkar *et al.* (2009)	Deosarkar *et al.* (2009)

Table 4. Contd...

Sr. No.	Character	Heterosis over mid parent	Heterosis over better parent	Heterosis over Standard check
6	Boll weight	Duhoon (1990) Nirania *et al.* (1991) Nirania *et al.* (1992) Dagaonkar and Malkhandale (1993) Rajkumari *et al.* (1996) Basha (1997) Sirugappa and Parameshwarappa (1998) Kajjidoni *et al.* (1999) Babar *et al.* (2001) Panhwar *et al.* (2002) Soomro and Baloch (2005) Maisuria *et al.* (2006) Natera *et al.* (2007) Deosarkar *et al.* (2009) Kancherla (2011)	Duhoon *et al.* (1983) Nirania *et al.* (1991) Patil *et al.* (1991) Singh and Singh (1993) Gencer and Kaynak (1994) Vijendradas and Shunmugavalli (1995) Basha (1997) Pavasia *et al.* (1999) Ahuja and Tuteja (2000) Solangi *et al.* (2001) Solangi *et al.* (2002) Ramlingam and Ponnusamy (2003) Kharde *et al.* (2004) Maisuria *et al.* (2006) Natera *et al.* (2007) Deosarkar *et al.* (2009) Kancherla (2011)	Bahtade and Rajeshwar (1994) Rajkumari *et al.* (1996) Babar *et al.* (2001) Muthu *et al.* (2005) Soomro and Baloch (2005) Giri *et al.* (2006) Verma *et al.* (2006) Kancherla (2011) Kumar *et al.* (2013) Tuteja *et al.* (2013)

Table 4. Contd…

Sr. No.	Character	Heterosis over mid parent	Heterosis over better parent	Heterosis over Standard check
7	Number of bolls per plant	Singh and Kalsy (1983) Patil and Chopde (1985) Rathinavelu and Premasekar (1990) Nirania *et al.* (1991) Nirania *et al.* (1992) Dagaonkar and Malkhandale (1993) Gencer and Kaynak (1994) Goudar *et al.* (1996) Basha (1997) Siruguppa and Parameswarappa (1998) Kajjidoni *et al.* (1999) Solangi *et al.* (2001) Ahmad *et al.* (2002) Solangi *et al.* (2002) Ramlingam and Ponnusamy (2003) Deshpande and Baig (2004) Soomro and Baloch (2005) Maisuria *et al.* (2006) Ganapathy and Nadarajan (2008) Pole *et al.* (2008), Deosarkar *et al.* (2009) Kancherla (2011)	Singh and Singh (1982) Duhoon *et al.* (1983) Duhoon (1990) Nirania *et al.* (1991) Patil *et al.* (1991) Singh and Singh (1993) Kalsy *et al.* (1994) Murthy *et al.* (1994) Basha (1997) Murthy *et al.* (1998) Pavasia *et al.* (1999) Ahuja and Tuteja (2000) Babar *et al.* (2001) Ahmad *et al.* (2002) Ramlingam and Ponnusamy (2003) Maisuria *et al.* (2006) Pole *et al.* (2008) Ganapathy and Nadarajan (2008) Deosarkar (2009) Kancherla (2011)	Bhatade and Rajeshwar (1994) Rajkumari *et al.* (1996) Meshram *et al.* (1998) Babar *et al.* (2001) Muthu *et al.* (2005) Soomro and Baloch (2005) Maisuria *et al.* (2006) Giri *et al.* (2006) Deosarkar *et al.* (2009) Tuteja *et al.* (2011) Kancherla (2011) Kumar *et al.* (2013) Tuteja *et al.* (2013)

Table 4. Contd…

Sr. No.	Character	Heterosis over mid parent	Heterosis over better parent	Heterosis over Standard check
8	Ginning percentage	Gururajarao *et al.* (1977) Singh and Singh (1982) Dani (1984) Singh *et al.* (1987b) Nirania *et al.* (1991) Gencer and Kaynak (1994) Kalsy *et al.* (1994) Patel *et al.* (1996) Basha (1997) Patel *et al.* (1998) Solangi *et al.* (2001) Solangi *et al.* (2002) Ganapathy *et al.* (2005) Maisuria *et al.* (2006) Kancherla (2011)	Gangneja (1968) Singh and Singh (1982) Duhoon *et al.* (1983) Dani (1984) Patil and Thombre (1990) Nirania *et al.* (1991) Jagtap (1994) Kalsy *et al.* (1994) Basha (1997) Kajjidoni *et al.* (1999) Pavasia *et al.* (1999b) Solangi *et al.* (2001) Solangi *et al.* (2002) Maisuria *et al.* (2006) Kancherla (2011)	Singh *et al.* (2003) Kancherla (2011)
9	Micronaire value	Prakash (1982) Gencer and Kaynak (1994) Jain (1996) Punitha *et al.* (1999a) Natera *et al.* (2007) Kancherla (2011)	Gencer and Kaynak (1994) Doss and Kadambavanasundaram (1997) Punitha *et al.* (1999a) Natera *et al.* (2007) Kancherla (2011)	Punitha *et al.* (1999a) Tuteja *et al.* (2005) Kancherla (2011)

Table 4. Contd…

Sr. No.	Character	Heterosis over mid parent	Heterosis over better parent	Heterosis over Standard check
10	Fibre length	Jain (1996) Ahuja and Tuteja (2000)		Jain (1996) Kumar *et al.* (2003) Tuteja *et al.* (2011) Tuteja *et al.* (2013)
11	Uniformity ratio	Punitha *et al.* (1999a) Kancherla (2011)	Patnaik *et al.* (2004) Kancherla (2011)	Patnaik *et al.* (2004) Tuteja *et al.* (2005) Kancherla (2011)
12	Fibre strength	Prakash (1982) Jain (1996) Punitha *et al.* (1999a) Khan (2002) Kancherla (2011)	Punitha *et al.* (1999a) Khan (2002) Kancherla (2011)	Punitha *et al.* (1999a) Tuteja *et al.* (2005) Kancherla (2011)
13	Seed cotton yield per plant	Al-Rawi and Kohel (1969) Baker and Verhalen (1975) Singh and Singh (1982) Singh and Kalsy (1983) Patil and Chopde (1985) Gunaseelan and Krishnaswamy (1988) Dani and Singh (1989) Nirania *et al.* (1991) Singh and Narayanan (1992)	Gangneja (1968) Singh *et al.* (1978b) Singh and Singh (1982) Gill and Singh (1982) Duhoon *et al.* (1983) Ranganathacharyulu and Rao (1986) Duhoon (1990) Nirania *et al.* (1991)	Bhatade and Rajeshwar (1994) Jain *et al.* (1996) Kajjidoni *et al.* (1999) Babar *et al.* (2001) Tuteja *et al.* (2001) Potdukhe *et al.* (2001) Solangi *et al.* (2001) Ahmad *et al.* (2002) Kumar *et al.* (2003)

Table 4. Contd…

Sr. No.	Character	Heterosis over mid parent	Heterosis over better parent	Heterosis over Standard check
		Kalsy *et al.* (1994) Das and Shunmugavalli (1996) Goudar *et al.* (1996) Jain (1996) Patel *et al.* (1996) Tuteja *et al.* (1996) Basha (1997) Siruguppa and Parameswarappa (1998) Kajjidoni *et al.* (1999) Punitha *et al.* (1999a) Babar *et al.* (2001) Ahmad *et al.* (2002) Solangi *et al.* (2002) Kumar *et al.* (2003) Deshpande and Baig (2004) Soomro and Baloch (2005) Natera *et al.* (2007) Pole *et al.* (2008) Deosarkar *et al.* (2009) Kaushik and Kapoor (2013)	Dagaonkar and Malkhandale (1993) Khadi *et al.* (1993) Singh and Singh (1993) Kalsy *et al.* (1994) Bhatade and Rajeshwar (1994) Das and Shunmugavalli (1996) Basha (1997) Kajjidoni *et al.* (1999) Babar *et al.* (2001) Ahmad *et al.* (2002) Panhwar *et al.* (2002) Solangi *et al.* (2002) Tuteja *et al.* (2005) Maisuria *et al.* (2006) Natera *et al.* (2007) Ganapathy and Nadarajan (2008) Deosarkar *et al.* (2009) Patel *et al.* (2009) Kaushik and Kapoor (2013)	Muthu *et al.* (2005) Tuteja *et al.* (2005) Giri *et al.* (2006) Maisuria *et al.* (2006) Tuteja *et al.* (2006) Natera *et al.* (2007) Deosarakar *et al.* (2009) Patel *et al.* (2009) Kumar *et al.* (2013) Tuteja *et al.* (2013)

2.4 Correlation

Yield is a polygenically controlled trait and highly influenced by the environment. Selection merely based on yield is not effective but selection based on its component characters has been reported to be more effective (Grafius, 1960). Correlation studies will establish the extent of association between yield and yield components which forms the basis for selection of genotypes for effective improvement. Unfavorable association between the desired attributes under selection may result in genetic slippage (Dickerson, 1955) and limit genetic advance. A sound knowledge on the magnitude and direction of association of character with yield components, among themselves and with yield as revealed through correlation coefficient estimates is being used very frequently in planning indirect selection for yield. Several workers have estimated correlation for yield and its components in cotton and contradictory association have been reported for some of the character pairs, probably because of the different experimental material handled. Information on correlation among characters with a set of genotypes over a number of environments is also scanty.

The available literature on correlation studies for yield and fibre quality characters is summarized below.

Kalsy *et al.* (1986) studied populations obtained from 33 progenies derived from diverse genotypes of ***hirsutum*** and noticed a positive relationship between yield and boll number, seed index and lint index.

Sandhu *et al.* (1986) reported in F_5 progenies derived from 12 crosses that yield of seed cotton is negatively correlated with 2.5% span length, but it showed positive genotypic correlation with boll number per plant, boll weight and seed index.

According to Sangwan and Yadava (1987) seed cotton yield is highly dependent on boll number. Yield was also significantly and positively associated with boll weight and number of sympodial branches.

Singh *et al.* (1987a) noticed that yield had a significant and positive association with number bolls per plant and boll weight but has no significant relationship with ginning percentage, 2.5% span length, seed index and lint index.

According to Goyal *et al.* (1987) seed cotton yield had a positive and significant association with yield component characters like number of bolls per plant, boll weight, lint yield per plant and total dry matter.

Chimanshette *et al.* (1990) noticed that seed cotton yield showed a positive and significant correlation with number of sympodia, number of bolls per plant, total dry matter. They also reported a positive association between total dry matter and bolls per plant, whereas number of sympodia per plant exhibited positive association with leaf area, 2.5% span length and number of bolls per plant.

According to Krishnarao and Mary (1990) positive association existed between seed cotton yield and other characters such as number of bolls per plant, boll weight, seed index, ginning outturn except fibre length, but fibre length had a negative correlation with micronaire value.

Katageri *et al.* (1992) reported significant and positive association between seed cotton yield and other yield component characters such as sympodial branches, number of bolls per plant, seed index, boll weight, ginning outturn and lint index in F_1 hybrids.

Rajarathinam *et al.* (1993) noticed that seed cotton yield was in positive association with bolls per plant, boll weight, lint index and 2.5% span length, whereas micronaire correlated negatively with 2.5% span length and seed cotton yield per plant. Boll weight exhibited a positive association with lint index and seed index, whereas bundle strength exhibited no significant correlation with seed cotton yield.

Shanti and Selvaraj (1993) reported significant and positive correlation of seed cotton yield with number of sympodia and number of bolls per plant and also observed the significant and positive association of number of sympodia with boll number and boll weight.

Kowsalya and Raveendran (1996) reported significant positive association of seed cotton yield with number of sympodia and number of bolls, whereas significant negative association was observed with days to 50% flowering. They also reported significant positive association of days to 50 % flowering with 2.5 % span length and bundle strength and number of sympodia with number of bolls.

Basha (1997) reported strong positive association of seed cotton yield with days to 50 % flowering, number of bolls and boll weight, whereas boll weight in turn was associated positively with days to 50 % flowering, number of sympodia, number of monopodia and ginning percentage and negatively correlated with boll number. Positive and significant association was also reported for 2.5 % span length with ginning percentage and days to 50 % flowering, number of monopodia with days to

50 % flowering and number of bolls with ginning percentage, number of sympodia and number of monopodia.

Hussain *et al.* (1998) evaluated twelve upland cotton (*G. hirsutum* L.) genotypes and noticed significant positive correlation between ginning percentage and lint, whereas, staple length was correlated with seed cotton yield.

Sangeetha (1998) reported significant positive correlation of yield with boll number and negative correlation with bundle strength, whereas boll weight exhibited significant positive association with number of seeds and negative association with boll number. They also noticed significant negative association between boll number and bundle strength and positive association of number of seeds with ginning percentage and 2.5 % span length with bundle strength.

Larik *et al.* (1999) reported significant correlation of seed cotton yield with bolls per plant at phenotypic level and with number of sympodia, bolls per plant, boll weight and lint index at genotypic level. Bolls per plant exhibited positive correlation with sympodia both at genotypic and phenotypic levels, whereas fibre strength showed positive correlation with staple length and ginning percentage at phenotypic level and strong negative association with staple length at genotypic level. Fibre fineness revealed strong positive and negative correlation with fibre strength and staple length respectively.

The correlation studies by Hussain *et al.* (2000) revealed that, plant height, monopodial branches and number of bolls per plant were significantly and positively correlated with seed cotton yield at genotypic level. They also reported strong correlation between number of bolls per plant and plant yield but ginning percentage exhibited non significant association with yield. In addition, plant height showed positive and significant correlation with number of sympodial branches, number of bolls per plant and ginning percentage, whereas number of monopodia was observed to be positively associated with number of sympodia.

Satange *et al.* (2000) observed positive significant correlation of number of boll per plant, sympodia per plant, seed index and boll weight with seed cotton yield per plant both at genotypic and phenotypic levels.

Afiah and Ghoneim (2000) reported positive correlation of number of fruiting branches, number of bolls per plant, boll weight and lint yield with seed cotton yield. The same relationship was found between lint yield and each of fruiting branches, number of boll per plant, boll weight, seed cotton yield and lint percentage.

The analysis of genotypic correlation using 56 F_2 families and their 8 parents of *G.hirsutum* by Ahmad and Azhar (2000) revealed that number of bolls and lint percentage had positive and significant relationship with seed cotton yield, boll weight, lint index, staple length and fibre fineness, whereas boll weight showed strong association with lint percentage, fibre fineness and seed cotton yield and staple length and fibre fineness exhibited positive correlation with seed cotton yield.

Baloch *et al.* (2001) reported positive phenotypic correlation of bolls per plant and lint percentage with yield, whereas boll weight exhibited significant but negative correlation.

Rao *et al.* (2001) reported significant positive correlation of yield with sympodia and boll number and negative correlation with boll weight. They also observed positive association of sympodia with boll number, boll weight and bundle strength, boll number with bundle strength and ginning percentage with micronaire value and negative association of boll weight with boll number and bundle strength.

Kaushik *et al.* (2003) evaluated 37 genotypes of American cotton and noticed significant positive association was observed for number of bolls per plant, sympodial branches per plant, plant height and monopodium branches per plant with seed cotton yield per plant. These components had positive inter- relationship among themselves.

Iqbal *et al.* (2003b) reported significantly positive correlation of node of first fruiting branches, number of monopodial branches, number of sympodial branches, number of bolls per plant, number of flowers, boll weight, micronaire value and fibre strength and non significant correlation of ginning percentage with seed cotton yield. They also reported positive and significant association between days to 50 % flowering and bundle strength, number of monopodia and number of bolls, number of sympodia and number of bolls and number of sympodia and 2.5 % span length, while 2.5 % span length was negatively associated with ginning percentage and micronaire value.

Narisireddy and Ratnakumari (2004b) reported significant positive correlation of seed cotton yield with number of bolls per plant at both phenotypic and genotypic levels whereas, days to 50% flowering exhibited significant positive association with plant height, and number of bolls per plant and negative significant association with number of sympodia per plant and boll weight.

Muthuswamy and Vivekanandan (2004) reported significant but negative association of ginning outturn with seed cotton yield. Plant height was positively correlated with number of sympodia, bolls per plant, lint index and ginning outturn, whereas number of sympodia was associated with boll number. Among the fibre quality traits, 2.5% span length showed positively significant association with strength and elongation.

Muthu *et al.* (2004) studied in 9x6 line x tester crosses of upland cotton revealed that seed cotton yield had positive and significant correlation with number of sympodia, bolls per plant, boll weight, locules per boll, seed index, lint index and bundle strength, whereas ginning percentage exhibited non significant association with yield. 2.5 % span length exhibited negative correlation with uniformity ratio, micronaire value and ginning percentage and positive association with bundle strength, while micronaire was associated positively with ginning percentage and uniformity ratio. They also reported positive correlation between sympodial branches and number of bolls and ginning percentage and uniformity ratio.

Rauf *et al.* (2004) noticed highly significant positive correlation of number of bolls per plant and sympodial branches with sed cotton yield at genotypic and phenotypic levels.

Naveed *et al.* (2004) reported that plant height and number of bolls were positively and significantly associated with yield of seed cotton at phenotypic and genotypic levels, respectively. Plant height and number of bolls were also positively and significantly correlated with each other at both the levels.

Ahuja *et al.* (2004) evaluated fifty one single plant selections of different coloured linted genotypes of cotton and reported that seed cotton yield per plant exhibited significant positive association with number of bolls per plant and plant height and non significant association with ginning percentage and bundle strength.

Rathore *et al.* (2004) evaluated 54 lines of American cotton (*Gossypium hirsutum* L.) and observed no correlation between seed cotton yield and 2.5% span length, uniformity ratio, micronaire value, fibre strength, fibre elongation, short fibre content and fibre quality index. But they observed positive association of FQI with 2.5% span length and fibre strength and negative association with micronaire value and short fibre content. They also reported negative association of 2.5 % span length with uniformity ratio and micronaire value and positive association of uniformity ratio with micronaire value.

Kaushik *et al.* (2005) studied ten diverse American cotton strains for correlation and path analysis. Correlation analysis showed that seed cotton yield per plant had significant and positive association with bolls per plant, plant height, sympodia per plant and seeds per boll and a significant and negative correlation with ginning percentage.

Gite *et al.* (2006) evaluated 14 genotypes of upland cotton to study character associations and path effects and revealed that seed cotton yield had positive and significant correlations both at genotypic and phenotypic level with number of bolls per plant, number of sympodia per plant, boll weight, plant height and number of monopodia per plant.

Murthy and Chamundeshwari (2006) reported seed cotton yield was found positively and strongly correlated with number of bolls per plant. This was further confirmed by path coefficient analysis. So, due weightage may be given to number of bolls per plant in yield improvement programme. Further, it is suggested that a balance should be struck between boll weight and number of bolls per plant, since they are negatively and significantly correlated with each other.

Iqbal *et al.* (2006) observed significant positive correlation for monopodial branches per plant with boll number and seed cotton yield per plant, whereas number of bolls per plant is negatively correlated with boll weight and positively correlated with seed cotton yield per plant, number of sympodia and ginning outturn.

Kaushik and Kapoor (2006) reported the seed cotton yield was positively and significantly correlated with plant height, number of sympodia per plant, number of bolls per plant and fibre fineness. The number of monopodia per plant was positively correlated with the number of days to flowering and plant height. The number bolls per plant showed a positive association with Plant height, number of sympodia per plant, number of monopodia per plant. The lint index was positively correlated with ginning outturn and seed index where as fibre fineness was positively associated with plant height.

Annapurve *et al.* (2007) reported that phenotypic and genotypic correlations are significant for almost all the characters like number of bolls per plant, days to 50% flowering, boll weight and yield per plant in American cotton (*G. hirsutum* L.).

Preetha and Raveendran (2007) reported positive and significant correlation of number of bolls, boll weight, days to first flowering, uniformity ratio and micronaire value with seed cotton yield, whereas bundle strength exhibited negative correlation and ginning percentage exhibited non significant association. They also noticed the positive inter correlation of number of bolls with 2.5% span length and bundle strength, ginning percentage exhibited non significant association. They also noticed the positive inter correlation of number of bolls with 2.5% span length and bundle strength, whereas negative inter correlation of 2.5% span length was observed with uniformity ratio, micronaire value and ginning percentage and bundle strength with boll weight, uniformity ratio and micronaire value.

Khan *et al.* (2009) reported correlation of seed cotton yield with other different traits was found significantly positive for majority of traits i.e. plant height, sympodia per plant, bolls per plant, and bolls weight. This type of correlation is desirable and little genetic gain in bolls per plant, boll weight and bolls per sympodia is great accomplishment. Cultivars CIM 499, CIM 473, CIM 496 and CIM 506 have larger genetic potential and enhancement of seed cotton yield.

Singh *et al.* (2009) reported that positive association of seed cotton yield was observed with boll numbers, sympodia per plant and plant height showed positive correlation among themselves. Monopodia per plant appeared to be an undesirable trait as it was negatively correlated with seed cotton yield as well as boll number.

Patnaik and Sial (2010) studied the correlation and indicated that number of sympodia per plant and number of bolls per plant had positive and significant correlation, while locules per boll had negative and significant association with seed cotton yield per plant.

Kancherla (2011) correlation studied revealed significant association in desired direction with seed cotton yield per plant for number of sympodia per plant, boll weight, number of bolls per plant and bundle strength (except for with uniformity ratio, micronaire value and ginning percentage).

Lal and Singh (2012) studied correlation analysis, revealed that number of sympodia per plant and number of bolls per plant had positive and significant correlations, while locules per boll had negative and significant association with seed cotton yield per plant.

Mendez- Natera *et al.* (2012) reported that seed cotton yield per plant was significantly positively correlated with bolls per plant at both phenotypic and environment level, while a genotypic level the correlation was significant and positive with fiber length, bolls per plant, boll weight, sympodial branches per plant, 100-seed weight and negative with fibre strength.

Rajamani *et al.* (2013) studied 41 genotypes of American cotton for correlation and path analysis and reported that analysis for seed cotton yield per plant had positive significant correlation with sympodia, number of bolls per plant, boll weight, seed index and lint index.

2.5 PATH ANALYSIS

Path coefficient analysis, a statistical device developed by Wright (1921) helps in partitioning of the correlation coefficients into direct and indirect effects of independent variable on dependent variable. As grain yield is a complex character influenced by several factors, selection based on simple correlation without taking into consideration between the component characters is not effective. Hence, path analysis is of much importance in any plant breeding programme. Correlation in combination with path analysis would give a better insight into cause and effect relationship between different pairs of characters. Dewey and Lu (1959) demonstrated the utility of path coefficient analysis in plant selection.

According to Singh *et al.* (1987a), bolls per plant and seed index had positive direct effect on seed cotton yield. They also reported positive and moderate direct influence of boll weight and ginning percentage on seed cotton yield.

Krishnarao and Mary (1990) in upland cotton recorded non significant direct effect of fibre traits on seed cotton yield.

Chimanshette *et al.* (1990) noticed strong positive direct influence of number of bolls per plant, boll weight, ginning percentage on seed cotton yield and positive indirect effects of leaf area on seed cotton yield through boll weight and ginning percentage.

Rajarathinam *et al.* (1993) reported that boll weight recorded significant and positive direct effect on seed cotton yield even though its indirect effects through other character were negative.

According to Murthy *et al.* (1995), bolls per plant had significant direct effect on seed cotton yield, whereas lint index had negative effect on seed cotton yield.

Sumathi and Nadarajan (1995) reported positive direct effect of number of bolls, ginning percentage and 2.5 % span length and negative direct effect of days to 50 % flowering, number of sympodia and boll weight on seed cotton yield, whereas indirect positive effect was reported on seed cotton yield by number of sympodia and boll weight via ginning outturn.

Kowsalya and Raveendran (1996) reported direct positive effect of days to 50 % flowering, number of sympodia, number of bolls, boll weight, ginning percentage, 2.5 % span length and bundle strength on seed cotton yield, whereas positive indirect effect on yield was exerted by number of bolls per plant via number of sympodia.

Basha (1997) reported positive direct effect of days to 50 % flowering, number of monopodia, number of bolls and boll weight on seed cotton yield per plant, whereas ginning percentage and 2.5 % span length exhibited negative direct effect.

Hussain *et al.* (1998) revealed greatest positive direct effect of lint index on seed cotton yield followed by staple length. Lint index also contributed to seed cotton yield via ginning percentage, staple length and seed index.

Sangeetha (1998) reported direct positive effect of number of sympodia, number of bolls, boll weight, number of seeds per boll and micronaire and direct negative effect of days to 50 % flowering, number of monopodia, ginning percentage, 2.5 % span length and bundle strength on seed cotton yield, whereas boll weight exerted positive indirect effect on yield via number of seeds per boll.

Hussain *et al.* (2000) reported positive direct effect of number of bolls per plant on seed cotton yield. Wheresas, monopodial, sympodial branches and ginning outturn exhibited negative direct effect on yield.

Ahmad and Azhar (2000) reported positive direct effect of number of bolls and boll weight with seed cotton yield. In addition boll weight, lint percentage, lint index, staple length and fibre fineness affects seed cotton yield through number of bolls.

Afiah and Ghoneim (2000) revealed that seed cotton yield was the major contributor to lint yield, followed by lint percentage and boll weight. Meanwhile, lint yield was the major contributor to seed cotton yield, and it was followed by lint percentage and boll weight.

Baloch *et al.* (2001) reported significant direct and indirect effect of bolls per plant and negligible effect of boll weight and lint percentage on the seed cotton yield per plant.

Rao *et al.* (2001) reported direct positive effect of number of sympodia, number bolls and micronaire value on seed cotton yield.

Kaushik *et al.* (2003) studied that path coefficient analysis at genotypic level revealed that sympodia per plant, monopodia per plant and boll weight had positive direct effect on cotton yield.

Pandey *et al.* (2003) revealed greater positive direct effect of plant height on seed cotton yield per plant and indirect effect via boll weight and ginning outturn, whereas boll weight showed positive direct effect on seed cotton yield per plant.

Iqbal *et al.* (2003b) revealed that number of sympodial branches, number of flowers per plant, number of bolls per plant and boll weight had maximum positive direct effects on seed cotton yield, whereas number of monopodial branches per plant, ginning outturn percentage and staple length had the negative direct effects on seed cotton yield. Indirect effect of number of bollsper plant on seed cotton yield via number of sympodia was also reported.

Rauf *et al.* (2004) observed maximum positive direct effect of number of bolls per plant on seed cotton yield.

Narisireddy and Ratnakumari (2004b) noticed highest direct effect of number of bolls per plant on seed cotton yield per plant followed by number of bolls per plant which also exhibited positive indirect effect via 50% flowing on seed cotton yield.

Rathore *et al.* (2004) reported positive direct of 2.5% span length and fibre strength and negative direct effect of micronaire value with fibre quality index (FQI). However, micronaire value also exhibited negative indirect effect on FQI via 2.5% span length and fibre strength, whereas uniformity ratio exhibited negligible positive direct effect on FQI and it had negative indirect effect via 2.5% span length and micronaire value.

Kaushik *et al.* (2005) studied ten diverse American cotton strains for correlation and path analysis. Path analysis showed that bolls per plant, plant height, sympodia per plant and seeds per boll had positive direct effect on seed cotton yield per plant.

Gite *et al.* (2006) studied path analysis at genotypic level revealed that number of bolls per plant exhibited the highest direct effect on seed cotton yield per plant, followed by plant height, ginning per cent and number of sympodia per plant.

Iqbal *et al.* (2006) reported direct positive effect of node of first fruiting branches, monopodial branches per plant, boll number and boll weight and direct negative effect of ginning outturn and staple length on seed cotton yield.

Preetha and Raveendran (2007) reported high direct positive influence of number of bolls, boll weight and days to first flowering on seed cotton yield.

Singh *et al.* (2009) partitioning of phenotypic correlation coefficients of various component traits with seed cotton yield into direct and indirect contributions and revealed that boll number had maximum direct effect upon seed cotton yield followed by boll weight and biomass. Although sympods per plant and plant height did not contribute directly to seed cotton yield but these contribute indirectly via boll number.

Patnaik and Sial (2010) revealed that bolls per plant and fibre strength should be given greater emphasis in cotton yield improvement programme, while number of sympodia per plant contributed maximum indirect effect through the bolls per plants.

Kancherla (2011) studied path matrix revealed that number of bolls per plant,boll weight and 2.5% span lenght was found to have maximum direct positive effect on seed cotton yield per plant .

Lal and Singh (2012) reported that bolls per plant and fiber strength had attributed maximum direct effect, while number of sympodia per plant contributed maximum indirect through the bolls per plant.

Rajamani *et al.* (2013) reported that number of bolls per plant, monopodia per plant and sympodia per plant, days to 50 % flowering, boll weight, ginning outturn, seed index, lint index, uniformity ratio and micronaire exhibited direct positive effect on seed cotton yield per plant signifying that these are the major yield contributing traits for improvement of seed cotton yield.

2.6 GENERATION MEAN ANALYSIS

The improvement of quantitative traits is a moving target. The expression of these traits is affected not only by large number of genes governing them but also by environmental effects. Frequently, these genes interact with each other causing distortions in Mendelian ratios and leading to novel phenotypes (Phillips, 1998). The term epistasis was coined by Bateson (1909) to describe a situation where in action of one gene masks the effect of other at different loci like the phenomenon of complete dominance in which one allele at same locus mask the effect of other.

The estimation of epistasis assumes more significance in view of the fact that in its presence, variance component estimates are likely to be biased, hence, inferences drawn from such estimates are more likely to be misleading. The magnitude of the bias depends upon the relative magnitude of epistatic effects comparatively to the deviation of 'd' and 'h' type of prevailing epistasis and direction of dominance. The existence of large array of interactions in a polygenic system cause over-estimation or under-estimation of heritability estimates (narrow sense), thereby, causing additional bias in predicted gains. Generation mean analysis is a powerful statistical procedure for detection of epistasis using several basic generations from a cross between two inbred lines.

The literature pertaining to the generation mean analysis and epistasis is summarized below

Nadarajan and Sreerangaswamy (1992) studied 6 generations (P_1, P_2, F_1, F_2, BC_1 and BC_2) derived from crosses of 5 genotypes with a Fuzzless-lintless type as the pollinator and reported that the traits 2.5% span length, uniformity ratio, fibre fineness and maturity coefficient were governed by additive, dominance and digenic non allelic interaction effects, with non-additive gene action predominating over additive gene action.

Pillai and Amirthadevarathinam (1997) carried out generation mean analysis in 6 generations of 3 crosses and opined that the scaling and joint scaling tests indicated the presence of non-allelic interaction for all the traits studied except seed index. Generation mean analysis showed the importance of dominance gene effects followed by other gene interactions.

Rajendrakumar and Raveendran (1999) studied gene action in P_1, P_2, F_1, F_2 and F_3 generations using 5-parameter model and observed presence of epistatic gene interactions for number of sympodia, number of bolls, boll weight, ginning percentage, 2.5 % span length and seed cotton yield per plant and all these traits except ginning percentage exhibited duplicate type of gene interaction.

Ahmmed and Mehra (2000) studied the generation mean analysis of an *intra-hirsutum* cross Pusa 45-3-6 x Pusa 19-27 revealed the presence of dominance and epistatic interactions in the genetic control of important yield components *viz.,* boll number, boll weight, number of sympodia, number of monopodia, plant height and biological yield, while only additive gene action was significant for first fruiting node number. They also observed duplicate type of interaction for number of bolls and boll weight.

Phogat and Singh (2000) evaluated cross combination of American glandless x HG 625 though generation mean analysis for gossypol and fibre properties. The result revealed that both additive x dominance type of gene effects control size of glands in petals, leaves and seed gossypol. Whereas for seed cotton yield per plant, lint (%), 2.5% span length, uniformity ratio, micronaire value, maturity coefficient and fibre strength were governed by all the three type of gene effects i.e. additive (d), dominance(h) and epistatic (i. j. and l).

Reddy *et al.* (2002) done generation mean analysis by using six parameter model for four crosses in upland cotton (*G. hirsutum* L.) for bolls per plant, boll weight and seed cotton yield and showed that all the three types of gene action were significant in crosses H.8 x H.16 and H.11 x H.12 for bolls per plant. Preponderance of dominance component over additive component was observed in H.11 x H.23 and H.11 x H.12. Genetic variance was entirely due to additive component in H.12 x H.12 for boll weight. Additive, dominance and epistatic components were significant in H.25 x H.11 for this trait.

Mehetre *et al.* (2003) studied nature and magnitude of gene action for seed cotton yield and fifteen chorarctres in intra hirsutm and interspecific crosses of cotton. Study indicated that magnitude of dominance effect was higher for almost all the characters. Epistatic components additive x additive (i) and dominance x dominance (l) were involved in the expression of most of the characters. Duplicate type of epistasis was observed for most of the characters in most of the crosses.

Iqbal and Nadeem (2003) studied genetic effects for seed cotton yield and number of sympodial branches per plant through generation mean analysis which revealed the presence of additive gene action in crosses S-12 x S-14, S-12 x Albacala (69)11, LRA 5166 x S-12 and LRA 5166 x S-14 for number of sympodial branches per plant, and dominance gene action in cross S-14 x S-12, whereas most of recessive alleles for seed cotton yield accumulated in Albacala (69)11 x S-12, which expressed the least positive degree of dominance. The scaling test revealed the involvement of epistasis in all the crosses except S-14 x LRA 5166 for seed cotton yield and the opposite sign of (h) and (I) in all the crosses suggested the duplicate type of epistasis.

Singh *et al.* (2005) observed epistatic type of gene interaction for the traits number of sympodia, number of bolls, boll weight, ginning percentage, 2.5 % span length, micronaire value, bundle strength and seed cotton yield per plant.

Bhatti *et al.* (2006) reported that the genes acting cumulatively were predominant in the inheritance of staple length, fibre strength and fibre fineness even though both additive and non-additive genes affected these traits. It was further revealed that additive x dominance and dominance x dominance epistasis component was important in the inheritance of these traits.

Ismail (2007) studied six generations P_1, P_2, F_1, F_2, BC_1 and BC_2 of two intraspecific crosses and reported epistatic gene interactions for the traits days to 50 % flowering, boll number, boll weight and seed cotton yield and also reported duplicate type of gene interaction and complementary type of interaction for days to 50 % flowering, boll number, boll weight and seed cotton yield per plant.

Singh *et al.* (2010) the generation mean analysis carried out to estimate the nature and magnitude of gene effects for yield and fibre quality traits in two crosses (*viz.*, LH1832 x CIM435 and LH 1832 x CIM 443) of upland cotton revealed the presence of epistasis for 2.5 % span length, boll weight, ginning out turn. The additive gene effects observed for seed cotton yield, bolls per plant and ginning outturn in cross-1 and for seed cotton yield in cross -2 may be fired in pure lines.

Kancherla (2011) estimated the gene effect through joint scaling test of three and six parameter and sequential fit model in six crosses for eleven charcters and noted that significance of epistasis interaction for days to 50% flowering, number of sympodia per plant, boll weight ,number of bolls per plant, ginning percentage, microniare value, uniformity ratio and seed cotton yield per plant were influnced by dominance x dominance (l) of gene interaction.

Nidagundi *et al.* (2012) studied the estimates of scaling tests along with gene effects based on joint scaling tests and best fit model for intervarietal cross GSHV 99/307 x Surabhi and reported that scaling as well as joint scaling test detected the presence of epistasis for seed cotton yield, boll weight, seed index and lint index, while simple additive dominance model was sufficient to explain the variation for ginning outturn.

Material and Methods

CHAPTER-III

MATERIAL AND METHODS

The present investigation on "Studies on heterosis, combining ability and gene action for fibre characters, yield and its components in intra and interspecific hybrids of upland cotton (*Gossypium sp.*) was undertaken with following objectives:

1. To estimate the magnitude of heterosis and combining ability of hybrids over parents for fibre quality and yield traits
2. To study the nature and magnitude of gene action involved in expression of fibre quality and yield characters by generation mean analysis
3. To study correlation and path analysis

3.1 LOCATION

The experiment was conducted at Cotton Research Scheme, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani. Geographically it is situated at an altitude of 408.50 m above mean sea level, 19^0 16" North latitude and 76^0 47" East longitude and comes under subtropical region of India.

3.2 EXPERIMENTAL MATERIAL

3.2.1 Selection of parents

The selfed seed of parental lines for the present study was obtained from Cotton Specialist, Cotton Research Station, Nanded. These genotypes were selected on the basis of genetic variation for morphological and fibre quality traits. The salient features of experimental material are summarized in Table 5.

Table 5. Morphological characters of parental lines

Sr.No.		SALIENT FEATURES
LINES :		
1.	NH 545	High ginner, medium staple length, tolerant to sucking pests
2.	NH 615	Drought tolerant, suitable for high density planting, sucking pest-tolerant, high ginner
3.	NH 630	Necked seeded, stay green character, high ginner
4.	NH 635	Higher yielder, tolerant to foliar diseases, good fibre quality
5.	PH 1060	Erect plant type, high yielder, better fibre quality
6.	PH 1076	Bold seeded, high yielder
7.	LRA 5166	Fibre quality
TESTERS :		
1.	NH 452	Medium staple length, with high ginner
2.	NH 625	Tolerant to sucking pest, high yielder
3.	PKV Rajat	Higher yielding and medium staple length
4.	Suvin	Extra long staple, finest fibre quality with spinnability up to 240 s count

Table 6. List of F_1 crosses (28)

Sr. No.	Hybrid	Sr. No.	Hybrid
1	NH 545 x NH 452	15	NH 635 x PKV Rajat
2	NH 545 x NH 625	16	NH 635 x Suvin
3	NH 545 x PKV Rajat	17	PH 1060 x NH 452
4	NH 545 x Suvin	18	PH 1060 x NH 625
5	NH 615 x NH 452	19	PH 1060 x PKV Rajat
6	NH 615 x NH 625	20	PH 1060 x Suvin
7	NH 615 x PKV Rajat	21	PH 1076 x NH 452
8	NH 615 x Suvin	22	PH 1076 x NH 625
9	NH 630 x NH 452	23	PH 1076 x PKV Rajat
10	NH 630 x NH 625	24	PH 1076 x Suvin
11	NH 630 x PKV Rajat	25	LRA 5166 x NH 452
12	NH 630 x Suvin	26	LRA 5166 x NH 625
13	NH 635 x NH 452	27	LRA 5166 x PKV Rajat
14	NH 635 x NH 625	28	LRA 5166 x Suvin

The present investigation was undertaken in *hirsutum* and *barbadense* cotton involving seven lines and four tester genotypes having wide variation in seed cotton yield and its associated traits. Crossing programme was undertaken in summer 2012 by using 7 lines and 4 testers and 28 hybrids (F_1's) were developed as per detailed list presented in Table 6. Seven lines, four testers, 28 F_1, 4 F_2, 4 BC_1 and 4 BC_2 s along with two checks (NHH 44 and DCH 32) were sown during *kharif*, 2013 at Cotton Research Scheme, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani.

3.2.2 Heterosis and combining ability studies:

The experiment material for heterosis and combining ability studies comprised of eleven (11) parents which included seven *Gossypium hirsutum* lines *viz.*, NH 545, NH 615, NH 630, NH 635, PH 1060, PH 1076, LRA 5166 and four testers out of which three were *Gossypium hirsutum viz.*, NH 452, NH 625, PKV Rajat and one was *barbadense* type i.e. Suvin and their 28 hybrids with two standard checks *viz.*, NHH 44 and DCH 32. Total 41entries including 28F_1's + 11 parents + 2 checks were evaluated during 2013-14, at Cotton Research Scheme, V.N.M.K.V., Parbhani.

3.2.3 Generation mean studies:

Four lines *viz.*, NH 545, NH 635, PH 1060 and LRA 5166 and three testers NH 452, PKV Rajat and Suvin and their four independent crosses were studied to assess the gene effects through generation mean analysis.

1. NH 545 x NH 452
2. NH 635 x PKV Rajat
3. PH 1060 x Suvin
4. LRA 5166 x Suvin

3.3 METHOD

During summer, 2012, the parents (seven lines and four testers) were sown in a crossing block at spacing of 120 x 60 cm (Plate 1). Crosses were effected in a line x tester design (7 x 4) to produce 28 F_1's crosses. Hybridization was carried out following hand emasculation and pollination method. Flower buds likely to open on next day were selected for emasculation. Emasculation was carried out between 3 to 6 pm and covered with red colored straw tube to prevent natural out crossing. The next day pollen from desirable testers were used for pollination. The operation was done from 9 to 11 am. Four to five emasculated buds of female parent were pollinated by one male flower. After pollination, the staminal column was covered with white colored straw tube for prevention of cross- pollination with undesirable pollen. A label with details of the cross was also tied on the pedicel for identification of cross. All recommended package of practices were adopted to obtain sufficient number of crossed bolls from each cross combination.

During *kharif* 2012, the material for generation means studies were generated. For this, four crosses (NH 545 x NH 452, NH 635 x PKV Rajat, PH

Plate 1. Crossing Block

1060 x Suvin and LRA 5166 x Suvin) were selected. These four selected crosses were selfed and backcrossed with their respective parents to obtain the F_2 and backcross (BC_1 and BC_2) seeds respectively. Selfed seed was also obtained for all the parents. Thus, six basic generations, P_1, P_2, F_1, F_2, BC_1 and BC_2 were developed for each of the four crosses.

In *kharif* 2013, two experiments were conducted. In one experiment, 28 F_1s, 11 parents along with two checks (NHH 44 and DCH 32) were evaluated for combining ability. The material was sown in Randomized Block Design in three replications (Plate 2). Parents and hybrids were sown in two rows with spacing of 60 x 60 cm. In another experiment evaluation of P_1, P_2, F_1, F_2, BC_1 and BC_2 generations of the selected four crosses was undertaken to understand the genetic nature of yield and yield contributing characters along with fiber quality through generation mean analysis. The F_2s were sown in ten rows and backcrosses in four rows, whereas parents and hybrid were sown in two rows each with a spacing of 60 x 60 cm.

3.4 OBSERVATIONS RECORDED

Fifty randomly selected plants in F_2, twenty plants in BC_1 and BC_2 and five randomly selected plants from other generations in generation mean analysis experiment from each plot in each replication were chosen and labeled for recording observations and the means were taken into consideration for statistical analysis. From F_1s along with parents and checks five plants were randomly selected for recording observations on fiber quality, yield and yield contributing characters.

A) Yield contributing traits

3.4.1 Days to 50 % flowering

Number of days required from sowing to the date on which 50 % of the plants flowered and average number of days to 50 % flowering was calculated.

Plate 2. Overall view of the experimental plot

3.4.2 Number of monopodia per plant

The number of vegetative branches on the main stem which are lateral, axillary in position with acropetal succession was counted at maturity stage, avoiding small sprouts.

3.4.3 Number of sympodia per plant

Reproductive branches which are auxiliary in position, normally horizontal with zigzag pattern of fruiting points were taken as sympodia. The number of such sympodia on main stem was counted on each of five plants at maturity and averaged.

3.4.5 Plant height (cm)

The main stem height was recorded in centimeters from the cotyledonary node to growing tip at the time of maturity and the averages were worked out.

3.4.5 Days to maturity

It was measured from date of sowing to days required for maturity of each genotype.

3.4.6 Boll weight (g)

The boll weight in gram was obtained by taking the average weight of seed cotton from 10 randomly collected bolls from each plant and averaged.

3.4.7 Number of bolls per plant

The total number of fully opened bolls harvested from each of five plants was counted and averaged.

3.4.8 Seed cotton yield per plant (g)

Weight of seed cotton in gram obtained from each plant of five randomly selected was recorded and averaged.

3.4.9 Seed cotton yield per plot (g)

Weight of seed cotton in gram obtained from each plot per replication was recorded.

3.4.10 Seed cotton yield qtl./ ha.

Weight of seed cotton obtained from each plot was multiply by the hector factor.

B) Fibre characters

3.4.11 Ginning (%)

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

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

3.4.12 Micronaire value (µg/ inch)

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

3.4.13 Fibre length (mm)

Determined by HVI (ICC Mode) instrument.

3.4.14 Uniformity ratio

Determined by HVI (ICC Mode) instrument. It is the ratio of 2.5 % span length and 50 per cent span length.

3.4.15 Fibre strength (g/tex)

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

3.5 STATISTICAL PROCEDURES

The data recorded on different traits were subjected to the following statistical analyses.

3.5.1 Analysis of variance

i) RBD analysis

The adopted design was Randomized Block Design (RBD) replied thrice. The analysis of variance was carried out by the method adopted by Panse and Sukhatme (1985).

$$Y_{ij} = m + g_i + v_j + e_{ij}$$

Where,

Y_{ij} = Phenotypic observation of i^{th} genotypic in j^{th} replication

m = General mean

g_i = Effect of j^{th} genotype

v_j = Effect of j^{th} replication

e_{ij} = Random error

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

ANOVA			
Source	**d.f**	**MS**	**F calculated**
Replications (r)	(r-l)	Mr	Mr/Me
Treatments (t)	(r-l)	Mt	Mt/Me
Error (e)	(r-l) (t-l)	Me	
Total	(rt-l)		

Where,

r = number of replications

t = number of treatments (genotypes)

Mr = mean sum of squares of replications

Mt = mean sum of squares of treatments

Me = mean sum of squares of error

d.f. = degrees of freedom

MS = mean sum of squares

The significant of mean sum of squares for each charactër was tested against the corresponding error degrees of freedom using 'F' test (Fisher and Yates, 1967).

ii) Line x Tester analysis

The data recorded on the material generated as per Line x Tester model of Kempthorne (1957) were subjected to analysis of variance as per the Line x Tester model given by Singh and Chaudhary (1985).

ANOVA for Line x Tester analysis

Source	**d.f**	**MS**
Replications (r)	(r-l)	
Genotypes (a)	(a-l)	
Parents (p)	(p-l)	
Crosses (c)	(c-l)	
Parents vs. crosses	L	
Males (m)	(m-l)	Mm
Females (f)	(f-l)	Mf
Males x females (m x f)	(m-l) (f-l)	M (m x f)
Error	(r-l) (a-l)	Me

Where,

r = number of replications

a = number of genotypes

p = number of parents

c = number of crosses

m = number of males

f = number of females

Mm = mean sum of squares of males

Mf = mean sum of squares of females

M (m x f) = mean sum of squares of males and females

Me = mean sum of squares of error

d.f. = degrees of freedom

MS = mean sum of squares

The significant differences among the genotypes and replications were verified by applying 'F' test (Fisher and Yates, 1967).

3.5.2 Variability, heritability and genetic advance

3.5.2.1 Genotypic and phenotypic coefficients of variation

The genotypic and phenotypic coefficients of variation were calculated according to the formula given by Falconer (1981).

$$\text{Genotypic coefficient of variation (GCV)} = \frac{\text{Genotypic standard deviation}}{\text{Mean}} \times 100$$

$$\text{Phenotypic coefficient of variation (GCV)} = \frac{\text{Phenotypic standard deviation}}{\text{Mean}} \times 100$$

3.5.2.2 Heritability

Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance in the total population. Heritability (h^2) in the broad sense was calculated according to the formula given by Allard (1960).

$$h^2 = \frac{\sigma^2 g}{\sigma^2 p}$$

h^2 = heritability in broad sense

$\sigma^2 g$ = genotypic variance

$\sigma^2 p$ = phenotypic variance ($\sigma^2 g + \sigma^2 e$)

3.5.2.3 Genetic advance

Genetic advance refers to the expected gain or improvement in the next generation by selecting the superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1952).

$$GA = K.\, h^2(b).\, \sigma p$$

Where,

GA = expected genetic advance

K = Selection differential, the value of which is 2.06 at 5 per cent selection intensity

σp = phenotypic standard deviation

$h^2(b)$ = heritability in broad sense

In order to visualize the relative utility of genetic advance among the characters, genetic advance as per cent for mean was computed.

$$\text{Genetic advance as per cent of mean} = \frac{GA}{\text{Grand mean}} \times 100$$

3.5.3 Estimation of combining ability

Combining ability was estimated based on the method of Kempthorne (1957). The estimates of general and specific combining ability and their variances were obtained by using covariance of half sibs and full sibs.

ANOVA				
Source	d.f	SS	MS	Expected mean squares
Replications	(r-l)	$\frac{X^2...k}{mf} - \frac{X^2...}{mfr}$		
Hybrids	(mf-l)	$\frac{X^2_{ij}}{r} - \frac{X^2...}{mfr}$		
Males	(m-l)	$\frac{X^2_{i..}}{fr} - \frac{X^2...}{mfr}$	M_1	σ^2 + r [Cov (F.S) – 2Cov (H.S) + fr Cov (H.S)]
Females	(f-l)	$\frac{X^2.j.}{mr} - \frac{X^2i..}{mfr}$	M_2	σ^2 + r [Cov (F.S) – 2Cov (H.S) + mr Cov (H.S)]
Males x Females	(m-l) (f-l)	$\frac{X^2_{(ij)}}{fr} - \frac{X^2...}{(H.S)]} - \frac{X^2_{.j.}}{mr} - \frac{X^2...}{mfr}$	M_3	σ^2 + r [Cov (F.S) – 2 Cov
Error	(r-l) (mf-l)	By difference	M_4	σ^2
Total	(mfr-l)	$X^2_{.(ij)k} - \frac{X^2...}{mfr}$		

Where,

$X...$ = Sum of all the (ij) hybrid combinations

$X_{..k}$ = Sum of k^{th} replication

$X_{(ij)}$ = Sum of ij^{th} hybrid combination over all replications

$X_{.j.}$ = Sum of j^{th} female parent over all males and replications

X_{ijk} = ij^{th} observation in k^{th} replication

Covariance of full sibs and covariance of half sibs were estimated by using the formula (Kempthorne, 1957) given below:

$$\text{Covariance of half sibs} = \frac{1}{r\,(2mf - f - m)}\left(\frac{(f-1)\,(m_1) + (m-1)(M_2)}{f+m-2}\right) - M3$$

$$\text{Covariance of full sibs} = \frac{(M_1 - M_4) + (M_2 - M_4) + (M_3 - M_4)}{3r}$$

$$+ \frac{6\,r\,Cov\,(H.S) - r\,(m+f) Cov\,(H.S)}{3r}$$

3.5.3.1 Estimation of variances

Using the covariances of half sibs and full sibs which were estimated by the above equations, variance due to general combining ability (σ^2 gca) and variance due to specific combining ability (σ^2 sca) were estimated as:

σ^2 gca = Covariance of half sibs

σ^2 sca = Covariance of full sibs – 2 Covariance of half sibs

3.5.3.2 Estimation of combining ability effects

The additive model used to estimate the gca and sca effects of the ijk observations were

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

Where,

μ = population mean

g_i = *gca* effect of i^{th} male parent

g_j = *gca* effect of j^{th} female parent

s_{ij} = *sca* effect of ij^{th} combination

e_{ijk} = error associated with the observation X_{ijk}

i = number of male parents

j = number of female parents

k = number of replications

The estimation of individual was as follows:

$$\mu = \frac{X...}{mfr}$$

Where,

X... = Total of all hybrid combinations over all replications

(i) Lines

$$g_i = \frac{X_{i..}}{fr} - \frac{X...}{mfr}$$

Where,

X_i = Total of i^{th} male parent over all females and replications

(ii) Testers

$$g_j = \frac{X_{.j.}}{mr} - \frac{X...}{mfr}$$

Where,

$X_{.j.}$=Total of j^{th} female parent over all male parents and replications

$$S_{ij} = \frac{X_{ij.}}{r} - \frac{X_{i..}}{fr} - \frac{X_{.j.}}{mr} - \frac{X...}{mfr}$$

Where,

$X_{ij.}$ = ij^{th} combination total over all replications

3.5.3.3 Standard errors for combining ability effects

The standard errors (SE) pertaining to gca and sca effects of different combinations were calculated as follows:

$$\text{SE } (g_i) \text{ female (gca for line)} = \left(\frac{\text{Error of variance}}{rm}\right)^{1/2}$$

$$\text{SE } (g_i) \text{ males (gca for tester)} = \left(\frac{\text{Error of variance}}{rf}\right)^{1/2}$$

$$SE(s_{ij}) \text{ male x female combination} = \left(\frac{\text{Error of variance}}{R} \right)^{1/2}$$

Where,

r = number of replications

m = number of males

f = number of females

The *gca* and *sca* effects were tested against zero for significance by calculating t-value, by using the following formulae.

$$\text{t-cal} = \frac{gi - 0}{SE(gi)}; \qquad \text{t-cal} = \frac{gj - 0}{SE(gj)};$$

$$\text{t-cal} = \frac{Sij - 0}{SE(Sij)};$$

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

3.5.4 Estimation of heterosis

Heterosis was estimated for 28 hybrids for 15 characters using the following formulae.

3.5.4.1 Heterosis over mid parent

Relative heterosis was expressed as per cent increase or decrease observed in the F_1 over the mid-parent as per following formula.

$$\text{Heterosis (\%) } (h_1) = \frac{\overline{F}_1 - \overline{MP}}{\overline{MP}} \times 100$$

Where,

$\overline{F}_1$ = Mean of F_1

$\overline{MP}$ = Mean of parents

3.5.4.2 Heterosis over better parent

Heterobeltiosis was expressed as per cent increase or decrease observed in F_1 over the better parent as per the formula of Liang *et al.* (1971).

$$\text{Heterosis (\%) } (h_2) = \frac{\overline{F}_1 - \overline{BP}}{\overline{BP}} \times 100$$

Where,

$\overline{BP}$ = Mean of better parent (for the characters like days to 50% flowering, earliness is desirable so the early parents are taken better parents).

3.5.4.3 Heterosis over standard checks

Standard heterosis was expressed as per cent increase or decrease observed in F_1 over standard checks.

$$\text{Standard heterosis (\%) } (h_3) = \frac{\overline{F}_1 - \text{Mean of check}}{\text{Mean of check}} \times 100$$

3.5.4.4 Test of significance of heterosis

To test the significance for different types of heterosis needs computation of standard error (SEm). For relative heterosis and heterobeltiosis, SEm were calculated based on error mean squares (EMS) from the ANOVA tables consisting parents and crosses, whereas, EMS from the RBD ANOVA (σ^2e) table based on all treatments (Parents, crosses and checks) was used for standard heterosis.

The significance of heterosis *viz.*, relative heterosis, heterobeltiosis and standard heterosis was then tested by comparing the calculated 't' – value with the tabulated student's 't' – value for appropriate error degrees of freedom at 5 per cent and 1 per cent level of significance (0.05 and 0.01 level of probability), respectively.

$$\text{'t'}_{cal} \text{ for Heterosis and heterobeltiosis} = \frac{\overline{F}_1 - \text{Mean of mid parents or better parent}}{\text{SEM}}$$

Where, $SEm = \sqrt{2EMS/r}$

EMS = Error mean of squares

r = Number of replications

$$\text{'t'}_{cal} \text{ for Standard heterosis} = \frac{\overline{F}_1 - \text{Mean of check}}{\text{SEM}\,\overline{SC}}$$

Where, $SEm\ \overline{SC} = \sqrt{2\sigma e2 / r}$

3.5.4.5 Least significance difference (critical difference) for heterosis

The significance of the difference between two estimates of heterosis were tested by computing the least significant difference (LSD) by multiplying the SEm with the appropriate student's 't' value of respective for degrees of freedom at desired level of probability.

CD = SEm x 't' table value at error degrees of freedom

3.5.5 Correlations

The data on 13 characters were utilized for the computation of correlation coefficients between quality, yield and yield component characters for all the genotypes. The formula suggested by Snedecor and Cochran (1967) was followed.

$$r(X_i \,.\, X_j) = \frac{Cov(X_i \,.\, X_j)}{\sqrt{(Var\ Xi) \,.\, (Var\ Xj)}}$$

Where,

$r(X_i \,.\, X_j)$ = Correlation coefficients between i^{th} and j^{th} character

$Cov(X_i \,.\, X_j)$ = Covariance between i^{th} and j^{th} character

$(Var\ X_i)(Var\ X_j)$ = Variance of i^{th} and j^{th} characters respectively

3.5.5.1 Phenotypic and genotypic correlations

Phenotypic and genotypic correlation coefficients were calculated for the characters by working out the variance components of each character and the covariance components for each pair of characters using the formulae suggested by Al-Jibouri *et al.* (1958).

$$\text{Genotypic correlation Coefficient } (r_g) = \frac{\text{Cov xy (genotypic)}}{\sqrt{(\text{Var x}).(\text{Var y})(\text{genotypic})}}$$

$$\text{Genotypic variance} = \frac{\text{Treatment MS} - \text{Error MS}}{\text{Number of replications}}$$

Similarly,

$$\text{Genotypic covariance} = \frac{\text{Treatment Cov} - \text{Error Cov}}{\text{Number of replications}}$$

$$\text{Phenotypic correlation Coefficient } (r_g) = \frac{\text{Cov xy (phenotypic)}}{\sqrt{(\text{Var x}).(\text{Var y})(\text{phenotypic})}}$$

The values of genotypic correlation exceeding unity should be considered as unit only (of same sign). To test the significance of correlation coefficients, the estimated values were compared with the table values of correlation coefficients (Fisher and Yates, 1967) at 5 per cent and 1 per cent levels of significance with (n-2) degrees of freedom, where 'n' is the number of genotypes used in the experiment.

3.5.6 Path coefficient analysis

Contribution of 13 component characters towards dependent character were calculated through path coefficient analysis as suggested by Wright (1921) and elaborated by Dewey and Lu (1959) at both phenotypic and genotypic levels.

$$\begin{pmatrix} r_{1y} \\ r_{2y} \\ : \\ : \\ : \\ r_{Iy} \end{pmatrix} \begin{matrix} = \\ = \\ \\ \\ \\ = \end{matrix} \begin{pmatrix} P_{1y} + r_{12} P_{2y} + r_{13} P_{3y} + \ldots\ldots\ldots\ldots + r_{1y} P_{Iy} \\ P_{2y} P_{1y} + P_{2y} + r_{23} P_{3y} + \ldots\ldots\ldots\ldots + r_{2y} P_{1y} \\ : \\ : \\ : \\ r_{11} P_{1y} + r_{12} P_{2y} + r_{13} P_{3y} + \ldots\ldots\ldots\ldots + P_{1y} \end{pmatrix}$$

Where,

r_{1y} to r_{Iy} = Coefficient of correlation between causal factor 1 to I and dependent character Y.

r_{12} to $r_{I\text{-}II}$ = Coefficient of correlation among causal factors

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

$$\underset{\textbf{A}}{\begin{pmatrix} r_{1y} \\ r_{2y} \\ : \\ : \\ : \\ r_{Iy} \end{pmatrix}} = \underset{\textbf{C}}{\begin{pmatrix} 1 & r_{12} & r_{13} & \ldots\ldots\ldots & r_{1i} \\ r_{12} & 1 & r_{13} & \ldots\ldots\ldots & r_{2i} \\ r_{31} & r_{13} & 1 & \ldots\ldots\ldots & r_{3i} \\ & & & & : \\ & & & & : \\ r_{I1} & r_{I2} & r_{I3} & \ldots\ldots\ldots & 1 \end{pmatrix}} \underset{\textbf{B}}{\begin{pmatrix} P_{1y} \\ P_{2y} \\ P_{3y} \\ \\ \\ P_{Iy} \end{pmatrix}}$$

Then $B = [C]^{-1} A$

Where C^{-1}

$$\begin{pmatrix} C_{11} & C_{12} & C_{13} & \ldots\ldots & C_{1I} \\ C_{21} & C_{22} & C_{23} & \ldots\ldots & C_{2I} \\ : & & & & \\ : & & & & \\ : & & & & \\ C_{I1} & C_{I2} & C_{I3} & \ldots\ldots & C_{Ii} \end{pmatrix}$$

The matrix was inverted using generalized inverse (G inverse).

Then, direct effects were calculated as follows:

$$P_{1Y} = \sum_{I=1}^{I} C_{1i}\, r_{iy}$$

$$P_{2Y} = \sum_{I=1}^{I} C_{2i}\, r_{iy}$$

$$P_{iY} = \sum_{I=1}^{I} C_{ij}\, r_{iy}$$

Residual effect (PR_y) which measures the contribution of the characters not considered in the causal scheme was obtained as,

$$\text{Residual effect } (PR_y) = (1-r^2)^{1/2}$$

$$r^2 = (P_{1y}\, r_{1y} + P_{2y}\, r_{2y} + \ldots\ldots\ldots + P_{1y}\, r_{1y})$$

3.5.7 Generation means and gene effects

The concept of Generation Mean Analysis (GMA) was developed by Hayman (1958) and Jinks and Hayman (1958) for the estimation of genetic components of variation; since this technique involves six different generations *viz.*, parents (P_1 and P_2), their F_1, F_2 and back (BC_1 and BC_2).

The means were computed for each generation of P_1, P_2, F_1, F_2, BC_1 and BC_2 for each cross over three replications. The variance and corresponding standard errors of the means were computed from the deviations of the individual values from the pooled mean for each of the generation in each cross.

3.5.7.1 Scaling test

The test which provides information regarding presence / absence of gene interaction is termed as scaling test. The test of adequacy of scales is important because in most of the cases the estimation of additive and dominance components of variances is made assuming the absence of gene interactions. Mather (1949), and Hayman and Mather (1955) gave four scaling tests.

The 't' values are calculated by dividing the scale effects of A, B and C by their respective standard error.

t cal for A-test = Scale A / S.E. A

t cal for B-test = Scale B / S.E. B

t cal for C-test = Scale C / S.E. C

t cal for D-test = Scale D / S.E. D

The calculated values of 't' are to be compared with 't' table values at 5 per cent and 1 per cent level of significance. If the calculated values of these scales is higher than 1.96, it is considered significant and vice versa. The significance of any scaling test indicates the presence of epitasis.

3.5.7.2 Components of generation means

The mean values over replication are used for the estimation of the gene effects. Owing to presence of six generations in each cross, Hayman's (1958) six parameter model was followed to estimate gene effects including epistatic interactions.

The six parameter model was first suggested by Hayman (1958) for estimation of various genetic components from the generation means. This method is used when non-allelic interactions are present. The analysis of this model is based on six generation *viz.*, P_1, P_2, F_1, F_2, BC_1 and BC_2 and six parameters are obtained. These parameters are mean (m), additive gene effects (d), dominance gene effects (h) and three types of non-allelic gene interactions *viz.*, additive x additive (i), additive x dominance (j) and dominance x dominance (l).

$$m = \overline{F}_2$$

$$d = \overline{B}_1 - \overline{B}_2$$

$$h = \overline{F}_1 - 4\overline{F}_2 - (1/2)\overline{P}_1 - (1/2)\overline{P}_2 + 2\overline{B}_1 + 2\overline{B}_2$$

$$i = 2\overline{B}_1 + 2\overline{B}_2 - 4\overline{F}_2$$

$$j = \overline{B}_1 - (1/2)\overline{P}_1 - \overline{B}_2 + (1/2)\overline{P}_2$$

$$l = \overline{P}_1 + \overline{P}_2 + 2\overline{F}_1 + 4\overline{F}_2 - 4\overline{B}_1 - 4\overline{B}_2$$

Where,

$\overline{P}_1$, $\overline{P}_2$, $\overline{F}_1$, $\overline{F}_2$, $\overline{B}_1$ and $\overline{B}_2$ are mean values of P_1 P_2, F_1, F_2, BC_1 and BC_2 generations, respectively.

3.5.7.3 Test of significance of various gene effects

The test of significance of the gene effects was done using 't' test for which variance and standard error of each estimates were calculated using following equations.

$$V_m = V(\overline{F}_2)$$

$$V_d = V(\overline{B}_1) + V(\overline{B}_2)$$

$$V_h = V(\overline{F}_1) + 16\,V(\overline{F}_2) + \tfrac{1}{4}\,V(\overline{P}_1) + \tfrac{1}{4}\,V(\overline{P}_2) + 4V(\overline{B}_1) + 4V(\overline{B}_2)$$

$$V_i = 4V(\overline{B}_1) + 4V(\overline{B}_2) + 16V(\overline{F}_2)$$

$$V_j = V(\overline{B}_1) + \tfrac{1}{4}\,V(\overline{P}_1) + V(\overline{B}_2) + \tfrac{1}{4}\,V(\overline{P}_2)$$

$$V_l = V(\overline{P}_1) + V(\overline{P}_2) + 4V(\overline{F}_1) + 16V(\overline{F}_2) + 16V(\overline{B}_1) + 16V(\overline{B}_2)$$

$V(P_1)$, $V(P_2)$, $V(F_1)$, $V(F_2)$, $V(B_1)$ and $V(B_2)$ are the variance of P_1, P_2, F_1, F_2, BC_1 and BC_2 generations, respectively.

The standard error of the gene effects was estimated as follows

$$S.E\,(m) = \sqrt{Vm}$$

$$S.E\,(d) = \sqrt{Vd}$$

$$S.E\,(h) = \sqrt{Vh}$$

$S.E(i) = \sqrt{Vi}$

$S.E(j) = \sqrt{Vj}$

$S.E(l) = \sqrt{Vl}$

The 't' values were worked out using following formulae

$t(m) = m / S.E(m)$

$t(d) = d / S.E(d)$

$t(h) = h / S.E(h)$

$t(i) = i / S.E(i)$

$t(j) = j / S.E(j)$

$t(l) = l / S.E(l)$

The significance for above parameter is tested with the help of 't' test. First standard error (S.E) is worked out for each component separately by taking the square root of the variance of the respective component. Then the 't' value is calculated for each component by dividing the gene effects of respective components by their S.E. The calculated value of 't' is compared with 1.96 which is the table value of 't' at 5 per cent level of significance. If the calculated value greater than 1.96, it is considered significant and vice versa.

3.5.7.4 Generation means and gene effects (Joint Scaling test)

The six families (P_1, P_2, F_1, F_2, BC_1 and BC_2) developed for four cross combinations were analyzed for generation mean analysis. The A, B, C and D scaling test of Mather (1949) and Hayman and Mather (1955) could not provide the detailed information. Separately on each parameter, namely:

i. additive x additive (i)

ii. additive x dominance (j)

iii. dominance x dominance (l)

Further, the six parameter model of Hayman (1958) can be employed to compute components of generation means, neither model can be tested nor the non-significant parameters can be eliminated from the model. Therefore, the data on seed yield and all possible ancillary traits were analyzed with the help of joint scaling test (Cavalli, 1952; Mather and Jinks, 1982) of three and six parameter models (to know non-significant parameters) where sequential model fit scheme was employed and the best model fit scheme was searched. The parameters m, [d] and [h] estimated from the observed mean of the available types of generations were compared with expected values derived from the estimates of these three parameters.

The six equations which are obtained by equating the observed family means to their expectations in terms of m, [d], [h], [i], [j] and [l] were used for estimating these parameters. Since, the number of equations is higher than the number of parameters to be estimated, least square technique was followed.

Further, the mean of various generations were not known with equal precision and hence, the generation means and their expectations were weighed, where the weight is estimated as

$$\text{Weight} = \frac{1}{(\text{Variance of generation mean})}$$

The weighed least square estimates of the three parameters were obtained from the three equations which were obtained after combining the six original equations and their weights. In order to assess first of these three equations, each of the original equation was multiplied by the coefficient of m which contained and by its weight and all the six equations were then summed to a single equation.

Similarly, the second and third equations were obtained by using the coefficients of [d] and [h] in turn the weights as the multipliers. These three simultaneous equations were solved by way of matrix inversion and the estimates of m, [d] and [h] were obtained.

The adequacy of the additive - dominance model was tested by determining the expected values of six different generations with help of estimates obtained from m, [d] and [h] and following the comparison between observed and expected means of these generations. Six deviations between the observed and expected values of each generation were obtained and by squaring each of these deviations and multiplying them by their corresponding weights tested the goodness of fit. The products were summed over all six types of families and tested against the values of n-p degrees of freedom; that is

$$\chi^2 = \sum_{i=l}^{6} \frac{(O-E)^2}{E} \times W \text{ for } (n-p) \text{d.f}$$

Where,

$\sum_{i=l}^{6}$	=	Represents the sum of all six products
O	=	Observed mean generations
E	=	Expected mean value of the generation
W	=	Corresponding weight of the generation
N	=	Number of equations and
P	=	Number of parameters to be used

χ^2 at (n-p) degrees of freedom (d, f) would indicate presence of epistasis. After confirmation of presence of epistasis, joint scaling test of parameter model significance estimates of m, [d], [h], [i], [j] and [l] was applied.

The weighed least square estimates of the six parameters were obtained for six equations which were obtained after combining the seven original equations and their weights. In order to assess first of these six equations each of the original equations was multiplied by the coefficients of m which it contained and by its weight all the six equations were then summed to give rise to a single equation.

Similarly, the second, third, fourth, fifth and sixth equations were obtained by using the coefficient of [d], [h], [i], [j] and [l] in turn the weights as the multipliers.

These six simultaneous equations were solved by way of matrix inversion and the estimates of m, [d], [h], [i], [j] and [l] were obtained.

The presence of the non-significant parameters in additive, dominance, additive x additive, additive x dominance and dominance x dominance model was searched and subsequently those were eliminated (χ^2) cannot be tested because degrees of freedom is zero.

Through sequential model fit scheme after eliminating the non-significant parameters of six parameter model best fit scheme was traced and tested through χ^2 at (n-p) degrees of freedom.

3.5.8 Chi-square test

χ^2 test was applied for testing the deviation of an observed segregation for theoretical observation. Chi-square was calculated using the formula

$$\chi^2 = \frac{\Sigma (O - E)^2}{E}$$

Where,

O	=	Observed frequency
E	=	Expected frequency
Σ	=	Summation of the data

If the calculated values of χ^2 is significant at 5 per cent level of significance, we can say that the fit is poor, one or more observed frequencies are not in accordance with the hypotheses assumed and vice versa. So, it is also known as goodness of fit. The degree of freedom (d. f) in χ^2 test is (n-1). Where n = number of classes.

Results

CHAPTER-IV

RESULTS

The results on "Studies on heterosis, combining ability and gene action for fibre characters, yield and its components in intra and inter specific hybrids of upland cotton (*Gossypium sp.*)" are presented under the following heads.

4.1 Mean performance of parents and crosses

4.2 Estimates of mean, range, PCV, GCV, heritability and genetic advance

4.3 Combining ability studies

4.4 Estimates of heterosis

4.5 Correlations

4.6 Path analysis

4.7 Generation mean analysis

4.1 MEAN PERFORMANCE OF PARENTS AND CROSSES

4.1.1 Analysis of variance

The mean data on fifteen characters *viz.,* days to 50% flowering, number of monopodia per plant, number of sympodia per plant, plant height (cm), days to maturity, boll weight (g), number of bolls per plant, ginning percentage, micronaire value (µg/inch), fibre length (mm), uniformity ratio, fibre strength (g/tax), seed cotton yield per plant (g), seed cotton yield per plot (g) and seed cotton yield qtl./ha were collected and analysed. Analysis of variance for fifteen characters is presented in Table 7.

The analysis of variance showed significant difference among the treatments (parents and crosses) for all the characters studied.

Table 7. Analysis of variance for yield, yield component and fibre quality characters in cotton

Source of variation	d.f.	Days to 50% flowering	Number of monopodia/ plant	Number of sympodia/ plant	Plant height (cm)	Days to maturity	Boll weight (g)	Number of bolls/ plant	Ginning percentage (%)	Micronaire value (µg/inch)	Fibre length (mm)	Uniformity ratio	Fibre strength (g/tex)	Seed cotton yield / plant (g)	Seed cotton yield / plot (g)	Seed cotton yield qt/ha
Replication	2	3.09	0.01	7.41	35.82	3.58	0.02	4.50	1.73	0.08	0.02	4.20	1.42	0.92	30.788	57404.59
Treatments	40	39.90**	0.10*	14.43**	416.96**	281.36**	0.21**	26.16**	19.07**	1.01**	31.84**	10.01**	10.64**	361.34**	121684.06**	231425.19**
Error	80	1.71	0.05	2.79	26.69	1.46	0.01	1.63	6.91	0.03	0.18	2.08	0.62	3.00	10803.86	22679.17

4.1.2 Mean performance

The mean performance of parents, crosses and checks for fifteen yield and fibre quality characters is presented in the Table 8.

4.1.2.1 Days to 50% flowering

The character days to 50% flowering recorded mean values ranging from 67.00 to 84.66 days in parents with an overall mean of 75.65 days. Among the parent, lines recorded mean value ranging from 67.00 (NH 545) to 78.00 days (NH 615), whereas for testers the values ranged from 72.33 (NH 452) to 84.66 days (Suvin). The cross NH 545 x NH 452 recorded lowest value (68.66 days, Plate 3) followed by NH 545 x NH 625 (71.66 days) and LRA 5166 x NH 625 (72.00 days) and the cross NH 630 x Suvin recorded the highest days to 50% flowering (82.33 days) with a mean of 76.06 days.

4.1.2.2 Number of monopodia per plant

The mean values of parents and hybrids for number of monopodia per plant ranged from 1.13 to 1.86. Among the females, the range was from 1.13 (NH 635) to 1.66 (LRA 5166), while for the males, it ranged from 1.20 (NH 625 and PKV Rajat) to 1.46 (Suvin). The mean values for hybrid ranged from 1.13 (LRA 5166 x Suvin) to 1.86 (NH 615 x NH 452). The cross NH 615 x NH 452 (1.86) recorded the highest monopodial values followed by NH 615 x NH 625 (1.80) and PH 1076 x Suvin (1.73).

4.1.2.3 Number of sympodia per plant

The mean of lines was 22.35 with a range of 19.68 (NH 630) to 24.66 (PH 1076). Among the testers the range was 23.06 (PKV Rajat) to 26.26 (Suvin) and among the crosses it ranged from 19.33 (LRA 5166 x PKV Rajat) to 28.26 (PH 1076 x PKV Rajat). The cross PH 1076 x PKV Rajat (28.26) recorded the highest mean value followed by LRA 5166 x NH 452 (27.59) and PH 1076 x NH 452 (27.40). The overall mean of parents

Table 8. Mean performance of parents, crosses and checks for different characters in cotton

	Days to 50% flowering	Number of monopodia /plant	Number of sym-Podia /plant	Plant height (cm)	Days to maturity	Boll weight (g)	Number of bolls /Plant	Ginning percentage (%)	Micronaire value (µg/inch)	Fibre length (mm)	Uniformity ratio	Fibre strength (g/tex)	Seed cotton yield / plant (g)	Seed cotton yield / plot (g)	Seed cotton yield qtl./ha
Lines															
NH 545	67.00	1.46	22.33	137.80	162.66	2.90	27.27	40.00	3.88	23.46	45.96	20.27	82.38	1483.00	20.59
NH 615	78.00	1.40	21.26	129.60	147.33	2.82	23.34	37.92	3.42	23.91	47.56	22.33	68.75	1237.66	17.18
NH 630	76.33	1.33	19.68	121.93	162.33	3.18	24.82	33.35	3.96	24.25	49.13	22.36	67.46	1214.33	16.86
NH 635	76.00	1.13	22.93	135.40	167.66	2.94	26.76	37.65	4.64	26.51	46.86	24.16	81.45	1466.33	20.36
PH- 1060	77.33	1.53	23.06	145.86	148.33	3.10	25.84	37.34	3.60	23.06	45.96	21.56	71.88	1294.00	17.97
PH 1076	75.00	1.40	24.66	167.13	152.33	3.12	25.50	38.34	4.63	23.16	47.36	22.30	78.00	1404.00	19.49
LRA 5166	74.33	1.66	22.53	162.73	164.33	3.16	26.68	38.27	3.30	24.93	47.40	25.60	79.55	1648.00	22.88
Lines mean	**74.76**	**1.42**	**22.35**	**142.92**	**157.85**	**3.03**	**25.74**	**37.55**	**3.92**	**24.18**	**47.18**	**22.65**	**75.63**	**1392.47**	**19.33**
Testers															
NH 452	72.33	1.26	25.66	136.26	163.66	2.98	24.72	39.98	3.98	24.20	45.93	21.18	73.47	1316.66	18.28
NH 625	74.00	1.20	24.66	133.33	166.33	3.05	23.82	40.16	4.42	23.30	49.36	21.82	67.75	1219.66	16.94
PKV Rajat	73.66	1.20	23.06	123.26	150.33	3.05	24.34	38.06	3.96	21.56	47.83	25.26	72.35	1302.33	18.07
Suvin	84.66	1.46	26.26	166.00	184.66	2.40	29.26	32.96	3.87	33.62	45.56	26.36	68.55	1234.00	17.13
Tester mean	**76.00**	**1.28**	**24.91**	**139.71**	**166.25**	**2.87**	**25.53**	**35.54**	**4.06**	**25.67**	**47.17**	**23.66**	**70.53**	**1268.16**	**17.61**
Parental mean	**75.33**	**1.36**	**23.28**	**141.75**	**160.90**	**2.97**	**25.66**	**36.82**	**3.97**	**24.72**	**47.17**	**23.02**	**73.78**	**1347.27**	**18.70**

Table 8. Contd...

CROSSES	Days to 50% flower-ing	Number of mono-podia /plant	Number of sym-Podia /plant	Plant height (cm)	Days to maturity	Boll weigh t (g)	Number of bolls /Plant	Ginning per-centage (%)	Micro-naire value (µg/inch)	Fibre length (mm)	Unifor-mity ratio	Fibre strength (g/tex)	Seed cotton yield / plant (g)	Seed cotton yield / plot (g)	Seed cotton yield qtl./ha
NH 545 x NH 452	68.66	1.40	25.46	145.13	161.33	3.15	26.20	40.56	3.88	24.43	46.53	22.10	80.72	1453.33	20.18
NH 545 x NH 625	71.66	1.33	24.73	150.20	163.66	3.15	24.35	40.33	4.30	23.96	48.73	21.76	74.20	1335.66	18.54
NH 545 x PKV Rajat	74.00	1.26	23.80	148.93	159.00	3.05	25.40	39.49	4.44	21.53	48.36	25.20	75.22	1354.00	18.80
NH 545 x Suvin	80.33	1.60	26.90	154.46	173.33	2.60	23.62	38.42	4.68	27.60	45.40	26.02	58.64	1073.66	14.90
NH 615 x NH 452	75.33	1.86	23.49	136.13	158.66	3.20	28.82	40.19	3.61	21.35	45.76	23.63	88.88	1600.00	22.21
NH 615 x NH 625	75.00	1.80	20.49	132.66	160.33	3.18	27.86	39.21	4.07	23.03	46.83	22.40	87.37	1572.66	21.84
NH 615 x PKV Rajat	80.00	1.63	23.26	138.06	154.66	3.12	32.84	38.42	4.50	23.16	44.76	25.38	99.87	1797.66	24.96
NH 615 x Suvin	80.33	1.40	25.86	136.46	177.33	2.52	27.90	37.52	3.81	28.75	40.50	26.12	67.37	1212.66	16.84
NH 630 x NH 452	75.00	1.20	22.73	142.80	165.00	2.81	26.40	41.30	3.94	24.51	46.36	22.17	71.14	1280.66	17.78
NH 630 x NH 625	76.66	1.53	21.63	146.20	164.00	3.00	22.54	41.73	4.99	22.63	44.06	21.96	64.53	1161.66	16.13
NH 630 x PKV Rajat	76.00	1.20	20.53	134.73	159.33	3.11	22.30	33.54	4.18	21.71	45.56	24.68	66.09	1189.66	16.52
NH 630 x Suvin	82.33	1.26	22.20	138.00	183.66	2.32	25.68	36.74	3.69	30.41	44.30	25.52	57.79	1040.33	14.50

Table 8. Contd...

CROSSES	Days to 50% flowering	Number of monopodia /plant	Number of sym-Podia /plant	Plant height (cm)	Days to maturity	Boll weight (g)	Number of bolls /Plant	Ginning percentage (%)	Micronaire value (µg/inch)	Fibre length (mm)	Uniformity ratio	Fibre strength (g/tex)	Seed cotton yield / plant (g)	Seed cotton yield / plot (g)	Seed cotton yield qtl./ha
NH 635 x NH 452	75.33	1.53	20.93	142.06	165.00	3.21	24.46	40.10	4.61	25.58	45.60	23.39	76.68	1380.33	19.16
NH 635 x NH 625	74.66	1.26	22.46	135.93	163.00	3.11	25.36	40.12	4.87	24.33	45.55	23.75	78.22	1408.00	19.55
NH 635 x PKV Rajat	75.00	1.33	23.94	140.26	160.00	3.03	24.53	39.40	3.77	23.93	44.80	23.88	73.64	1331.66	18.49
NH 635 x Suvin	79.66	1.33	23.93	137.06	178.66	2.55	23.28	35.34	4.02	25.43	43.74	24.53	58.09	1045.66	14.70
PH 1060 x NH 452	77.00	1.33	24.51	158.16	156.33	3.18	21.52	40.54	3.60	24.45	47.53	22.20	67.00	1206.00	16.75
PH 1060 x NH 625	73.66	1.46	23.15	149.26	163.00	3.24	26.98	42.05	3.04	24.23	46.33	22.13	83.12	1406.33	19.53
PH 1060 x PKV Rajat	75.00	1.53	27.02	160.46	146.66	3.09	29.42	40.33	3.08	20.10	45.40	23.75	86.93	1565.33	21.73
PH 1060 x Suvin	79.00	1.33	22.26	158.46	175.66	2.70	23.28	36.09	2.99	30.70	43.70	27.46	61.35	1104.33	15.33
PH 1076 x NH 452	73.00	1.66	27.40	158.60	154.33	3.28	30.90	40.25	4.39	28.60	45.70	21.51	97.29	1751.33	24.32
PH 1076 x NH 625	74.33	1.60	24.06	155.00	156.33	3.05	27.40	41.70	4.48	22.33	46.66	23.08	81.72	1471.00	20.42
PH 1076 x PKV Rajat	76.33	1.40	28.26	162.40	150.66	3.20	34.72	41.43	4.48	22.70	43.76	23.93	109.33	1968.00	27.33
PH 1076 x Suvin	79.33	1.73	22.46	159.20	184.66	2.40	28.36	35.83	3.19	31.51	45.26	26.76	66.90	1204.33	16.72

Table 8. Contd...

CROSSES	Days to 50% flowering	Number of monopodia/ plant	Number of sympodia/ plant	Plant height (cm)	Days to maturity	Boll weight (g)	Number of bolls/ plant	Ginning percentage (%)	Micronaire value (µg/inch)	Fibre length (mm)	Uniformity ratio	Fibre strength (g/tex)	Seed cotton yield / plant (g)	Seed cotton yield / plot (g)	Seed cotton yield qtl./ha
LRA 5166 x NH-45	74.00	1.53	27.59	149.20	164.33	3.22	26.58	41.03	4.23	25.66	45.90	23.62	82.24	1480.33	20.55
LRA 5166 x NH 625	72.00	1.60	21.56	153.46	165.66	2.90	27.64	39.33	4.58	21.70	46.73	24.33	77.72	1399.00	19.42
LRA 5166 x PKV Rajat	75.66	1.46	19.33	152.66	157.00	2.65	22.81	40.69	4.69	23.96	44.23	25.19	69.38	1249.00	17.34
LRA 5166 x Suvin	81.33	1.13	20.73	157.00	174.00	2.80	30.70	34.41	3.04	32.46	44.20	27.50	77.25	1390.66	19.31
Cross mean	**76.06**	**1.45**	**23.59**	**147.60**	**164.13**	**2.97**	**26.49**	**39.15**	**4.04**	**25.03**	**45.44**	**24.07**	**76.38**	**1372.76**	**19.07**
General mean	**75.65**	**1.42**	**23.47**	**145.41**	**163.17**	**2.98**	**26.07**	**38.54**	**3.98**	**25.05**	**45.93**	**23.66**	**75.61**	**1365.52**	**18.95**
NHH 44	67.66	1.46	22.76	135.73	161.33	3.15	23.18	34.54	3.59	24.65	48.50	20.72	78.88	1454.00	19.66
DCH 32	75.00	1.20	23.13	133.93	164.00	3.00	21.74	35.04	2.66	30.18	42.16	22.05	70.84	1234.33	17.71
SE m±	**0.75**	**0.15**	**0.96**	**2.98**	**0.68**	**0.05**	**0.73**	**1.51**	**0.10**	**0.24**	**0.82**	**0.45**	**1.00**	**60.01**	**0.87**
CD(5%)	**2.12**	**0.38**	**2.71**	**8.39**	**1.93**	**0.14**	**2.07**	**4.27**	**0.30**	**0.68**	**2.32**	**1.28**	**2.81**	**168.89**	**2.45**

Plate 3. A cross showing early flowering
(NH 545 x NH 452)

and hybrids was 23.28 and 23.59 respectively, while the check DCH 32 recorded 23.13 numbers of sympodia per plant.

4.1.2.4 Plant height (cm)

Among the females, the range was for plant height 121.93 (NH 630) to 167.13 cm (PH 1076), while for the males it ranged from 123.26 (PKV Rajat) to 166.00 cm (Suvin). The mean values for hybrids ranged from 132.66 (NH 615 x NH 625) to 162.40 cm (PH 1076 x PKV Rajat), while the check NHH 44 recorded 135.73 cm of plant height. The cross PH 1076 x PKV Rajat (162.40 cm) exhibited highest plant height followed by PH 1060 x PKV Rajat (160.46 cm) and PH 1076 x NH 452 (158.60 cm).

4.1.2.5 Days to maturity

The character days to maturity recorded mean values ranging from 146.66 to 184.66 days in parents with an overall mean of 163.17 days. Among the parents, lines recorded mean value ranging from 147.33 (NH 615) to 167.66 days (NH 635), whereas, for testers the values ranged from 150.33 (PKV Rajat) to 184.66 days (Suvin). Among the crosses, PH 1060 x PKV Rajat recorded lowest value (146.66 days, Plate 4) followed by PH 1076 x PKV Rajat (150.66 days) and PH 1076 x NH 452 (154.33 days). The cross PH 1076 x Suvin recorded late days to maturity (184.66 days) than check NHH 44 (161.33 days).

4.1.2.6 Boll weight (g)

The boll weight among the parents and hybrids ranged between 2.32 and 3.28 g, while the check NHH 44 recorded 3.15 g. This character ranged from 2.82 (NH 615) to 3.18 g (NH 630) in lines with a mean of 3.03 g, while in testers the range was from 2.40 (Suvin) to 3.05 g (NH 625 and PKV Rajat) with a mean of 2.87 g. The overall mean of

Plate 4. Early maturing hybrid (PH 1060 x PKV Rajat)

parents and crosses was 2.97 and 2.97 g, respectively. The cross PH 1076 x NH 452 recorded the maximum boll weight (3.28 g).

4.1.2.7 Number of bolls per plant

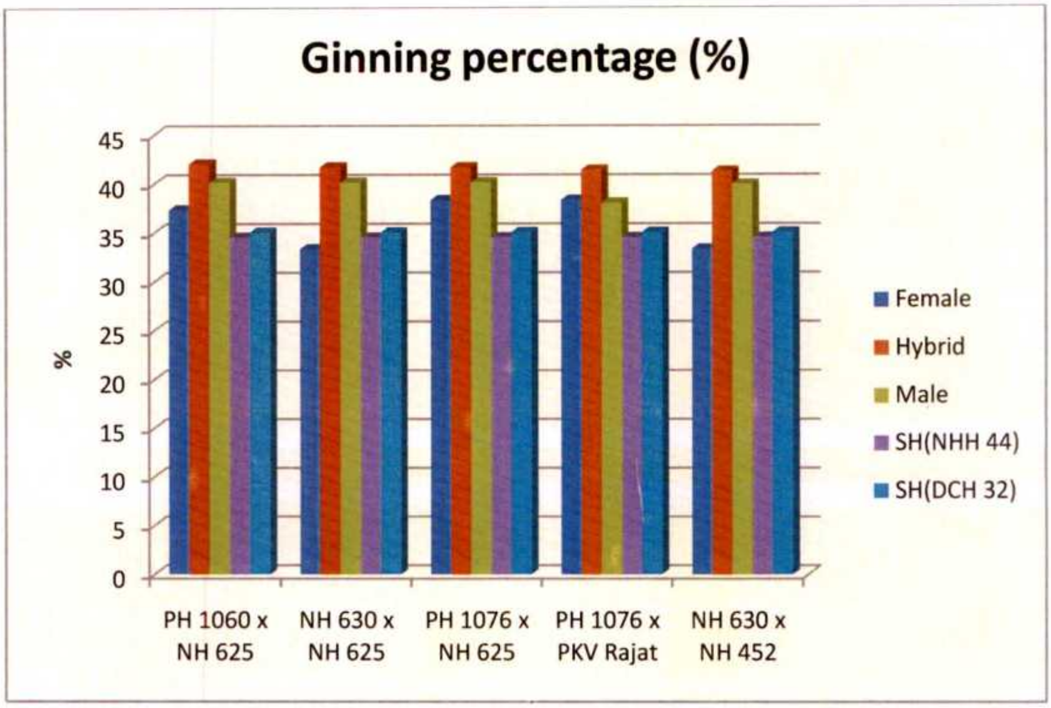
The overall mean values for number of bolls per plant ranged from 21.52 to 34.72 hybrids. In lines, number of bolls per plant ranging from 23.34 (NH 615) to 27.27 (NH 545) with mean of 25.74, whereas for the testers, the values ranged from 23.82 (NH 625) to 29.26 (Suvin) with a mean of 25.53. The cross PH 1076 x PKV Rajat recorded the highest bolls per plant (34.72) followed by NH 615 x PKV Rajat (32.84) and PH 1076 x NH 452 (30.90). However, the check NHH 44 recorded 23.18 numbers of bolls per plant.

4.1.2.8 Ginning percentage (%)

The ginning percentage varied from 32.96 to 42.05. The female parents exhibited a range of 33.35 (NH 630) to 40.00 per cent (NH 545), while the male parents were in the range of 32.96 (Suvin) to 40.16 per cent (NH 625) with a mean of 37.55 and 35.54 per cent of lines and testers respectively. Among the hybrids, PH 1060 x NH 625 recorded highest ginning per cent (42.05%, Fig. 1) followed by NH 630 x NH 625 (41.73%) and PH 1076 x NH 625 (41.70%). The cross NH 630 x PKV Rajat recorded the lowest ginning percentage (33.54%).

4.1.2.9 Micronaire value (μg/inch)

Mean micronaire values were recorded 3.92 μg/inch, 4.06 μg/inch and 4.04 μg/inch for lines, testers and crosses, respectively. Among the lines, LRA 5166 recorded the minimum value (3.30 μg/inch), whereas NH 635 recorded the maximum (4.64 μg/inch), while in testers, Suvin recorded minimum values (3.87 μg/inch) and NH 625 recorded the maximum (4.42 μg/inch), corresponding to the parental mean of 3.97



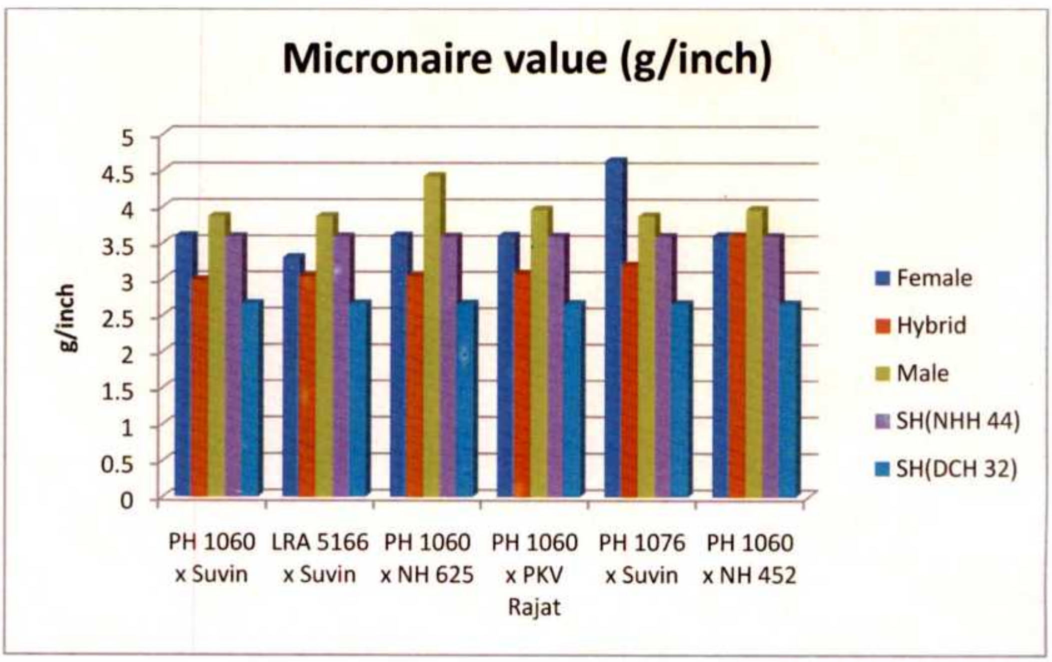


Fig. 1. Performance of promising hybrids for fiber properties

μg/inch. In crosses, PH 1060 x Suvin recorded lowest value of 2.99 μg/inch followed by PH 1060 x NH 625 (3.04 μg/inch) and LRA 5166 x Suvin (3.04 μg/inch).The cross NH 630 x NH 625 recorded highest micronaire value (4.99 μg/inch). The check DCH 32 recorded 2.66 μg/inch (Fig. 1).

4.1.2.10 Fibre length (mm)

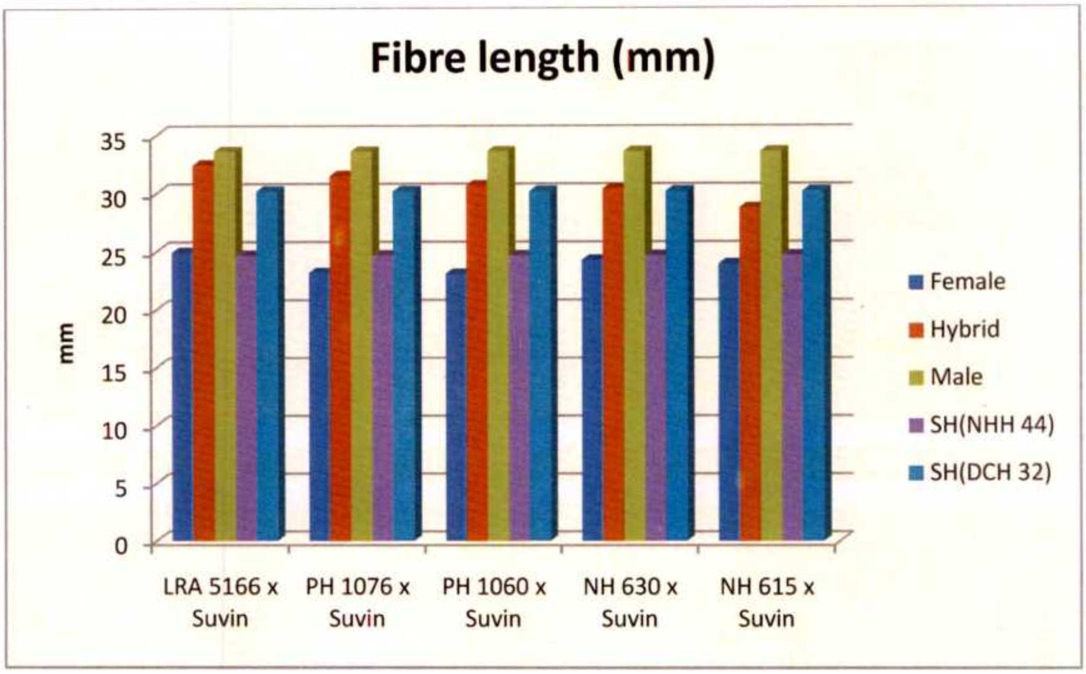
This character ranged from 23.06 (PH 1060) to 26.51 mm (NH 635) in lines with a mean of 24.18 mm, while in testers the range was from 21.56 (PKV Rajat) to 33.62 mm (Suvin) with a mean of 25.67 mm. The overall mean of parents and crosses was 24.72 mm and 25.03 mm respectively. The cross LRA 5166 x Suvin recorded the maximum fibre length of 32.46 mm followed by PH 1076 x Suvin (31.51 mm) and PH 1060 x Suvin (30.70 mm) Fig. 2.

4.1.2.11 Uniformity ratio

Among the parents and hybrids the mean values of uniformity ratio ranged from 40.50 to 49.36. Among the lines, the character ranged from 45.96 (PH 1060 and NH 545) to 49.13 (NH 630) and from 45.56 (Suvin) to 49.36 (NH 625) in testers with a mean values of 47.18 and 47.17 respectively. Among the crosses, the values varies from 40.50 (NH 615 x Suvin) to 48.73 (NH 545 x NH 625) with a mean of 45.44, while NH 545 x NH 625 (48.73) recorded highest uniformity ratio followed by NH 545 x PKV Rajat (48.36) and PH 1060 x NH 452 (47.53) Fig. 2.

4.1.2.12 Fibre strength (g/tex)

For fibre strength, the lines, testers and crosses exhibited mean values of 22.65 (g/tex), 23.66 (g/tex) and 24.07 (g/tex) respectively. The parent NH 545 recorded minimum value of 20.27 (g/tex), whereas LRA 5166 recorded the maximum (25.60 g/tex) among the females. Among the males, the value varied from NH 452 (21.18 g/tex) to Suvin (26.36 g/tex) for the check DCH 32 the fibre strength recorded was 22.05 g/tex. Among the



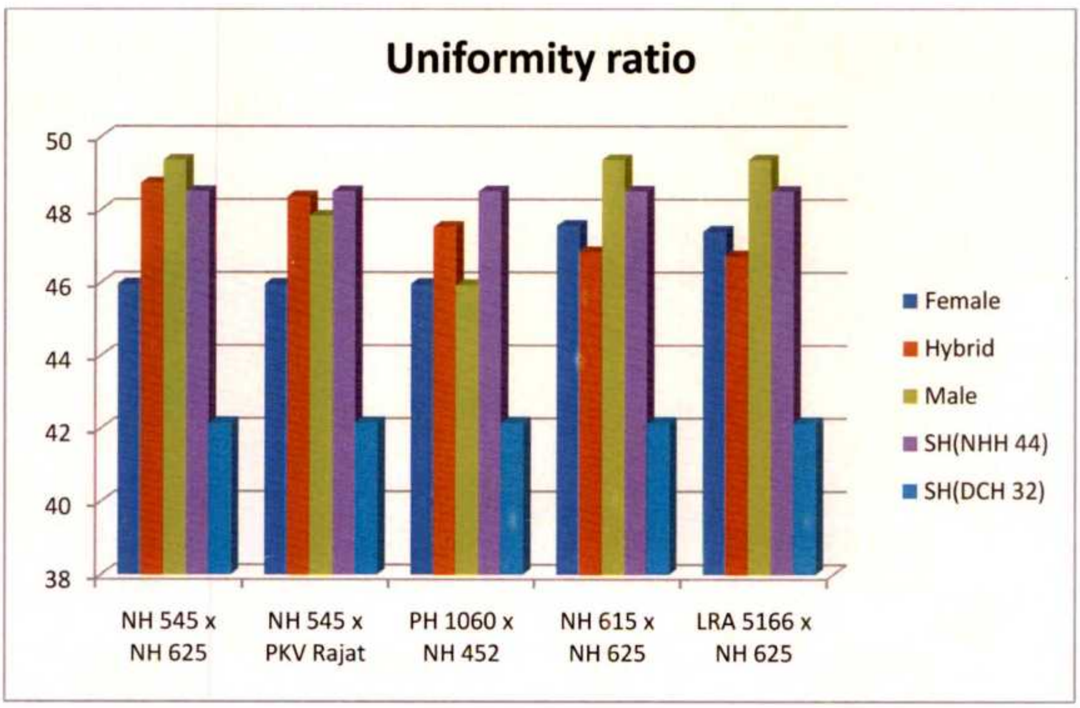


Fig. 2. Performance of promising hybrids for fibre properties

hybrids, LRA 5166 x Suvin recorded highest value of 27.50 g/tex followed by PH 1060 x Suvin (27.46 g/tex) and PH 1076 x Suvin (26.76 g/tex) Fig. 3.

4.1.2.13 Seed cotton yield per plant (g)

Among the lines, the seed cotton yield per plant values varied from 67.46 (NH 630) to 82.38 g (NH 545), whereas in testers NH 625 recorded lowest yield of 67.72 g and NH 452 recorded the highest value of 73.47 g. The hybrid, NH 630 x Suvin recorded the lowest value of 57.79 g and the hybrid PH 1076 x PKV Rajat recorded the highest yield of 109.33 g followed by NH 615 x PKV Rajat (99.87 g) and PH 1076 x NH 452 (97.29 g) (Plate 5 and Fig. 4). The check NHH 44 recorded the seed cotton yield of 78.88 g per plant.

4.1.2.14 Seed cotton yield per plot (g)

Among the lines, the seed cotton yield per plot varied from 1214.33 (NH 630) to 1648.00 g (LRA 5166), whereas in testers NH 452 recorded the highest 1316.66 g followed by 1302.33 (PKV Rajat) and 1234.00 g (Suvin). The hybrid PH 1076 x PKV Rajat recorded the highest yield of 1968.00 g followed by NH 615 x PKV Rajat (1797.66 g) and PH 1076 x NH 452 (1751.33 g) as compare to check NHH 44 (1454.00 g).

4.1.2.15 Seed cotton yield qtl./ ha

Among the lines, the seed cotton yield qtl./ ha varied from 16.86 (NH 630) to 22.88 qtl./ha (LRA 5166), whereas in testers NH 452 (18.28) recorded the highest qtl./ha seed cotton yield followed by PKV Rajat (18.07 qtl./ha) and Suvin (17.13 qtl./ha). The hybrid PH 1076 x PKV Rajat recorded the highest yield seed cotton 27.33 qtl./ha followed by NH 615 x PKV Rajat (24.96 qtl./ha) and PH 1076 x NH 452 (24.32 qtl./ha) whereas, the check NHH 44 recorded 19.66 qtl./ha (Fig. 4). The interspecific cross LRA 5166 x Suvin recorded the highest seed cotton yield (19.31 qt/ha) among the interspecific crosses with better fibre quality (Plate 6).

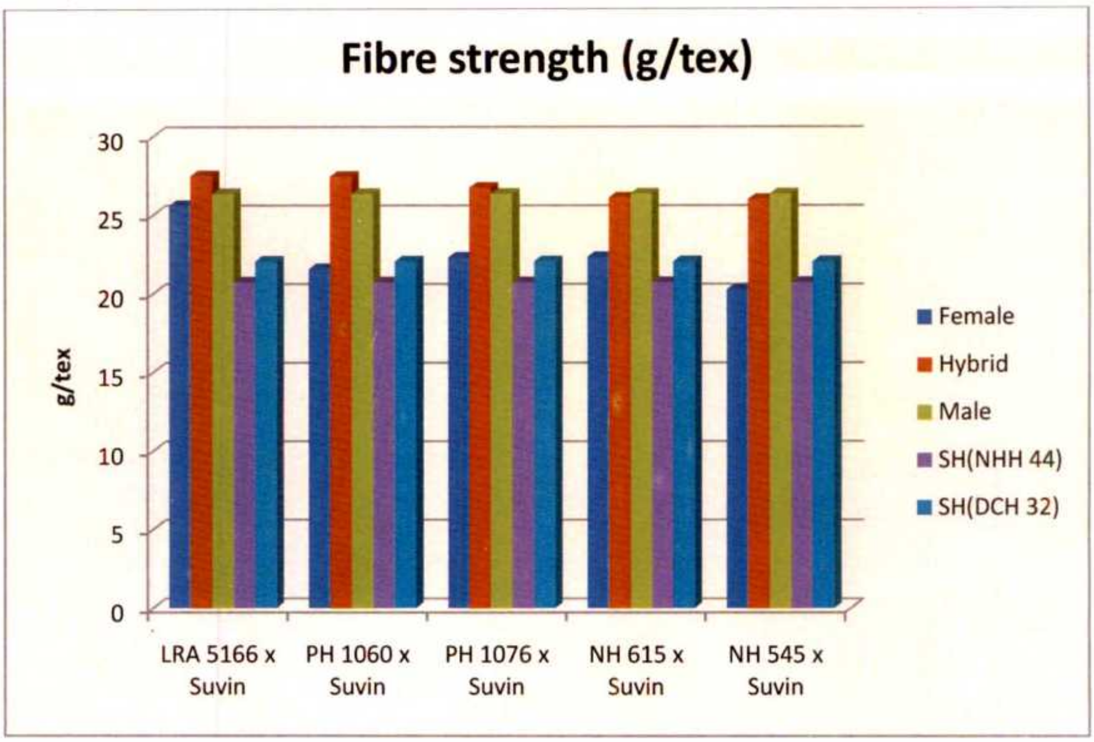
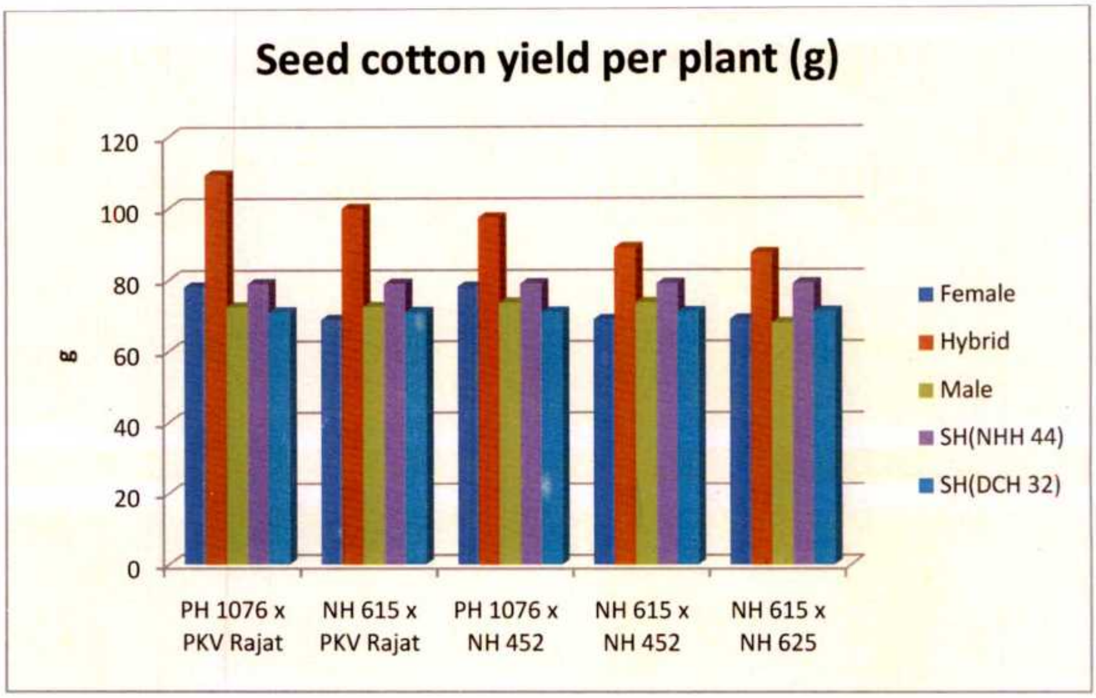


Fig. 3. Performance of promising hybrids for fiber properties



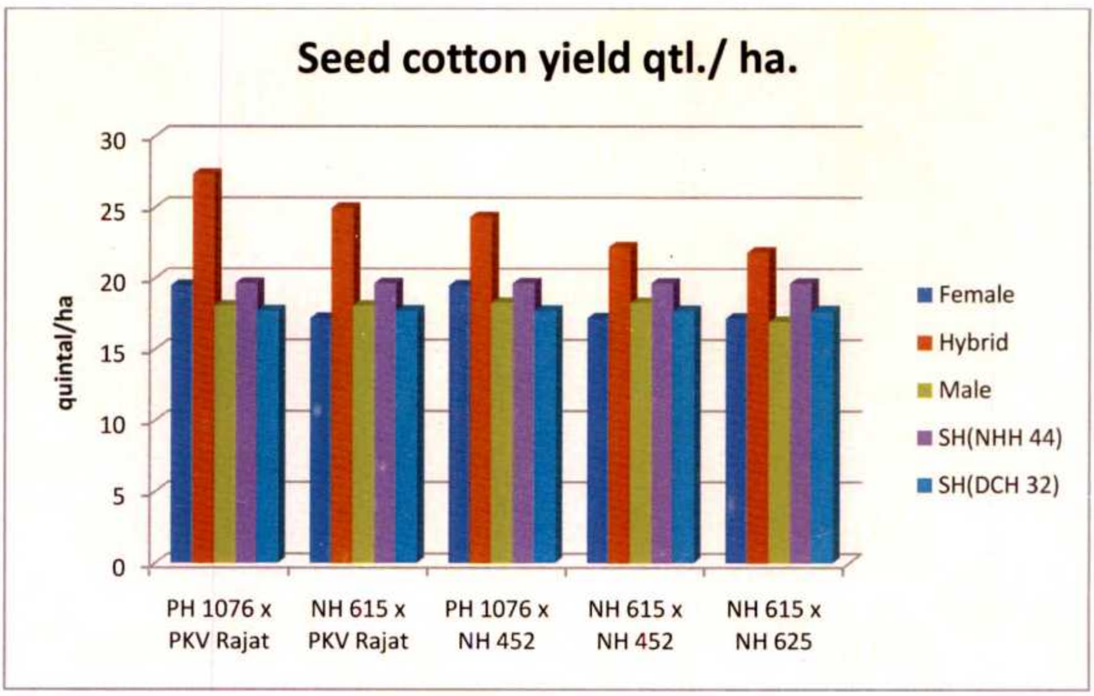


Fig. 4. Performance of promising hybrids for seed cotton yield

Plate 5. A promising intraspecific cross for seed cotton yield (PH 1076 x PKV Rajat)

Plate 6. A promising interspecific cross for fibre quality and yield (LRA 5166 x Suvin)

4.2 MEAN, RANGE, GENOTYPIC COEFFICIENT OF VARIATION (GCV), PHENOTYPIC COEFFICIENT OF VARIATION (PCV), HERITABILITY (h^2) AND GENETIC ADVANCE (GA) IN COTTON

The results are furnished in Table 9.

4.2.1 Days to 50% flowering

The overall mean for this character was 75.65 days with a range from 67.00 to 84.66 days. Genotypic coefficient of variation and phenotypic coefficient of variation were 4.71 and 5.02 respectively. Broad sense heritability recorded was 88.13 per cent with low genetic advance of 9.12.

4.2.2 Number of monopodia per plant

Range for this character was from 1.13 to 1.86, with mean of 1.42. GCV and PCV values recorded were 8.53 and 18.52 respectively. The heritability recorded low (21.24 per cent) with low genetic advance (8.10) was observed for this trait.

4.2.3 Number of sympodia per plant

The character ranged from 19.33 to 28.26 with a mean of 23.47. The values recorded for GCV, PCV, heritability and genetic advance were 8.38, 11.00, 58.99 per cent and 16.87 respectively.

4.2.4 Plant height

The overall mean for this character was 145.41 cm with a range from 121.93 to 167.13 cm. For this character GCV was 7.84, PCV was 8.61 whereas high heritability 82.97 per cent and high genetic advance (14.71) was recorded.

4.2.5 Days to maturity

The overall mean for this character was 163.17 days with a range from 146.66 to 184.66 day. The low GCV (5.91) and PCV (5.96) was

Table 9. Mean, range, genotypic coefficient of variation, phenotypic coefficient of variation, heritability and genetic advance for different characters in cotton

Character	Mean	Range		GCV	PCV	h^2	GA (% over mean)
		Minimum	Maximum				
Days to 50% flowering	75.65	67.00	84.66	4.71	5.02	88.13	9.12
Number of monopodia / plant	1.42	1.13	1.86	8.53	18.52	21.24	8.10
Number of sympodia / plant	23.47	19.33	28.26	8.38	11.00	58.99	16.87
Plant height (cm)	145.41	121.93	167.13	7.84	8.61	82.97	14.71
Days to maturity	163.17	146.66	184.66	5.91	5.96	98.45	12.09
Boll weight (g)	2.98	2.32	3.28	8.70	9.23	88.84	16.90
Number of bolls/plant	26.07	21.52	34.72	10.96	12.01	83.32	20.61
Ginning percentage (%)	38.54	32.96	42.05	5.22	8.59	36.92	6.53
Micronaire value (µg/ inch)	3.98	2.66	4.99	14.31	15.04	90.50	28.04
Fibre length (mm)	25.05	20.10	33.62	12.96	13.07	98.27	26.47
Uniformity ratio	45.93	40.50	49.36	3.54	4.73	55.93	5.45
Fibre strength (g/tex)	23.66	20.27	27.50	7.72	8.41	84.28	14.61
Seed cotton yield / plant (g)	75.61	57.79	109.79	14.45	14.63	97.55	29.40
Seed cotton yield / plot (g)	1364.52	1040.33	1968.00	14.08	16.01	77.38	25.53
Seed cotton yield qtl./ha	18.95	14.50	27.33	13.91	16.02	75.42	24.89

found for this character. However, high heritability (98.45 per cent) with high genetic advance (12.09) was recorded for days to maturity.

4.2.6 Boll weight

The overall mean for this character was 2.98 g with a range from 2.32 to 3.28 g. GCV and PCV recorded for this character was 8.70 and 9.23, respectively. The high heritability (88.84 per cent) with moderate genetic advance (16.90) was recorded for this trait.

4.2.7 Number of bolls per plant

Range for number of bolls per plant was 21.52 to 34.72 with an average value of 26.07. The GCV for this character was 10.96 and PCV was 12.01. The high heritability and high genetic advance was recorded (83.32 per cent and 20.61, respectively) for this trait.

4.2.8 Ginning percentage

The mean value recorded for ginning percentage was 38.54 per cent, whereas a range was from 32.96 to 42.05 per cent. GCV, PCV, heritability and genetic advance recorded were 5.22, 8.59, 36.92 per cent and 6.53, respectively.

4.2.9 Micronaire value

For the trait micronaire value, the mean was 3.98 µg/inch, whereas the range was from 2.66 to 4.99 µg/inch. GCV and PCV recorded were 14.31 and 15.04 respectively. High genetic advance (28.04) and high heritability (90.50 per cent) recorded for this trait.

4.2.10 Fibre length

For this character, 25.05 mm was the mean value recorded with a range from 20.10 to 33.62 mm. Both GCV (12.96) and PCV (13.07) recorded high values, while heritability (98.27 per cent) and genetic advance (26.47) was observed to be very high.

4.2.11 Uniformity ratio

The trait uniformity ratio ranged from 40.50 to 49.36 with an average value of 45.93. Both GCV (3.54) and PCV (4.73) recorded low value, while heritability was moderate (55.93 per cent) and genetic advance very low (5.45).

4.2.12 Fibre strength

The overall mean for this character was 23.66 g/tex with a range from 20.27 to 27.50 g/tex. Both GCV (7.72) and PCV (8.41) recorded moderate values, while heritability was high (84.28) and low genetic was recorded (14.61).

4.2.13 Seed cotton yield per plant

This character has recorded a mean value of 75.61 g with a range of 57.79 to 109.79 g per plant. Both GCV (14.45) and PCV (14.63) were found to be moderate coupled with high heritability (97.55 per cent) and high genetic advance (29.40).

4.2.14 Seed cotton yield per plot

The overall mean for this character was 1364.52 g with range from 1040.33 to 1968.00 g per plot. GCV recorded was 14.08 and PCV was 16.01. High heritability 77.38 per cent and high genetic advance (25.53) were recorded for these trait.

4.2.15 Seed cotton yield qtl./ ha

For this character 18.95 qt/ha was the mean value recorded with a range from 14.50 to 27.33 qtl./ha. Both GCV (13.91) and PCV (16.02) recorded moderate values, while moderate heritability (75.42) per cent with high genetic advance was observed (24.89) recorded.

4.3 COMBINING ABILITY

4.3.1 Analysis of variance

Analysis of variance for combining ability revealed significant differences for most of the characters within parents and crosses. In lines, significant differences were observed for number of monopodia per plant, plant height, number of bolls per plant, micronaire value, seed cotton yield per plant, seed cotton yield per plot and seed cotton yield quintal per ha., where as in testers significant differences were recorded for days to 50% flowering, days to maturity, boll weight, ginning percentage, fibre length, uniformity ratio, fibre strength, seed cotton yield per plant, seed cotton yield per plot and seed cotton yield qtl./ ha. (except for number of monopodia per plant, number of sympodia per plant, plant height, number of bolls per plant and micronaire value). In line x tester significant differences were noted for all the characters (except for number of monopodia per plant and ginning percentage). However, in parents vs crosses significant differences were observed for all the traits studied, except for number of monopodia per plant, boll weight, micronaire value, seed cotton yield per plot and seed cotton yield quintal per ha (Table10).

4.3.2 Combining ability variances and gene action

The estimates of general combining ability (GCA) and specific combining ability (SCA) variances, their ratios and gene action are presented in Table 11. General combining ability is generally associated with additive gene action while specific combining ability is genetically due to dominance and epistasis.

In the present study, the result revealed that the variance due to SCA were higher in magnitude than the variance due to GCA for the characters days to 50% flowering, number of monopodia per plant, number

Table 10. Analysis of variance for combining ability for yield, yield component and fibre quality characters in cotton

Source of variation	Degree of freedom	Days to 50% flowering	Number of monopodia/ plant	Number of sympodia/ plant	Plant height (cm)	Days to maturity	Boll weight (g)	Number of bolls/plant	Ginning percentage (%)	Micro-naire value (µg/inch)	Fibre length (mm)	Unifor-mity ratio	Fibre strength (g/tex)	Seed cotton yield /plant (g)	Seed cotton yield / plot (g)	Seed cotton yield qtl./ha
Replication	2	2 67	0.04	9 01	55 80	3.39	0.022	3.06	2.03	0.06	0.03	4 69	1.15	1.23	32960.77	60086.11
Treatments	38	36.78**	0.10	15.14**	420.19**	295 84**	0.21**	25.29**	17.72**	0.90**	31.38**	8 89**	10.27**	377.71**	126114.92**	241981.34**
Parents	10	55 13**	0.07	11.12**	818.52**	357.53**	0.14**	8 97**	17.67*	0.59**	30.68**	4.93*	12.02**	95.57**	57254.05**	110463.58**
Parents vs Crosses	1	13 75*	0.17	2.34*	811.02**	240.51**	0.09	16 17*	55 26**	0.12	1 99**	71 63**	26 11**	160.26**	15392 84	30890.27
Crosses	27	30.83**	0.10	17.10**	258 18**	275.84**	0 25**	31 67**	16 35**	1.05**	32.73**	8 04**	9.04**	490.26**	155719.66**	298509 87**
Lines	6	21.17	0.21*	25.12	1014.73**	90.53	0 07	73 33*	4 10	1.89*	7.96	9.57	3 48	839.45**	273090 59**	524839.51**
Testers	3	185.87**	0 08	14.28	26.46	2034 82**	1.11**	8 78	86.75**	1.87	211.18**	28 10**	61.39**	1531.71**	483337.26**	920794.00**
Lines x Testers	18	8 21**	0.07	14.90**	44 62*	43.26**	0 17**	21.59**	8.70	0.63**	11.24**	4.18*	2.17**	200.28**	61993.23**	119352.64**
Error	76	1.72	0.05	2 83	26.13	1 48	0.01	1.66	7.19	0 03	0.18	2.15	0.60	2.68	11300.04	23531.74
Total	116	13.22	0.06	6.97	155.73	97.95	0.08	9.42	10 55	0.32	10 40	4 40	3.78	125.51	49285 28**	95723.06

Table 11. Estimates of general and specific combining ability variances and their ratios in cotton

Characters	δ^2 gca	δ^2sca	δ^2gca/ δ^2 sca
Days to 50% flowering	0.5027	2.1626	0.2324
Number of monopodia/ plant	0.0007	0.0070	0.1000
Number of sympodia/ plant	0.0490	4.0246	0.0121
Plant height (cm)	4.7458	6.1627	0.7700
Days to maturity	5.1509	13.9267	0.3698
Boll weight (g)	0.0019	0.0543	0.0349
Number of bolls/plant	0.2239	6.6459	0.03336
Ginning percentage (%)	0.1700	0.5056	0.3366
Micronaire value (µg/ inch)	0.0093	0.1993	0.0456
Fibre length (mm)	0.4775	3.6848	0.1295
Uniformity ratio	0.0856	0.6791	0.1260
Fibre strength (g/tex)	0.1527	0.5246	0.2910
Seed cotton yield / plant (g)	6.4438	65.8670	0.0978
Seed cotton yield / plot (g)	2082.812	16897.728	0.1232
Seed cotton yield qt./ha	3981.271	32546.717	0.1223

of sympodia per plant, days to maturity, plant height, number of bolls per plant, boll weight, ginning percentage, uniformity ratio, fibre length, micronaire value, bundle strength, seed cotton yield per plant, Seed cotton yield per plot (g) and Seed cotton yield qtl./ha which indicated the predominance of non-additive gene action.

4.3.3 Combining ability effects

The combining ability effects were estimated for all the characters as they had significant contribution in total variance. The effects due to general combining ability and specific combining ability are presented under following sub-heads.

4.3.3.1 General combining ability effects

The GCA effects of eleven parents for fifteen characters are presented in Table 12. The GCA effects are the numerical values assigned to parents according to their average performance in series of cross combinations.

4.3.3.1.1 Days to 50% flowering

Among seven female lines, only three lines exhibited the significant GCA effects. The line NH 545 (-2.429) has recorded significant negative GCA effects for this character and considered to be good conferring earliness to the hybrids, while NH 615 (1.571) and NH 630 (1.405) recorded significant positive effects.

Among the testers, NH 452 (-2.048) and NH 625 (-2.095) exhibited significant negative desirable GCA effects, whereas Suvin (4.238) has recorded undesirable GCA effects.

4.3.3.1.2 Number of monopodia per plant

Among the lines, NH 615 (0.219) and PH 1076 (0.144) recorded significant positive GCA effects, whereas NH 630 (-0.156)

Table 12. General combining ability (gca) effects of parents in cotton

PARENTS	Days to 50% flowering	Number of monopodia /plant	Number of sym-Podia /plant	Plant height (cm)	Days to maturity	Boll weight (g)	Number of bolls /Plant	Ginning percentage (%)	Micronaire value (µg/inch)	Fibre length (mm)	Uniformity ratio	Fibre strength (g/tex)	Seed cotton yield / plant (g)	Seed cotton yield / plot (g)	Seed cotton yield qtl./ha
Lines															
NH 545	-2.429**	-0.056	1.627**	2.075	-0.012	0.008	-1.603**	0 535	0.284**	-0.718**	1.818**	-0.300	-4 187**	-68.595*	-96.130*
NH 615	1.571**	0.219**	-0.320	-11.775**	-1.345**	0.025	2 860**	-0.330	-0 042	-0.943**	-0 975*	0.312	9 490**	172.988**	239.619**
NH 630	1.405**	-0.156*	-1.823**	-7.175**	3.905**	-0.170**	-2.265**	-0.837	0.159**	-0.197	-0.365	-0.485*	-11.495**	-203.679**	-283.464**
NH 635	0.071	-0.089	-0 780	-8 775**	2.571**	-0.002	-2 088**	-0 426	0.276**	-0.197	-0.517	-0.181	-4.723**	-81.345*	-108.964*
PH- 1060	0.071	-0 039	0.640	8.983**	-3.679**	0.073**	-1 119**	0.586	-0.864**	-0 147	0.302	-0.186	-1.781**	-52.262	-73.214
PH 1076	-0 345	0.144*	1 950**	11.192**	-2.595**	0 003	3 850**	0.636	0.093	1.270**	-0.090	-0.249	12.428**	225.905**	313.202**
LRA 5166	-0.345	-0.023	-1.293*	5 475**	1.155**	0.063*	0 437	-0.163	0.094	0 932**	-0 173	1.090**	0.267	6.988	8.952
SE(gi)	0 37	0 06	0.48	1.47	0.35	0.02	0.37	0 77	0.05	0.12	0.42	0.22	0.47	30.68	42.53
CD at 5%	0.76	0.13	0.97	2.95	0 70	0.05	0.74	1 55	0.10	0.25	0.84	0 45	0.94	61.62	88.78
Testers															
NH 452	-2.048**	0 049	0.992**	-0.165	-3.381**	0.171**	-0 084	1.403*	-0 004	-0.075	0.759*	-1.410**	4.182**	77.524**	106 953**
NH 625	-2.095**	0.058	-1.012**	-1.504	-1.952**	0.111**	-0 476	1.550*	0.293**	-1.842**	0.977**	-1.296**	1.745**	20.714	28.048
PKV Rajat	-0.095	-0.051	0.139	0.611	-8 762**	0 057**	0.937**	-0 124	0.121**	-2 573**	-0.169	0.503**	6.542**	120 857**	167 238**
Suvin	4.238**	-0 056	-0.118	1.058	14 095**	-0.338**	-0.378	-2.829**	-0.409**	4 489**	-1.567**	2 203**	-12.469**	-219.095**	-302 238**
SE(gi)	0.28	0 05	0.36	1.11	0.26	0.01	0.28	0 58	0.04	0.09	0.32	0.16	0.35	23 19	32.15
CD at 5%	0.57	0 10	0.73	2 23	0.54	0.03	0.56	1.17	0.08	0 19	0 64	0.34	0.71	46.50	67.11

* Significant at 5% level, ** Significant at 1% level, respectively.

recorded significant negative GCA effects. Among the testers NH 452 (0.049) and NH 625 (0.058) exhibited positive GCA effect.

4.3.3.1.3 Number of sympodia per plant

Among the seven lines, only four lines showed highly significant GCA effects. The GCA effects were found to be negative and significant for LRA 5166 (-1.293) and NH 630 (-1.823) and positively significant for NH 545 (1.627) and PH 1076 (1.950).

In case of testers, NH 452 (0.992) recorded significant and positive GCA effects, whereas NH 625 (-1.012) has produced undesirable GCA effects. PKV Rajat (0.194) and Suvin (-0.118) exhibited non-significant GCA effects.

4.3.3.1.4 Plant height (cm)

Among seven female lines, six lines exhibited the significant GCA effects. The line PH 1076 (11. 192) exhibited the highly significant positive GCA effects followed by PH 1060 (8.983) and LRA 5166 (5.475). Whereas, the line, NH 615 (-11.775) recorded the highest negative GCA effect for this traits followed by NH 635 (-8.775) and NH 630 (-7.175). Among the testers, none of tester reported significant GCA effects.

4.3.3.1.5 Days to maturity

Among seven lines, only six lines exhibited the significant GCA effects. The line PH 1060 (-3.679) showed highly negative and significant GCA effect for this traits followed by PH 1076 (-2.595) and NH 615 (-1.345). The lines NH 630 (3.905), NH 635 (2.571) and LRA 5166 (1.155) were produced undesirable and positive GCA effects.

In case of testers, PKV Rajat (-8.762) recorded significant and negative GCA effect followed by NH 452 (-3.381) and NH 625 (-1.952), whereas, Suvin (14.095) had produced significant and positive GCA effects.

4.3.3.1.6 Boll weight

The GCA effects were found to be significant and negative for NH 630 (-0.170). Whereas, the lines PH 1060 (0.073) and LRA 5166 (0.063) exhibited significant and positive GCA effect.

The testers, NH 452 (0.171), NH 625 (0.111) and PKV Rajat (0.057) exhibited significant desirable positive GCA effects, while Suvin (-0.338) had recorded undesirable negative GCA effects.

4.3.3.1.7 Number of bolls per plant

For this trait, among the lines PH 1076 (3.850) and NH 615 (2.860) exhibited positive and significant GCA effects. The lines, NH 630 (-2.265), NH 635 (-2.088), NH 545 (-1.603) and PH 1060 (-1.119) recorded negative and significant GCA effects. Among the tester, PKV Rajat (0.937) was found to be showing positively significant GCA effects.

4.3.3.1.8 Ginning percentage

Among seven lines, none of line exhibited the significant GCA effects. The line PH 1076 (0.636) has recorded non-significant positive GCA effects for this character followed by PH 1060 (0.586) and NH 545 (0.535).

Among the tester, NH 625 (1.550) exhibited significant positive GCA effects followed by NH 452 (1.403). The tester, Suvin (-2.829) recorded negatively significant for this character.

4.3.3.1.9 Micronaire value

Among seven lines, only four lines exhibited the significant GCA effects. The line NH 545 (0.284) exhibited positive significant GCA effects followed by NH 635 (0.276) and NH 630 (0.159). Whereas PH 1060 (-0.864) exhibited significant negative effects.

Among the testers, NH 625 (0.293) and PKV Rajat (0.121) recorded positive and significant GCA effects, while Suvin (-0.409) was found to be good combiner and negative significant GCA effect.

4.3.3.1.10 Fibre length

For this character, among the lines, PH 1076 (1.270) and LRA 5166 (0.932) were good general combiners and with significant positive GCA effect, while lines NH 545 (-0.718) and NH 615 (-0.943) recorded negative GCA effects.

Among the testers, Suvin (4.489) was found to exhibit good general combining ability effects, while PKV Rajat (-2.573) and NH 625 (-1.842) recorded significant negative GCA effect.

4.3.3.1.11 Uniformity ratio

Among seven lines, only two lines exhibited the significant GCA effect. The line NH 545 (1.818) exhibited positive significant GCA effects, while NH 615 (-0.975) recorded significant and negative effect for this trait.

In case of testers, NH 625 (0.977) found to be good combiner followed by NH 452 (0.759) and Suvin (-1.567) recorded negative and significant effects for this character.

4.3.3.1.12 Fibre strength

Among seven lines, only two lines exhibited the significant GCA effect. The line LRA 5166 (1.090) exhibited significantly positive GCA effects, whereas NH 630 (-0.485) exhibited significant negative effects.

Among the testers, Suvin (2.203) and PKV Rajat (0.503) recorded significant positive effects, whereas NH 452 (-1.410) and NH 625 (-1.296) exhibited significantly negative GCA effect for this trait.

4.3.3.1.13 Seed cotton yield per plant

For seed cotton yield per plant, among the lines, PH 1076 (12.428) was observed to be good general combiner (Plate 7a). The lines NH 630 (-11.495) recorded highest significant and negative GCA effects.

Among the testers, PKV Rajat (6.542, Plate 7b), NH 452 (4.182) and NH 625 (1.743) were found to exhibit good general combining ability effects. While, Suvin (-12.469) recorded significant negative GCA effects.

4.3.3.1.14 Seed cotton yield per plot

Among the seven lines, PH 1076 (225.905) and NH 615 (172.988) recorded significantly positive GCA effects, whereas, NH 630 (-203.679) exhibited significant highest negative effects.

Among the testers, PKV Rajat (120.857) and NH 452 (77.524) recorded significant positive effects and Suvin (-219.095) recorded significant negative GCA effects.

4.3.3.1.15 Seed cotton yield qtl./ ha

Among the seven lines, PH 1076 (313.202) and NH 615 (239.619) recorded significant positive GCA effects, whereas NH 630 (-283.464) exhibited highest significantly negative effects.

Among the testers, PKV Rajat (167.238) and NH 452 (106.953) exhibited significant and positive GCA effects. The Suvin (-302.238) exhibited highest significantly negative effects.

4.3.3.2 Specific combining ability effects

The SCA effects of twenty eight hybrids estimated for fifteen characters under study are presented in Table 13.

Plate 7a. A promising line for seed cotton yield per plant (PH 1076)

Plate 7b. A promising tester for seed cotton yield per plant (PKV Rajat)

Table 13. Specific combining ability (sca) effects for different crosses in cotton

CROSSES	Days to 50% flowering	Number of monopodia /plant	Number of sympodia /plant	Plant height (cm)	Days to maturity	Boll weight (g)	Number of bolls /Plant	Ginning percentage (%)	Micronaire value (µg/inch)	Fibre length (mm)	Uniformity ratio	Fibre strength (g/tex)	Seed cotton yield / plant (g)	Seed cotton yield / plot (g)	Seed cotton yield qt/ha
NH 545 x NH 452	-2.952**	-0.049	-0.754	-4.385	0 631	-0.008	1.391	-0 541	-0 441**	0.208	-1.484	-0.263	4.343**	71 643	100.466
NH 545 x NH 625	0.095	-0 125	0 520	2.020	0 536	0.052	-0.067	-0 921	-0.321**	1.508**	0.498	-0 710	0.260	10.786	15.702
NH 545 x PKV Rajat	0 429	-0.082	-1.561	-1.361	3.679**	0.006	-0.430	-0.087	-0.006	-0.194	1.277	0 925*	-3.517**	-71.024	-98.155
NH 545 x Suvin	2.429**	0.256	1.796	3.725	-4 845**	-0.049	-0.895	1.549	0 767**	-1.523**	-0.291	0.048	-1.086	-11 405	-18.012
NH 615 x NH 452	-0.286	0.143	-0 778	0 465	-0.702	0 024	-0.451	-0.046	-0 382**	-2 650**	0.536	0.658	-1.175	-23.274	-31.953
NH 615 x NH 625	-0.571	0 067	-1 770	-1.663	-0 464	0 064	-1 019	-1.176	-0.218*	0.800**	1.392	-0.689	-0.247	6 202	9.286
NH 615 x PKV Rajat	2.429**	0.010	. -0.155	1.623	0.679	0.058	2.548**	-0 295	0.377**	1.664**	0.470	0.496	7.455**	131 060*	182.762*
NH 615 x Suvin	-1.571*	-0 219	2 703**	-0.425	0.488	-0 147**	-1 077	1.517	0.223*	0.186	-2.398**	-0 464	-6 033**	-113.988	-160.095
NH 630 x NH 452	-0 452	-0.149	-0.034	2.532	0.381	-0 171**	2 254**	1.571	-0.259*	-0.229	0.533	-0.001	2 070*	34.060	47.797
NH 630 x NH 625	1.262	0 175	0 870	7.270*	-2.048**	0 079	-1 214	1.851	0.501**	-0.346	-1.985*	-0.325	-2.102*	-28.131	-38.298
NH 630 x PKV Rajat	-1.405	-0.049	-1.381	-6.311*	0 095	0.243**	-2.867**	-4 665**	-0 137	-0.532*	0.660	0.593	-5.340**	-100 274	-138 821
NH 630 x Suvin	0.595	0.023	0.546	-3 492	1.571*	-0.152**	1.828*	1.244	-0.104	1.107**	0.792	-0.267	5 372**	94.345	129.322
NH 635 x NH 452	1.214	0.118	-2.877**	3.399	1.714*	0.065	0.136	-0.043	0.294**	0.838**	-0.082	0.911*	0.839	11.393	11.631
NH 635 x NH 625	0.595	-0 158	0.657	-1 396	-1.714*	0 025	1.428	-0 167	0.264*	1.354**	-0 350	. 1.161*	4.816**	95.869	129.203
NH 635 x PKV Rajat	-1 071	0.018	0.986	0.823	2.095**	-0 001	-0 815	0.784	-0.667**	1.685**	0.045	-0.511	-4.555**	-80 607	-115 655
NH 635 x Suvin	-0.738	0 023	1.233	-2.825	-2.095**	-0 089	-0 750	-0.574	0 109	-3.877**	0 387	-1.561**	-1.100	-26.655	-25.178

Table 13. Contd...

CROSSES	Days to 50% flowering	Number of monopodia /plant	Number of sympodia /plant	Plant height (cm)	Days to maturity	Boll weight (g)	Number of bolls /Plant	Ginning percentage (%)	Micronaire value (µg/inch)	Fibre length (mm)	Uniformity ratio	Fibre strength (g/tex)	Seed cotton yield / plant (g)	Seed cotton yield / plot (g)	Seed cotton yield qtL./ha
PH 1060 x NH 452	2.881**	-0 132	-0.717	1.740	-0.702	-0.043	-3.700**	-0.618	0.428**	-0.346	1.033	-0 277	-11.783**	-192.024**	-265 786**
PH 1060 x NH 625	-0 405	-0.008	-0.073	-5.821	4.536**	0.077	2.159**	0 745	-0.433**	1.204**	-0 385	-0.457	6 775**	65 119	91.119
PH 1060 x PKV Rajat	-1.071	0.168	2.646**	3.264	-4.988**	-0.019	3.186**	0.706	-0.221*	-2.198**	-0.173	-0.636	5 790**	123.976*	172 595*
PH 1060 x Suvin	-1.405	-0.027	-1.857	0 817	1.155	-0.014	-1.645*	-0.832	0.226*	1.340**	-0.475	1.371**	-0.782	2.929	2.072
PH 1076 x NH 452	-0.702	0.018	0.863	-0 035	-3.786**	0 127*	0.639	-0.955	0.257*	2.388**	-0.409	-0.901*	4.298**	75.143	105 131
PH 1076 x NH 625	0.679	-0.058	-0 473	-2.296	-3 214**	-0.043	-2.469**	0.345	0.051	-2.113**	0.340	0 555	-8 835**	-148 381*	-205.631*
PH 1076 x PKV Rajat	0.679	-0 149	2 576*	2 989	-2 071**	0.161**	3 438**	1 749	0.223*	-1.015**	-1 415	-0 394	13.978**	248.476**	345.845**
PH 1076 x Suvin	-0 655	0.189	-2 967**	-0.658	9.071**	-0.244**	-1.607*	-1.139	-0 531**	0.740**	1.484	0.740	-9.441**	-175 238**	-245.345**
LRA 5166 x NH 452	0.298	0 051	4.296**	-3.718	2.464**	0.007	-0.269	0.633	0.103	-0.208	-0.126	-0.127	1.409	23.060	32 174
LRA 5166 x NH 625	-1.655*	0.108	0 270	1.887	2.369**	-0.253**	1 183	-0 677	0.156	-2.408**	0.490	0.466	-0.667	-1.464	-1.381
LRA 5166 x PKV Rajat	0.012	0.085	-3.111**	-1.027	0.512	-0.449**	-5.060**	1.808	0.431**	0 589*	-0 865	-0.473	-13.811**	-251.607**	-348.571**
LRA 5166 x Suvin	1 345	-0 244	-1.454	2.858	-5.345**	0 696**	4.145**	-1.764	-0.689**	2.027**	0.500	0.134	13.070**	230.012**	317.238**
SE(sij)	0 75	0.13	0.97	2.95	0.70	0 05	0 74	1.54	0.10	0 25	0.84	0.44	0.94	61.37	85.07
CD at 5%	1 52	0 26	1 94	5.91	1.41	0.10	1.49	3.10	0.21	0.50	1 69	0.90	1.89	123 04	177.56

* Significant at 5% level, ** Significant at 1% level, respectively.

4.3.3.2.1 Days to 50% flowering

Among cross combinations, SCA effects ranged from -2.952 (NH 545 x NH 452) to 2.881 (PH 1060 x NH 452). Out of twenty eight hybrids, three hybrids exhibited significant and positive SCA effects and three hybrids exhibited significant and negative SCA effects. The cross NH 545 x NH 452 (-2.952) exhibited the highest significant negative SCA effects followed by LRA 5166 x NH 625 (-1.655) and NH 615 x Suvin (-1.571) and were found to be good for earliness.

4.3.3.2.2 Number of monopodia per plant

The SCA effects ranged from -0.219 to 0.256. None of the crosses recorded significantly positive or negative SCA effects for this character. The cross NH 545 x Suvin (0.256) recorded highest positive SCA effects followed by PH 1076 x Suvin (0.189) and NH 630 x NH 625 (0.175).

4.3.3.2.3 Number of sympodia per plant

The range of SCA effects among twenty eight hybrids was from -3.111 (LRA 5166 x PKV Rajat) to 4.296 (LRA 5166 x NH 452). Seven crosses exhibited significant SCA effects. Out of seven crosses, four crosses exhibited positive and three crosses recorded negative significant SCA effects. The cross LRA 5166 x NH 452 (4.296) exhibited highest significant positive SCA effects followed by cross NH 615 x Suvin (2.703) and PH 1060 x PKV Rajat (2.646).

4.3.3.2.4 Plant height

Among the twenty eight cross combinations, the cross NH 630 x NH 625 (7.270) showed the highest significant positive SCA effect and the cross NH 630 x PKV Rajat (-6.311) showed significant negative SCA effects.

4.3.3.2.5 Days to maturity

Among cross combinations studied, eight crosses exhibited significant positive SCA effects and nine crosses exhibited significant negative SCA effects. The cross LRA 5166 x Suvin (-5.345) exhibited highest significant negative SCA effects followed by PH 1060 x PKV Rajat (-4.988) and NH 545 x Suvin (-4.845). The cross PH 1076 x Suvin (9.071) recorded the highest significant and positive SCA effects for this trait.

4.3.3.2.6 Boll weight

For this character, ten crosses exhibited significant SCA effects. Among the crosses, four crosses recorded significant and positive effects *viz.*, LRA 5166 x Suvin (0.696), NH 630 x PKV Rajat (0.243), PH 1076 x PKV Rajat (0.161) and PH 1076 x NH 452 (0.127) and six crosses recorded significant negative SCA effects.

4.3.3.2.7 Number of bolls per plant

Out of twenty eight crosses studied, seven crosses exhibited significant positive SCA effects and six crosses exhibited significant and negative SCA effects. Among the interspecific crosses significant and positive effects were exhibited by, LRA 5166 x Suvin (4.145) followed by PH 1076 x PKV Rajat (3.438) and PH 1060 x PKV Rajat (3.184). The highest significant and negative values were recorded for intraspecific crosses LRA 5166 x PKV Rajat (-5.060) and PH 1060 x NH 452 (-3.700).

4.3.3.2.8 Ginning percentage

For this character, SCA effects ranged from -4.665 (NH 630 x PKV Rajat) to 1.851 (NH 630 x NH 625). The maximum positive SCA effects were recorded by crosses NH 630 x NH 625 (1.851), LRA 5166 x PKV Rajat (1.808) and PH 1060 x PKV Rajat (1.749). However, one cross NH 630 x PKV Rajat (-4.665) recorded negative significant SCA effects.

4.3.3.2.9 Micronaire value

Out of twenty eight crosses studied, eleven crosses exhibited significant positive SCA effects and ten crosses exhibited significant and negative SCA effects. The highest significant and negative values were recorded in the interspecific cross LRA 5166 x Suvin (-0.689) followed by intraspecific cross NH 635 x PKV Rajat (-0.667) and interspecific cross PH 1076 x Suvin (-0.531). The highest positive significant SCA effect recorded by an interspecific cross NH 545 x Suvin (0.767) followed by intraspecific crosses NH 630 x NH 625 (0.501) and LRA 5166 x PKV Rajat (0.431).

4.3.3.2.10 Uniformity ratio

The SCA effects ranged from -2.398 (NH 615 x Suvin) to 1.484 (PH 1076 x Suvin). The crosses PH 1076 x Suvin (1.484), NH 615 x NH 625 (1.392) and NH 545 x PKV Rajat (1.277) recorded positive SCA effects for uniformity ration. Two crosses, NH 615 x Suvin (-2.398) and NH 630 x NH 625 (-1.985) recorded significant and negative SCA effects for this trait.

4.3.3.2.11 Fibre length

The SCA effects ranged from -3.877 (NH 635 x Suvin) to 2.388 (PH 1076 x NH 452). Out of twenty eight crosses, thirteen crosses had recorded significant positive and eight crosses had recorded significant negative SCA effects. The highest positive significant values were recorded by cross PH 1076 x NH 452 (2.388) followed by LRA 5166 x Suvin (2.027) and NH 635 x PKV Rajat (1.685).

4.3.3.2.12 Fibre strength

Four crosses, PH 1060 x Suvin (1.371), NH 635 x NH 625 (1.161), NH 545 x PKV Rajat (0.925) and NH 635 x NH 452 (0.911) exhibited positive significant SCA effects. Whereas, two crosses, NH 635 x

Suvin (-1.561) and PH 1076 x NH 452 (-0.901) recorded negative significant SCA effects.

4.3.3.2.14 Seed cotton yield per plant

The SCA effects ranged from -13.811 to 13.978. Nineteen crosses exhibited significant SCA effects. Out of twenty eight hybrids, ten hybrids recorded positive values and nine hybrids had recorded negative SCA effects. The highest positive significant values were recorded by an intraspecific cross, PH 1076 x PKV Rajat (13.978) followed by LRA 5166 x Suvin (13.070) and NH 615 x PKV Rajat (7.455). The highest significant negative values were observed in the cross LRA 5166 x PKV Rajat (-13.811).

4.3.3.2.15 Seed cotton yield per plot

The SCA effects ranged from -251.607 to 248.476. Eight crosses exhibited significant SCA effects. Out of twenty eight hybrids, four hybrids had positive SCA effects and four had negative effects. The highest positive significant value was recorded by an intraspecific cross, PH 1076 x PKV Rajat (248.476) followed by LRA 5166 x Suvin (230.012) and NH 615 x PKV Rajat (131.060). Whereas, the highest significant and negative effect was observed in the cross LRA 5166 x PKV Rajat (-251.607).

4.3.3.2.16 Seed cotton yield qtl./ ha

Eight crosses exhibited significant SCA effects ranged from -348.571 to 345.845. Out of twenty eight hybrids, four hybrids recorded positive values and four had negative effects. The highest positive significant value recorded by an intraspecific cross, PH 1076 x PKV Rajat (345.845) followed by LRA 5166 x Suvin (317.238) and NH 615 x PKV Rajat (182.762). Whereas, the highest significant negative value was observed in the cross LRA-5155 x PKV Rajat (-348.571).

4.4 ESTIMATES OF HETEROSIS

The magnitude of heterosis exhibited by twenty eight hybrids was measured as per cent increase or decrease over the mean of parents (relative or mid parental heterosis), over the better parent (heterobeltiosis) and over the standard check (standard heterosis) NHH 44 and DCH 32 for all the fifteen characters are presented in the Table 14.1 to 14.8. The parents with lower values were considered as better parents for the estimation of heterobeltosis for days to 50 per cent flowering when earliness is considered as useful trait, while for other characters parents with higher values were considered as better parent except micronaire value. The results obtained on the magnitude of heterosis are presented below.

4.4.1 Days to 50% flowering

The negative heterosis of this trait is of interest to the breeders as it indicates earliness. The relative heterosis ranged from -2.92 (LRA 5166 x NH 625) to 5.93 per cent (NH 545 x Suvin) Table 14.1. Out of twenty eight crosses, eight crosses had exhibited significant mid parental heterosis, among which five crosses had exhibited positive heterosis and three exhibited negative heterosis. Top three crosses early in flowering were LRA 5166 x NH 625 (-2.92%), PH 1060 x NH 625 (-2.64%) and PH 1060 x Suvin (-2.47).

Heterobeltosis ranged from -6.69 (PH 1060 x Suvin) to 2.56 per cent (NH 615 x PKV Rajat). For this trait fourteen crosses showed significant negative heterobeltosis. Among the intrespecific crosses, the cross PH 1060 x Suvin (-6.69 %) was found to be early followed by crosses PH 1076 x Suvin (-6.30%) and NH 635 x Suvin (-5.91%).

For standard heterosis, the values varied from -1.48 (NH 545 x NH 452) to 21.67 per cent (NH 630 x Suvin) and from -8.44 (NH 545 x NH 452) to 9.78 per cent (NH 630 x Suvin) over NHH 44 and DCH 32. Twenty seven crosses recorded significant positive heterosis over check NHH 44.

Table 14.1. Estimates of heterosis over mid parent (MP), better parent (BP) and standard check (SH) for days to 50% flowering and number of monopodia per plant

Crosses	Days to 50% flowering				Number of monopodia/ plant			
	MP	BP	SH(NHH44)	SH(DCH 32)	MP	BP	SH(NHH44)	SH(DCH 32)
NH 545 x NH 452	-1.44	-5.07**	1.48	-8.44**	2.44	-4.55	-4.55	16.67
NH 545 x NH 625	1.65	-3.15*	5.91**	-4.44**	0.00	-9.09	-9.09	11.11
NH 545 x PKV Rajat	5.21**	0.45	9.36**	-1.33	-5.00	-13.64	-13.64	5.56
NH 545 x Suvin	5.93**	-5.12**	18.72**	7.11**	9.09	9.09	9.09	-33.33
NH 615 x NH 452	0.22	-3.42*	11.33**	0.44	40.00**	33.33*	27.27*	55.56**
NH 615 x NH 625	-1.32	-3.85**	10.84**	0.00	38.46**	28.57*	22.73	50.00**
NH 615 x PKV Rajat	5.49**	2.56	18.23**	6.67**	25.64	16.67	11.36	36.11*
NH 615 x Suvin	-1.23	-5.12**	18.72**	7.11**	-2.33	-4.55	-4.55	16.67
NH 630 x NH 452	0.90	-1.75	10.84**	0.00	-7.69	-10.00	-18.18	0.00
NH 630 x NH 625	2.00	0.44	13.30**	2.22	21.05	15.00	4.55	27.78
NH 630 x PKV Rajat	1.33	-0.44	12.32**	1.33	-5.26	-10.00	-18.18	0.00
NH 630 x Suvin	2.28	-2.76*	21.67**	9.78**	-9.52	-13.64	-13.64	5.56
NH 635 x NH 452	1.57	-0.88	11.33**	0.44	27.78*	21.05	4.55	27.78
NH 635 x NH 625	-0.44	-1.75	10.34**	-0.44	8.57	5.56	-13.64	5.56
NH 635 x PKV Rajat	0.22	-1.32	10.84**	0.00	14.29	11.11	-9.09	11.11
NH 635 x Suvin	-0.83	-5.91**	17.73**	6.22**	2.56	-9.09	-9.09	11.11
PH 1060 x NH 452	2.90*	-0.43	13.79**	2.67	-4.76	-13.04	-9.09	11.11
PH 1060 x NH 625	-2.64*	-4.74**	8.87**	-1.78	7.32	-4.35	0.00	22.22
PH 1060 x PKV Rajat	-0.66	-3.02*	10.84**	0.00	12.20	0.00	4.55	27.78
PH 1060 x Suvin	-2.47*	-6.69**	16.75**	5.33**	-11.11	-13.04	-9.09	11.11
PH 1076 x NH 452	-0.90	-2.67	7.88**	-2.67	25.00*	19.05	13.64	38.89*
PH 1076 x NH 625	-0.22	-0.89	9.85**	-0.89	23.08	14.29	9.09	33.33
PH 1076 x PKV Rajat	2.69*	1.78	12.81**	1.78	7.69	0.00	-4.55	16.67
PH 1076 x Suvin	-0.63	-6.30**	17.24**	5.78**	20.93	18.18	18.18	44.44*
LRA 5166 x NH 452	0.91	-0.45	9.36**	-1.33	4.55	-8.00	4.55	27.78
LRA 5166 x NH 625	-2.92*	-3.14*	6.40**	-4.00**	11.63	-4.00	9.09	33.33
LRA 5166 x PKV Rajat	2.25	1.79	11.82**	0.89	2.33	-12.00	0.00	22.22
LRA 5166 x Suvin	2.31	-3.94**	20.20**	8.44**	-27.66*	-32.00*	-22.73	-5.56
SE±	0.92	1.07	1.07	1.07	0.16	0.18	0.18	0.18
CD at 5%	1.86	2.15	2.15	2.15	0.32	0.37	0.37	0.37

*Significant at 5% level, **Significant at 1% level, respectively.

Among the eleven crosses, eight crosses showed significantly positive heterosis, while only three crosses were found to be negative over DCH 32. The cross NH 545 x NH 452 (-8.44 %) recorded the highest negative and significant heterosis followed by NH 545 x NH 625 (-4.44%) and LRA 5166 x NH 625 (-4.00%) over DCH 32.

4.4.2 Number of monopodia per plant

For this character range varied from -27.66 to 40.00 per cent, -32.00 to 33.33 per cent, -22.73 to 27.27 per cent and -5.56 to 55.56 per cent for relative heterosis, heterobeltosis and standard heterosis over NHH 44 and DCH 32, respectively (Table 14.1).

Out of twenty eight hybrids, four hybrids registered significant positive values over mid parent and two crosses over better parent. The cross NH 615 x NH 452 (40.00 and 33.33%) exhibited the highest positive significant heterosis over mid parent and better parent followed by NH 615 x NH 625 (38.46 and 28.57% respectively).

In case of standard heterosis, the cross NH 615 x NH 452 (27.27 %) registered significant value over check NHH 44 and five crosses *viz.*, NH 615 x NH 452 (55.56%), NH 615 x NH 625 (50.00%), PH 1076 x Suvin (44.44%), PH 1076 x NH 452 (38.89%) and NH 615 x PKV Rajat (36.11%) recorded positive and significant heterosis over DCH 32.

4.4.3 Number of sympodia per plant

Heterosis over mid parent ranged from -15.20 (LRA 5166 x PKV Rajat) to 18.44 per cent (PH 1076 x PKV Rajat). Out of ten significant crosses, four showed positive heterosis and six crosses exhibited negative heterosis over mid parent. The intraspecific crosses PH 1076 x PKV Rajat (18.44 %) recorded significant positive heterosis followed by PH 1060 x PKV Rajat (17.17 %) and LRA 5166 x NH 452 (14.51 %) over mid parent (Table 14.2).

Table 14.2. Estimates of heterosis over mid parent (MP), better parent (BP) and standard check (SH) for number of sympodia per plant and plant height.

Crosses	Number of sympodia /plant				Plant height (cm)			
	MP	BP	SH(NHH44)	SH(DCH 32)	MP	BP	SH(NHH44)	SH(DCH 32)
NH 545 x NH 452	6.11	-0.78	11.83	10.06	5.91*	5.32	6.93*	8.36**
NH 545 x NH 625	5.26	0.28	8.62	6.90	10.79**	9.00**	10.66**	12.15**
NH 545 x PKV Rajat	4.87	3.21	4.54	2.88	14.10**	8.08*	9.72**	11.20**
NH 545 x Suvin	10.72*	2.44	18.16**	16.28**	1.69	-6.95**	13.80**	15.33**
NH 615 x NH 452	0.13	-8.46	3.18	1.54	2.41	-0.10	0.29	1.64
NH 615 x NH 625	-10.74*	-16.90**	-9.99	-11.41	0.91	-0.50	-2.26	-0.95
NH 615 x PKV Rajat	4.96	0.87	2.17	0.55	9.20**	6.53	1.72	3.06
NH 615 x Suvin	8.84	-1.52	13.59*	11.79	-7.67**	-17.79**	0.54	1.89
NH 630 x NH 452	0.26	-11.42*	-0.16	-1.74	10.61**	4.79	5.21	6.62*
NH 630 x NH 625	-2.44	-12.29*	-4.99	-6.50	14.55**	9.65**	7.71*	9.16**
NH 630 x PKV Rajat	-3.93	-10.97	-9.82	-11.25	9.90**	9.30**	-0.74	0.60
NH 630 x Suvin	-3.35	-15.46**	-2.49	-4.03	-4.14	-16.87**	1.67	3.04
NH 635 x NH 452	-13.85**	-18.43**	-8.07	-9.52	4.59	4.26	4.67	6.07
NH 635 x NH 625	-5.61	-8.92	-1.35	-2.91	1.17	0.39	0.15	1.49
NH 635 x PKV Rajat	4.11	3.83	5.15	3.49	8.45**	3.59	3.34	4.73
NH 635 x Suvin	-2.70	-8.87	5.11	3.44	-9.05**	-17.43**	0.98	2.34
PH 1060 x NH 452	0.62	-4.48	7.66	5.95	12.12**	8.43**	16.53**	18.09**
PH 1060 x NH 625	-2.98	-6.12	1.68	0.07	6.92**	2.33	9.97**	11.45**
PH 1060 x PKV Rajat	17.17**	17.17**	18.68**	16.80	19.25**	10.01**	18.22**	19.81**
PH 1060 x Suvin	-9.73*	-15.23**	-2.23	-3.78	1.62	-4.54	16.75**	18.32**
PH 1076 x NH 452	8.90	6.78	20.35**	18.44	4.55	-5.11*	16.85**	18.42**
PH 1076 x NH 625	-2.43	-2.43	5.68	4.01	3.17	-7.26**	14.19**	15.73**
PH 1076 x PKV Rajat	18.44**	14.69*	24.13**	22.16**	11.85**	-2.83	19.65**	21.25**
PH 1076 x Suvin	-11.78*	-14.47**	-1.35	-2.91	-4.42*	-4.75	17.29**	18.87**
LRA 5166 x NH 452	14.51**	7.52	21.19**	19.27**	-0.20	-8.32**	9.92**	11.40**
LRA 5166 x NH 625	-8.62	-12.57*	-5.30	-6.80	3.67	-5.69*	13.06**	14.58**
LRA 5166 x PKV Rajat	-15.20**	-16.18**	-15.10*	-16.44**	6.76**	-6.19*	12.48**	13.99**
LRA 5166 x Suvin	-15.02**	-21.06**	-8.95	-10.39	-4.48*	-5.42*	15.67**	17.22**
SE±	1.18	1.37	1.37	1.37	3.61	4.17	4.17	4.17
CD at 5%	2.38	2.75	2.75	2.75	7.24	8.36	8.36	8.36

*Significant at 5% level, **Significant at 1% level, respectivel

Heterosis over better parent ranged from -21.06 (LRA 5166 x Suvin) to 17.17 per cent (PH 1060 x PKV Rajat). Twelve crosses recorded significant heterosis over better parent. The cross PH 1060 x PKV Rajat (17.17%) recorded the highest positive significant heterosis followed by PH 1076 x PKV Rajat (14.69 %) over better parent.

The range of standard heteosis varied from -15.10 (LRA 5166 x PKV Rajat) to 24.13 per cent (PH 1076 x PKV Rajat) and -16.44 (LRA 5166 x PKV Rajat) to 22.16 per cent (PH 1076 x PKV Rajat) over standard check NHH 44 and DCH 32, respectively. Out of twenty eight crosses, six and three crosses recorded significant positive heterosis over standard check NHH 44 and DCH 32, respectively. The crosses PH 1076 x PKV Rajat (24.13 and 22.16 %) and LRA 5166 x NH 452 (21.19 and 19.27 %) recorded the highest positive and significant heterosis over checks NHH 44 and DCH 32, respectively.

4.4.4 Plant height (cm)

For this character the range varied from -9.05 to 19.25 per cent, -17.79 to 10.01 per cent, -2.26 to 19.65 per cent and form -0.95 to 21.25 per cent for relative heterosis, heterobetosis and standard heterosis over NHH 44 and over DCH 32, respectively (Table 14.2).

Out of twenty eight crosses, thirteen crosses registered significant positive values over mid parent and six crosses over better parent. The intraspecific cross PH 1060 x PKV Rajat exhibited the highest positive significant heterosis over mid parent (19.25 %) and better parent (10.01%) followed by NH 630 x NH 625 (14.55 and 9.65 %), respectively.

In standard heterosis, out of twenty eight crosses, seventeen exhibited significant heterosis over check NHH 44 and eighteen crosses exhibited significant heterosis over DCH 32. The highest significant positive heterosis was observed for PH 1076 x PKV Rajat (19.65 and 21.25 %) followed by PH 1060 x PKV Rajat (18.22 and 19.81 %) and PH 1076 x Suvin (17.29 and 18.87 %) over check NHH 44 and DCH 32, respectively.

4.4.5 Days to maturity

The relative heterosis ranged from -2.40 (NH 635 x NH 625) to 9.59 per cent (PH 1076 x Suvin) Table 14.3. Out of twenty eight hybrids, eighteen hybrids exhibited significant mid parental heterosis, among which twelve hybrids exhibited positive heterosis and six hybrids exhibited negative heterosis over mid parent. The crosses NH 635 x NH 625 (-2.40 %), PH 1076 x NH 452 (-2.32 %), PH 1076 x NH 625 (-1.88 %) and PH 1060 x PKV Rajat (-1.79 %) were found early in maturity.

Heterobeltiosis ranged from -6.14 (NH 545 x Suvin) to 2.88 per cent (NH 615 x PKV Rajat). Twenty one hybrids showed significant negative heterobeltiosis. The interspecific cross NH 545 x Suvin (-6.14%) was found to be early followed by PH 1076 x NH 625 (-6.01 %) and LRA 5166 x Suvin (-5.78%).

For standard heterosis the values varied from -9.09 (PH 1060 x PKV Rajat) to 14.46 per cent (PH 1076 x Suvin) over check NHH 44 and from -10.57% (PH 1060 x PKV Rajat) to 12.60 per cent (PH 1076 x Suvin) over check DCH 32. Ten and thirteen crosses showed significantly negative and positive heterosis over check NHH 44. Whereas, thirteen and seven crosses showed significantly negative and positive heterosis over check DCH 32. The cross, PH 1060 x PKV Rajat (-9.09 and -10.57 per cent) recorded the highest negative significant heterosis followed by PH 1076 x PKV Rajat (-6.61 and -8.13 per cent) over checks NHH 44 and DCH 32, respectively.

4.4.6 Boll weight (g)

Heterosis over mid parent ranged from -16.85 (NH 630 x Suvin) to 22.30 per cent (LRA 5166 x Suvin). Out of sixteen crosses exhibited significant heterosis, eleven crosses showed positive heterosis and five crosses showed negative heterosis over mid parent. The cross LRA 5166 x Suvin

Table 14.3. Estimates of heterosis over mid parent (MP), better parent (BP) and standard check (SH) for days to maturity and boll weight

Crosses	Days to maturity				Boll weight			
	MP	BP	SH(NHH44)	SH(DCH 32)	MP	BP	SH(NHH44)	SH(DCH 32)
NH 545 x NH 452	-1.12*	-1.43*	0.00	-1.63**	7.14**	5.70*	0.00	5.00*
NH 545 x NH 625	-1.11*	-2.20**	0.83	-0.81	5.88**	3.28	0.00	5.00*
NH 545 x PKV Rajat	1.60**	-2.25**	-1.45*	-3.05**	2.52	0.00	-3.17	1.67
NH 545 x Suvin	-0.19	-6.14**	7.44**	5.69**	-1.89	-10.34**	-17.46**	-13.33**
NH 615 x NH 452	2.04**	-3.05**	-1.65**	-3.25**	10.34**	7.38**	1.59	6.67**
NH 615 x NH 625	2.23**	-3.61**	-0.62	-2.24**	8.35**	4.26	0.95	6.00*
NH 615 x PKV Rajat	3.92**	2.88**	-4.13**	-5.69**	6.30**	2.30	-0.95	4.00
NH 615 x Suvin	6.83**	-3.97**	9.92**	8.13**	-3.45	-10.64**	-20.00**	-16.00**
NH 630 x NH 452	1.23*	0.81	2.27**	0.61	-8.77**	-11.64**	-10.79**	-6.33*
NH 630 x NH 625	-0.20	-1.40*	1.65**	0.00	-3.69	-5.66*	-4.76*	0.00
NH 630 x PKV Rajat	1.92**	-1.85**	-1.24*	-2.85**	-0.16	-2.20	-1.27	3.67
NH 630 x Suvin	5.86**	-0.54	13.84**	11.99**	-16.85**	-27.04**	-26.35**	-22.67**
NH 635 x NH 452	-0.40	-1.59**	2.27**	0.61	8.56**	7.83**	2.01	7.11**
NH 635 x NH 625	-2.40**	-2.78**	1.03	-0.61	3.95	2.08	-1.16	3.78
NH 635 x PKV Rajat	0.63	-4.57**	-0.83	-2.44**	1.28	-0.55	-3.70	1.11
NH 635 x Suvin	1.42**	-3.25**	10.74**	8.94**	-4.49	-13.27**	-19.05**	-15.00**
PH 1060 x NH 452	0.21	-4.48**	-3.10**	-4.67**	4.61*	2.58	0.95	6.00*
PH 1060 x NH 625	3.60**	-2.00**	1.03	-0.61	5.37*	4.52	2.86	8.00**
PH 1060 x PKV Rajat	-1.79**	-2.44**	-9.09**	-10.57**	0.49	-0.32	-1.90	3.00
PH 1060 x Suvin	5.55**	-4.87**	8.88**	7.11**	-1.82	-12.90**	-14.29**	-10.00**
PH 1076 x NH 452	-2.32**	-5.70**	-4.34**	-5.89**	7.54**	5.13*	4.13	9.33**
PH 1076 x NH 625	-1.88**	-6.01**	-3.10**	-4.67**	-1.13	-2.24	-3.17	1.67
PH 1076 x PKV Rajat	-0.44	-1.09	-6.61**	-8.13**	3.73	2.56	1.59	6.67**
PH 1076 x Suvin	9.59**	0.00	14.46**	12.60**	-13.04**	-23.08**	-23.81**	-20.00**
LRA 5166 x NH 452	0.20	0.00	1.86**	0.20	4.89*	1.90	2.22	7.33**
LRA 5166 x NH 625	0.20	-40	2.69**	1.02	-6.60**	-8.23**	-7.94**	-3.33
LRA 5166 x PKV Rajat	-0.21	-4.46**	-2.69**	-4.27**	-14.65**	-16.14**	-15.87**	-11.67**
LRA 5166 x Suvin	-0.29	-5.78**	7.85**	6.10**	22.30**	7.59**	7.94**	13.33**
SE±	0.86	0.99	0.99	0.99	0.06	0.07	0.07	0.07
CD at 5%	1.73	1.99	1.99	1.99	0.12	0.14	0.14	0.14

*Significant at 5% level, **Significant at 1% level, respectively.

(22.30%) recorded significant and positive heterosis followed by NH 615 x NH 452 (10.34%) and NH 635 x NH 452 (8.56%) over mid parent.

For heterobeltosis the values ranged from -27.04 (NH 630 x Suvin) to 7.83 per cent (NH 635 x NH 452). Among the crosses, the ten crosses exhibited significantly negative heterosis and five crosses recorded significant positive heterosis over better parent. The cross NH 635 x NH 452 (7.83%) and LRA 5166 x Suvin (7.59 %) recorded highest significant positive heterosis respectively over better parents (Table 14.3).

For boll weight, ten crosses showed significant negative and one cross LRA 5166 x Suvin (7.94%) recorded positive and significant heterosis over the check NHH 44. Out of nineteen crosses, eleven crosses recorded positive and eight crosses recorded significant negative heteosis over check DCH 32. The cross LRA 5166 x Suvin (13.33 %) exhibited the highest significant heterosis followed by cross PH 1076 x NH 452 (9.33 %) and PH 1060 x NH 625 (8.00 %) over DCH 32.

4.4.7 Number of bolls per plant

The heterosis over mid parent ranged from -16.89 (NH 635 x Suvin) to 39.33 per cent (PH 1076 x PKV Rajat) and over better parent it varied between -20.44 (NH 635 x Suvin) to 36.16 per cent (PH 1076 x PKV Rajat). Sixteen and eighteen crosses exhibited significant heterosis over mid parent and better parents. Out of sixteen, ten crosses recorded significant positive and six crosses recorded significant negative heterosis over mid parent and six and eleven crosses recorded significant positive and negative heterosis over better parent, respectively. The intraspecific cross, PH 1076 x PKV Rajat (39.33 and 36.16 %) recorded highest positive significant heterosis followed by cross NH 615 x PKV Rajat (37.73 and 34.92%) and PH 1076 x NH 452 (23. 06 and 21.18 %) over mid and better parent, respectively (Table 14.4).

Table 14.4. Estimates of heterosis over mid parent (MP), better parent (BP) and standard check (SH) for number of bolls per plant and ginning percentage

Crosses	Number of bolls/plant				Ginning percentage (%)			
	MP	BP	SH(NHH44)	SH(DCH 32)	MP	BP	SH(NHH44)	SH(DCH 32)
NH 545 x NH 452	0.79	-3.92	13.03**	20.48**	1.43	1.40	17.44**	15.77*
NH 545 x NH 625	-4.68	-10.71**	5.05	11.97*	0.62	0.42	16.76*	15.11*
NH 545 x PKV Rajat	-1.57	-6.86	9.58*	16.80**	1.18	-1.28	14.33*	12.71*
NH 545 x Suvin	-16.43**	-19.28**	1.90	8.61	5.31	-3.96	11.23	9.66
NH 615 x NH 452	19.92**	16.59**	24.33**	32.53**	3.19	0.53	16.37*	14.72*
NH 615 x NH 625	18.13**	16.96**	20.19**	28.11**	0.43	-2.37	13.52*	11.91
NH 615 x PKV Rajat	37.73**	34.92**	41.67**	51.01**	1.12	0.95	11.22	9.65
NH 615 x Suvin	6.07	-4.65	20.36**	28.30**	5.87	-1.05	8.64	7.10
NH 630 x NH 452	6.58	6.37	13.89**	21.40**	12.65*	3.31	19.58**	17.88**
NH 630 x NH 625	-7.32	-9.19*	-2.76	3.65	13.53*	3.91	20.81**	19.10**
NH 630 x PKV Rajat	-9.28*	-10.15*	-3.80	2.54	-6.06	-11.87*	-2.89	-4.27
NH 630 x Suvin	-5.03	-12.24**	-10.79*	18.09**	10.82	10.17	6.38	4.87
NH 635 x NH 452	-4.97	-8.59*	5.52	12.48*	3.31	0.30	16.10*	14.45*
NH 635 x NH 625	0.28	-5.23	9.40*	16.62**	3.14	-0.09	16.16*	14.52*
NH 635 x PKV Rajat	-3.99	-8.33*	5.82	12.80*	4.09	3.53	14.07*	12.45
NH 635 x Suvin	-16.89**	-20.44**	0.43	7.05	0.09	-6.14	2.31	0.86
PH 1060 x NH 452	-14.87**	-16.72**	-7.16	-1.04	4.86	1.39	17.36**	15.70*
PH 1060 x NH 625	8.69*	4.44	16.42**	24.10**	8.15	4.70	21.73**	20.01**
PH 1060 x PKV Rajat	17.28**	13.88**	26.95**	35.32**	6.99	5.98	16.77*	15.12*
PH 1060 x Suvin	-15.50**	-20.44**	0.43	7.05	2.67	-3.34	4.49	3.01
PH 1076 x NH 452	23.06**	21.18**	33.30**	42.09**	2.79	0.68	16.53*	14.88*
PH 1076 x NH 625	11.11**	7.45	18.21**	26.00**	6.24	3.83	20.72**	19.01**
PH 1076 x PKV Rajat	39.33**	36.16**	49.78**	59.66**	8.46	8.06	19.94**	18.24**
PH 1076 x Suvin	3.58	-3.08	22.35**	30.41**	0.51	-6.53	3.74	2.27
LRA 5166 x NH 452	3.42	-0.37	14.67**	22.23**	4.89	2.65	18.82**	17.13**
LRA 5166 x NH 625	9.47*	3.60	19.24**	27.10**	1.69	-0.71	15.45*	13.81*
LRA 5166 x PKV Rajat	-10.58**	-14.51**	-1.60	4.89	6.61	6.31	17.79**	16.12*
LRA 5166 x Suvin	9.76**	4.92	32.44**	41.17**	-3.39	-10.09	-0.38	-1.79
SE±	0.91	1.05	1.05	1.05	1.89	2.18	2.18	2.18
CD at 5%	1.82	2.10	2.10	2.10	3.80	4.38	4.38	4.38

*Significant at 5% level, **Significant at 1% level, respectively.

The range of standard heterosis varied form -10.79 (NH 630 x Suvin) to 49.78 per cent (PH 1076 x PKV Rajat) over check NHH 44 and from -1.04 (PH 1060 x NH 452) to 59.66 per cent (PH 1076 x PKV Rajat) over check DCH 32.

Out of twenty eight crosses, seventeen and twenty one crosses recorded significant and positive heterosis over checks NHH 44 and DCH 32, respectively. The cross PH 1076 x PKV Rajat (49.78 and 59.66%) exhibited significant positive heterosis followed by cross NH 615 x PKV Rajat (41.67 and 51.01 %) and PH 1076 x NH 452 (33.30 and 42.09 %) over standard check NHH 44 and DCH 32, respectively.

4.4.8 Ginning (%)

The relative heterosis ranged from -3.39 (LRA 5166 x Suvin) to 13.53 per cent (NH 630 x NH 625) for this trait (Table 14.4). It was observed significant and positive values in two crosses. In intraspecific cross, NH 630 x NH 625 recorded the highest significant positive value of 13.53 per cent followed by NH 630 x NH 452 (12.65%).

The extent of heterobeltosis for this trait was between -11.87 (NH 630 x PKV Rajat) to 8.06 per cent (PH 1076 x PKV Rajat). Only one cross *viz.,* NH 630 x PKV Rajat (-11.87%) recorded significant and negative heterobeltosis for this trait.

Standard heterosis for ginning percentage ranged from -2.89 (NH 630 x PKV Rajat) to 21.73 per cent (PH 1060 x NH 625). Out of twenty eight crosses, nineteen crosses recorded significant and positive values over the check NHH 44. The intraspecific cross PH 1060 x NH 625 (21.73%) registered the highest positive significant heterosis followed by NH 630 x NH 625 (20.81%) and PH 1076 x NH 625 (20.72%) over standard check NHH 44.

Standard heterosis over check DCH 32 for ginning percentage ranged from -4.27 (NH 630 x PKV Rajat) to 20.01 per cent (PH 1060 x NH

625). Seventeen crosses recorded significant and positive values over the check DCH 32. The cross PH 1060 x NH 625 (20.01%) recorded the highest positive significant heterosis followed by NH 630 x NH 625 (19.10%) and PH 1076 x NH 625 (19.01%) over check DCH 32.

4.4.9 Micronaire value (µg/inch)

The heterosis ranged from -24.81 (PH 1076 x Suvin) to 29.08 per cent (LRA 5166 x PKV Rajat) over mid parent and from -31.27 (PH 1060 x NH 625) to 20.69 per cent (NH 545 x Suvin) over better parent (Table 14.5). Out of twenty eight crosses, seven and five crosses recorded significant positive and six and ten crosses recorded significant negative heterosis over mid parent and better parent, respectively. The cross PH 1076 x Suvin recorded the highest significant negative heterosis -24.81 per cent over mid parent followed by PH 1076 x NH 625 (-24.25%) and PH 1060 x Suvin (-19.84%). The cross PH 1060 x NH 625 (-31.27%) recorded the highest significant negative heterosis over better parent followed by PH 1066 x Suvin (-30.96%) and PH 1060 x Suvin (-22.63%).

In case of standard heterosis, seventeen and five crosses recorded significant positive and negative heterosis over check NHH 44, respectively and twenty eight crosses recorded significant positive heterosis over check DCH 32. The cross PH 1060 x Suvin (-16.60%) recorded highest negative and significant heterosis followed by LRA 5166 x Suvin (-15.40%) and PH 1060 x NH 625 (-15.40 %) over check NHH 44. The cross PH 1060 x Suvin recorded lowest significant positive values 12.38 per cent over check DCH 32.

4.4.10 Fibre length (mm)

The range of heterosis over mid parent ranged from -15.41 (NH 635 x Suvin) to 20.76 per cent (PH 1076 x NH 452) and over better parent it varied between -24.35 (NH 635 x Suvin) to 18.18 per cent (PH 1076 x NH 452). Significant and positive values in ten and four crosses were recorded over mid and better parents, respectively (Table 14.5).

Table 14.5. Estimates of heterosis over mid parent (MP), better parent (BP) and standard check (SH) for microniare value and fibre length

Crosses	Microniare value(µg/inch)				Fibre length (mm)			
	MP	BP	SH(NHH44)	SH(DCH 32)	MP	BP	SH(NHH44)	SH(DCH 32)
NH 545 x NH 452	-1.27	-2.51	8.07	45.63**	2.52	0.96	-0.88	-19.05**
NH 545 x NH 625	3.53	-2.79	19.67**	61.25**	2.49	2.13	-2.77	-20.60**
NH 545 x PKV Rajat	13.21**	12.02**	23.65**	66.63**	-4.37**	-8.24**	-12.64**	-28.66**
NH 545 x Suvin	20.84**	20.69**	30.43**	75.75**	-3.30**	17.91**	11.97**	-8.56**
NH 615 x NH 452	-2.38	-9 21*	0.65	35.63**	-11.26**	-11.78**	-13.39**	-29.27**
NH 615 x NH 625	3.86	-7.84*	13.45**	52.88**	-2.44	-3.69*	-6.56**	-23.69**
NH 615 x PKV Rajat	21.73**	13.45**	25.23**	68.75**	1.87	-3.14*	-6.02**	-23.25**
NH 615 x Suvin	4.57	-1.46	6.22	43.13**	-0.06	-14.49**	16.63**	-4.75**
NH 630 x NH 452	-0.88	-1.09	9.65*	47.75**	1.20	1.10	-0.54	-18.77**
NH 630 x NH 625	19.11**	12.96**	39.05**	87.38**	4.80**	-6.67**	-8.18**	-25.01**
NH 630 x PKV Rajat	5.55	5.55	16.51**	57.00**	-5.20**	-10.45**	-11.90**	-28.05**
NH 630 x Suvin	-5.87	-6.97	2.69	38.38**	5.12**	-9.53**	23.39**	0.77
NH 635 x NH 452	6.92*	-0.65	28.29**	72.88**	0.89	-3.52**	3.79**	-15.24**
NH 635 x NH 625	7.61*	5.10	35.71**	82.88**	-2.31	-8.23**	-1.28	-19.38**
NH 635 x PKV Rajat	-12.32**	-18.68**	5.01	41.50**	-0.45	-9.74**	-2.91*	-20.71**
NH 635 x Suvin	-5.56	-13.36**	11.87**	50.75**	-15.41**	-24.35**	3.18*	-15.74**
PH 1060 x NH 452	-5.01	-9.54*	0.28	35.13**	3.46**	1.03	-0.81	-19.00**
PH 1060 x NH 625	-24.25**	-31.27**	-15.40**	14.00*	4.53**	4.01**	-1.69	-19.71**
PH 1060 x PKV Rajat	-18.63**	-22.35**	-14.29**	15.50**	-9.93**	-12.86**	-18.46**	-33.41**
PH 1060 x Suvin	-19.84**	-22.63**	-16.60**	12.38*	8.31**	-8.69**	24.54**	1.71
PH 1076 x NH 452	1.93	-5.18	22.17**	64.63**	20.76**	18.18**	16.02**	-5.25**
PH 1076 x NH 625	-1.03	-3.24	24.68**	68.00**	-3.87**	-4.15**	-9.40**	-26.01**
PH 1076 x PKV Rajat	4.23	-3.24	24.68**	68.00**	1.49	-2.01	-7.91**	-24.79**
PH 1076 x Suvin	-24.81**	-30.96**	-11.04*	19.88**	11.00**	-6.26**	27.86**	4.42**
LRA 5166 x NH 452	16.34**	6.36	17.90**	58.88**	4.48**	2.94*	4.12**	-14.96**
LRA 5166 x NH 625	18.77**	3.69	27.64**	72.00**	-10.02**	-12.97**	-11.97**	-28.11**
LRA 5166 x PKV Rajat	29.08**	18.24**	30.52**	75.88**	3.08*	-3.88**	-2.77	-20.60**
LRA 5166 x Suvin	-15.24**	-21.51**	-15.40**	14.00*	10.90**	-3.43**	31.71**	7.56**
SE±	0.13	0.15	0.15	0.15	0.30	0.35	0.35	0.35
CD at 5%	0.26	0.30	0.30	0.30	0.61	0.71	0.71	0.71

*Significant at 5% level, **Significant at 1% level, respectively.

The cross PH 1076 x NH 452 (20.76%) registered significant positive heterosis followed by PH 1076 x Suvin (11.00%) and LRA 5166 x Suvin (10.90%) over mid parent. Only four crosses *viz.*, PH 1076 x NH 452 (18.18%), NH 545 x Suvin (17.91%), PH 1060 x NH 625 (4.01%) and LRA 5166 x NH 452 (2.94%) exhibited significant positive heterosis over better parent.

For standard heterosis, the range varied from -18.46 (PH 1060 x PKV Rajat) to 31.71% (LRA 5166 x Suvin) and -31.41 (PH 1060 x PKV Rajat) to 7.56 % (LRA 5166 x Suvin) over standard check NHH 44 and DCH 32, respectively. Out of twenty eight crosses, ten recorded significant positive and eleven recorded negative heterosis over check NHH 44. The interspecific cross LRA 5166 x Suvin (31.71%) recorded highest significant positive heterosis followed by PH 1076 x Suvin (27.86%) and PH 1060 x Suvin (24.54%). Two interspecific crosses *viz.*, LRA 5166 x Suvin (7.56%) and PH 1076 x Suvin (4.42%) exhibited significantly positive heterosis over DCH 32.

4.4.11 Uniformity ratio

The distribution of heterosis for uniformity ratio varied from -13.03 to 3.45 per cent, -14.86 to 3.41 per cent, -16.49 to 0.84 per cent and -8.85 to 9.68 per cent for relative heterosis, heterobeltosis, over standard checks NHH 44 and DCH 32, respectively (Table 14.6).

Out of twenty eight crosses, eleven and seventeen crosses recorded significant and negative heterosis over mid parent and better parent, respectively. None of the cross recorded positive and significant heterosis over mid and better parent. The cross NH 615 x Suvin (-13.03 and -14.86%) registered the significant and negative heterosis followed by NH 630 x NH 625 (-10.52 and -10.74%) and PH 1076 x PKV Rajat (-8.05 and 8.50%) over mid and better parent, respectively.

Table 14.6 Estimates of heterosis over mid parent (MP), better parent (BP) and standard check (SH) for uniformity ratio and fibre strength

Crosses	Uniformity ratio				Fibre strength (g/tex)			
	MP	BP	SH(NHH44)	SH(DCH 32)	MP	BP	SH(NHH44)	SH(DCH 32)
NH 545 x NH 452	1.27	1.23	-4.05	10.36**	6.61*	4.33	6.64*	0.23
NH 545 x NH 625	2.24	-1.28	0.48	15.58**	3.40	-0.27	5.03	-1.28
NH 545 x PKV Rajat	3.13	1.11	-0.27	14.71**	10.66**	-0.26	21.60**	14.29**
NH 545 x Suvin	-0.80	-1.23	-6.39*	7.68**	11.58**	-1.30	25.58**	18.02**
NH 615 x NH 452	-2.12	-3.80	-5.65*	8.53**	8.62**	5.82*	14.04**	7.18*
NH 615 x NH 625	-3.37	-5.13*	-3.44	11.08**	1.45	0.30	8.09*	1.59
NH 615 x PKV Rajat	-6.15**	-6.41*	-7.70**	6.17*	6.65**	0.46	22.49**	15.12**
NH 615 x Suvin	-13.03**	-14.86**	-16.49**	-3.94	7.28**	-0.92	26.06**	18.47**
NH 630 x NH 452	-2.45	-5.63*	-4.40	9.97**	1.84	-0.85	7.01*	0.57
NH 630 x NH 625	-10.52**	-10.74**	-9.14**	4.51	-0.59	-1.79	6.00	-0.38
NH 630 x PKV Rajat	-6.02**	-7.26**	-6.05*	8.07**	3.64	-2.31	19.11**	11.94**
NH 630 x Suvin	-6.44**	-9.84**	-8.66**	5.07	4.75*	-3.20	23.16**	15.75**
NH 635 x NH 452	-1.72	-2.70	-5.98*	8.15**	3.17	-3.20	12.88**	6.09*
NH 635 x NH 625	-5.33*	-7.73**	-6.08*	8.03**	3.30	-1.70	14.64**	7.74**
NH 635 x PKV Rajat	-5.39*	-6.34*	-7.63**	6.25*	-3.37	-5.47*	15.25**	8.31**
NH 635 x Suvin	-5.35*	-6.66*	-9.81**	3.75	-2.90	-6.95**	18.39**	11.26**
PH 1060 x NH 452	3.45	3.41	-1.99	12.74**	3.86	2.94	7.13*	0.68
PH 1060 x NH 625	-2.80	-6.14*	-4.47	9.89**	2.01	1.41	6.80*	0.38
PH 1060 x PKV Rajat	-3.20	-5.09*	-6.39*	7.68**	1.44	-5.99*	14.62**	7.72**
PH 1060 x Suvin	-4.52	-4.93	-9.90**	3.64	14.58**	4.15	32.51**	24.54**
PH 1076 x NH 452	-2.04	-3.52	-5.77*	8.39**	-1.05	-3.53	3.81	-2.43
PH 1076 x NH 625	-3.51	-5.47*	-3.78	10.68**	4.62	3.51	11.39**	4.69
PH 1076 x PKV Rajat	-8.05**	-8.50**	-9.76**	3.80	0.63	-5.28*	15.49**	8.54**
PH 1076 x Suvin	-2.58	-4.43	-6.67**	7.36*	10.00**	1.52	29.16**	21.39**
LRA 5166 x NH 452	-1.64	-3.16	-5.36*	8.86**	1.00	-7.71**	14.01**	7.15*
LRA 5166 x NH 625	-3.41	-5.33*	-3.64	10.84**	2.61	-4.95	17.42**	10.36**
LRA 5166 x PKV Rajat	-7.11**	-7.53**	-8.80**	4.91	-0.94	-1.59	21.57**	14.26**
LRA 5166 x Suvin	-4.91*	-6.75**	-8.87**	4.83	5.84**	4.30	32.70**	24.70**
SE±	1.03	1.19	1.19	1.19	0.54	0.63	0.63	0.63
CD at 5%	2.08	2.40	2.40	2.40	1.10	1.27	1.27	1.27

*Significant at 5% level, **Significant at 1% level, respectively.

For standard heterosis the values varied from -16.49 (NH 615 x Suvin) to 0.48 per cent (NH 545 x NH 625). Twenty crosses noted significant and positive values over the check DCH 32. The cross NH 545 x NH 625 (15.58 %) showed the highest significant positive heterosis followed by cross NH 545 x PKV Rajat (14.71 %) and PH 1060 x NH 452 (12.74 %) over check DCH 32.

4.4.12 Fibre strength (g/tex)

The relative heterosis for fibre strength ranged from -3.37 (NH 635 x PKV Rajat) to 14.58 per cent (PH 1060 x Suvin). Ten crosses recorded positive significant heterosis over mid parent. The highest mid parental heterosis was observed in PH 1060 x Suvin (14.58%) followed by NH 545 x Suvin (11.58%) and NH 545 x PKV Rajat (10.66%) Table 14.6.

For heterobeltiosis the range observed from -7.71 (LRA 5166 x NH 452) to 5.82 per cent (NH 615 x NH 452). Only one cross *viz.*, NH 615 x NH 452 (5.82%) exhibited significant positive heterosis over better parent, while five crosses recorded negative heterosis over better parent.

For standard heterosis, the range varied from 3.81 (PH 1076 x NH 452) to 32.70 per cent (LRA 5166 x Suvin) and from -2.43 (PH 1076 x NH 452) to 24.70 per cent (LRA 5166 x Suvin) over check NHH 44 and DCH 32, respectively. Out of twenty eight crosses, twenty five and nineteen crosses recorded significantly positive heterosis over checks NHH 44 and DCH 32.

The cross LRA 5166 x Suvin (32.70 and 24.70%) recorded the highest significantly positive heterosis followed by PH 1060 x Suvin (32.51 and 24.54%) and PH 1076 x Suvin (29.16 and 21.39%) over checks NHH 44 and DCH 32, respectively.

4.4.13 Seed cotton yield per plant (g)

For seed cotton yield per plant, the mid parent heterosis ranged from -22.55 (NH 545 x Suvin) to 45.43 per cent (PH 1076 x PKV Rajat). Out of twenty eight crosses, thirteen crosses recorded positive heterosis value and ten crosses recorded significant negative heterosis over mid parental value. The intraspecific hybrid PH 1076 x PKV Rajat (45.43%) exhibited highest significant positive heterosis followed by NH 615 x PKV Rajat (41.56%) and PH 1076 x NH 452 (28.46%) over mid parent value (Table 14.7).

The estimates of heterobeltiosis for seed cotton yield per plant ranged from -28.82 (NH 545 x Suvin) to 40.17 per cent (PH 1076 x PKV Rajat). Out of twenty eight crosses, eight and fourteen crosses recorded positive and negative significant values over better parent, respectively. The cross PH 1076 x PKV Rajat (40.17%) registered the highest positive significant heterosis followed by NH 615 x PKV Rajat (38.04%) and NH 615 x NH 625 (27.08%) over better parent.

Standard heterosis over check NHH 44 ranged from -26.74 (NH 630 x Suvin) to 38.60 per cent (PH 1076 x PKV Rajat). Twenty three crosses recorded significant heterosis over check NHH 44. Out of which nine crosses were found positively significant and fourteen were negatively significant over check NHH 44. Standard heterosis over check DCH 32 ranged from -18.42 (NH 630 x Suvin) to 54.33 (PH 1076 x PKV Rajat). Out of twenty eight crosses, seventeen crosses recorded positive significant heterosis over DCH 32. The cross PH 1076 x PKV Rajat (38.60 and 54.33%) recorded highest positive significant heterosis followed by NH 615 x PKV Rajat (26.61 and 40.98%) and PH 1076 x NH 452 (23.34 and 37.34%) over check NHH 44 and DCH 32, respectively.

Table 14.7. Estimates of heterosis over mid parent (MP), better parent (BP) and standard check (SH) for seed cotton yield per plant and seed cotton yield per plot

Crosses	Seed cotton yield/plant (g)				Seed cotton yield per plot (g)			
	MP	BP	SH(NHH44)	SH(DCH 32)	MP	BP	SH(NHH44)	SH(DCH 32)
NH 545 x NH 452	3.58*	-2.02	2.33	13.95**	3.82	-2.00	-0.05	17.74*
NH 545 x NH 625	-1.15	-9.93**	-5.93**	4.74*	-1.16	-9.93	-8.14	8.21
NH 545 x PKV Rajat	-2.77	-8.69**	-4.64**	6.18**	-2.78	-8.70	-6.88	9.69
NH 545 x Suvin	-22.30**	-28.82**	-25.66**	-17.22**	-20.97*	-27.60**	-26.16**	-13.02
NH 615 x NH 452	24.99**	20.97**	12.68**	25.47**	25.28**	21.52**	10.04	29.62**
NH 615 x NH 625	28.01**	27.08**	10.76**	23.33**	28.00**	27.07**	8.16	27.41**
NH 615 x PKV Rajat	41.56**	38.04**	26.61**	40.98**	41.55**	38.03**	23.64**	45.64**
NH 615 x Suvin	-1.86	-2.21	-14.59**	-4.90*	-1.87	-2.02	-16.60**	-1.76
NH 630 x NH 452	0.96	-3.18	-9.81**	0.42	1.20	-2.73	-11.92	3.75
NH 630 x NH 625	-4.55*	-4.75*	-18.19**	-8.91**	-4.55	-4.79	-20.11**	-5.89
NH 630 x PKV Rajat	-5.46**	-8.65**	-16.21**	-6.71**	-5.46	-8.65	-18.1 8**	-3.62
NH 630 x Suvin	-15.02**	-15.70**	-26.74**	-18.42**	-14.69*	-15.37*	-28.18**	-15.39*
NH 635 x NH 452	-1.01	-5.86**	-2.79	8.24**	-0.80	-5.86	-5.07	11.83
NH 635 x NH 625	4.85**	-3.97*	-0.84	10.42**	4.84	-3.98	-3.16	14.07
NH 635 x PKV Rajat	-4.23**	-9.58**	-6.63**	3.96*	-3.80	-9.18	-8.41	7.89
NH 635 x Suvin	-22.55**	-28.68**	-26.36**	-18.00**	-22.55**	-28.69**	-28.08**	-15.28*
PH 1060 x NH 452	-7.81**	-8.81**	-15.06**	-5.42**	-7.61	-8.41	-17.06**	-2.30
PH 1060 x NH 625	19.06**	15.64	5.38**	17.33**	11.89	8.68	-3.28	13.93
PH 1060 x PKV Rajat	20.55**	20.16**	10.21**	22.72**	20.58**	20.19**	7.66	26.82**
PH 1060 x Suvin	-12.63**	-14.65**	-22.22**	-13.40**	-12.63*	-14.66*	-24.05**	-10.53
PH 1076 x NH 452	28.46**	24.73**	23.34**	37.34**	28.74**	24.74**	20.45**	41.88**
PH 1076 x NH 625	12.14**	4.77**	3.60*	15.36**	12.13*	4.77	1.17	19.17**
PH 1076 x PKV Rajat	45.43**	40.17**	38.60**	54.33**	45.44**	40.17**	35.35**	59.44**
PH 1076 x Suvin	-8.70**	-14.23**	-15.19**	-5.56**	-8.68	-14.22*	-17.17**	-2.43
LRA 5166 x NH 452	7.49**	3.38*	4.26*	16.09**	-0.13	-10.17	1.81	19.93**
LRA 5166 x NH 625	5.54**	-2.29	-1.46	9.72**	-2.43	-15.11**	-3.78	13.34
LRA 5166 x PKV Rajat	-8.65**	-12.78**	-12.04**	-2.06	-15.33**	-24.21**	-14.10*	1.19
LRA 5166 x Suvin	4.32**	-2.89	-2.07	9.05**	-3.49	-15.61**	-4.36	12.67
SE±	1.15	1.33	1.33	1.33	75.16	86.79	86.79	86.79
CD at 5%	2.32	2.68	2.68	2.68	150.69	174.01	174.01	174.01

*Significant at 5% level, **Significant at 1% level, respectively

4.4.14 Seed cotton yield per plot (g)

For seed cotton yield per plot, the mid parental heterosis ranged from -22.55 (NH 635 x Suvin) to 45.44 per cent (PH 1076 x PKV Rajat). Out of twenty eight crosses, seven crosses recorded positive heterosis and five crosses recorded significant negative heterosis over mid parental value. The intraspecific hybrid PH 1076 x PKV Rajat (45.44%) exhibited highest significant positive heterosis over mid parent value followed by NH 615 x PKV Rajat (41.55%) and PH 1076 x NH 452 (28.74%).

The estimates of heterobeltiosis for seed cotton yield per plot ranged from –28.69 (NH 635 x Suvin) to 40.17 per cent (PH 1076 x PKV Rajat). Out of twenty eight crosses, six and eight crosses recorded positive and negative significant heterosis over better parent. The cross PH 1076 x PKV Rajat (40.17%) recorded the highest positive heterosis followed by NH 615 x PKV Rajat (38.03%) and NH 615 x NH 625 (27.07%) over better parent (Table 14.7).

Standard heterosis over check NHH 44 ranged from -28.18 (NH 630 x Suvin) to 20.45 per cent (PH 1076 x PKV Rajat). Thirteen crosses recorded significant heterosis over NHH 44. Out of these three crosses were found positively significant over check NHH 44. Standard heterosis over DCH 32 ranged from -15.39 (NH 630 x Suvin) to 59.44 per cent (PH 1076 x PKV Rajat).Out of eleven significant crosses, nine crosses recorded significantly positive heterosis over check DCH 32. The cross PH 1076 x PKV Rajat (35.35 and 59.44 %) recorded the highest positive heterosis followed by NH 615 x PKV Rajat (23.64 and 45.64%) and PH 1076 x NH 452 (20.45 and 41.88 %) over checks NHH 44 and DCH 32, respectively.

4.4.15 Seed cotton yield qtl./ ha

Mid parent heterosis ranged from -21.56 (NH 635 x Suvin) to 45.49 per cent (PH 1076 x PKV Rajat). Out of twenty eight crosses, seven crosses recorded positive heterosis value and five crosses recorded significant negative heterosis over mid parental value. The intraspecific hybrid PH 1076 x PKV Rajat (45.49 %) exhibited the highest significant positive heteros followed by NH 615 x PKV Rajat (41.61%) and PH 1076 x NH 452 (28.75%) over mid parent value (Table 14.8).

The estimates of heterobeltiosis for seed cotton yield quintal per ha ranged from -27.78 (NH 635 x Suvin) to 40.19 per cent (PH 1076 x PKV Rajat). Out of twenty eight crosses, six and eight crosses recorded positive and negative significant values over better parent. The cross PH 1076 x PKV Rajat (40.19%) recorded the highest positive heterosis followed by NH 615 x PKV Rajat (38.12%) and NH 615 x NH 625 (27.10%) over better parent, respectively.

Standard heterosis over check NHH 44 ranged from -26.22 (NH 630 x Suvin) to 39.02 per cent (PH 1076 x PKV Rajat). Thirteen crosses recorded significant heterosis. Out of which four crosses were found to be positively significant and nine were negatively significant over check NHH 44. Standard heterosis over check DCH 32 ranged from -18.09 (NH 630 x Suvin) to 54.34 per cent (PH 1076 x PKV Rajat). Out of twenty eight crosses, eight crosses recorded significantly positive heterosis over check DCH 32.The cross PH 1076 x PKV Rajat (39.02 and 54.34%) recorded the highest positive heterosis followed by NH 615 x PKV Rajat (26.98 and 40.97%) and PH 1076 x NH 452 (23.71 and 37.34%) over checks NHH 44 and DCH 32, respectively.

Table 14.8. Estimates of heterosis over mid parent (MP), better parent (BP) and standard check (SH) for seed cotton yield quintal per ha

Crosses	Seed cotton yield qt/ha			
	MP	BP	SH(NHH44)	SH(DCH 32)
NH 545 x NH 452	3.81	-2.01	2.65	13.97
NH 545 x NH 625	-1.18	-9.95	-5.67	4.72
NH 545 x PKV Rajat	-2.78	-8.72	-4.38	6.15
NH 545 x Suvin	-20.99**	-27.63**	-24.19**	-15.83*
NH 615 x NH 452	25.27**	21.49**	12.99*	25.45**
NH 615 x NH 625	28.01**	27.10**	11.08	23.32**
NH 615 x PKV Rajat	41.61**	38.12**	26.98**	40.97**
NH 615 x Suvin	-1.85	-1.98	-14.34*	-4.89
NH 630 x NH 452	1.18	-2.75	-9.56	0.41
NH 630 x NH 625	-4.56	-4.76	-17.95**	-8.90
NH 630 x PKV Rajat	-5.45	-8.61	-15.98*	-6.72
NH 630 x Suvin	-14.68*	-15.35*	-26.22**	-18.09*
NH 635 x NH 452	-0.82	-5.88	-2.52	8.23
NH 635 x NH 625	4.83	-3.98	-0.55	10.41
NH 635 x PKV Rajat	-3.73	-9.17	-5.93	4.44
NH 635 x Suvin	-21.56**	-27.78**	-25.20**	-16.96*
PH 1060 x NH 452	-7.60	-8.40	-14.81*	-5.42
PH 1060 x NH 625	11.89	8.68	-0.67	10.28
PH 1060 x PKV Rajat	20.60**	20.25**	10.55	22.74**
PH 1060 x Suvin	-12.63*	-14.65*	-22.00**	-13.40
PH 1076 x NH 452	28.75**	24.76**	23.71**	37.34**
PH 1076 x NH 625	12.12*	4.77	3.89	15.34*
PH 1076 x PKV Rajat	45.49**	40.19**	39.02**	54.34**
PH 1076 x Suvin	-8.68	-14.21*	-14.93*	-5.55
LRA 5166 x NH 452	-0.15	-10.18	4.55	16.07*
LRA 5166 x NH 625	-2.44	-15.12**	-1.20	9.69
LRA 5166 x PKV Rajat	-15.31**	-24.21**	-11.78	-2.05
LRA 5166 x Suvin	-3.51	-15.63**	-1.79	9.03
SE±	108.47	125.25	125.25	125.25
CD at 5%	289.61	334.41	334.41	334.41

*Significant at 5% level, **Significant at 1% level, respectively.

4.5 CORRELATIONS

Phenotypic and genotypic correlations were worked out for yield, yield contributing and fibre quality characters in twenty eight crosses and their eleven parents. In general, genotypic correlations were found higher than phenotypic correlations. The results are presented in Table 15.

4.5.1 Days to 50% flowering

The character days to 50 % flowering exhibited significant positive phenotypic and genotypic correlation with the days to maturity (0.4600/0.4859), fibre length (0.5252/0.5696), fibre strength (0.6206/ 0.7363), while it registered significant negative correlation with uniformity ratio (-0.3531/-0.5503), boll weight (-0.5010/-0.5303), ginning percentage (-0.3278/-0.5599) and seed cotton yield per plant (-0.3460/-0.3650) at phenotypic and genotypic level.

4.5.2 Number of monopodia per plant

Number of monopodia per plant registered significant positive association with plant height (0.2078/0.4251), number of bolls per plant (0.2527/0.5546) and seed cotton yield per plant (0.2589/0.5435) both at phenotypic and genotypic level and while it had recorded significant positive association with number of sympodia per plant (0.1948), ginning percentage (0.6284) and registered negative significant association with fibre length (-0.2106) at genotypic level.

4.5.3 Number of sympodia per plant

Number of sympodia per plant exhibited significant positive association with number of bolls per plant (0.2932/0.4030), ginning percentage (0.1841/0.4059) and seed cotton yield per plant (0.2710/0.3480) at phenotypic and genotypic level and it registered significant positive correlation with plant height (0.4720) at genotypic level.

Table 15. Phenotypic and Genotypic correlation coefficients among seed cotton yield per plant and other characters in cotton

Characters	Number of monopodia/ plant	Number of sympodia/ plant	Plant height (cm)	Days to maturity	Boll weight (g)	Number of bolls/plant	Ginning percentage (%)	Micronaire value (µg/ inch)	Fibre length (mm)	Uniformity ratio	Fibre strength (g/tex)	Seed cottc yield / pla (g)
Days to 50% flowering	0 0014 (-0.0899)	0 0085 (-0.0377)	0.1562 (0.1966*)	0 4600** (0.4859**)	-0.5010** (-0.5303**)	0.1223 (0.1598)	-0.3278** (-0.5599**)	-0.0939 (-0.1291)	0 5252** (0.5696**)	-0.3531** (-0.5503**)	0 6206** (0.7363**)	-0.3460** (-0 3650**
Number of monopodia/plant		0.0168 (0.1948*)	0 2078* (0.4251**)	-0 0672 (-0.1496)	0.0388 (0.0381)	0.2527** (0 5546**)	0 0446 (0 6284**)	-0.0039 (0.1151)	-0 0878 (-0.2106*)	-0.0263 (-0 0107)	-0 0518 (0.0162)	0.2589** (0.5435**
Number of sympodia/ plant			0.1295 (0.4720**)	-0.0500 (-0.0635)	-0 0075 (0 0224)	0.2932** (0.4030**)	0 1841* (0.4059**)	0 0751 (0 0622)	0 0371 (0.0571)	-0 0668 (-0.1487)	-0.0513 (-0 0794)	0.2710** (0 3480**
Plant height (cm)				0.0847 (0.0858)	-0.0245 (-0.0515)	0.2862** (0.3687**)	0 1324 (0.2215*)	-0.0364 (-0.0342)	0 2298* (0.2532**)	-0.1096 (-0 1289)	0.2519** (0.3120**)	0.1650 (0 1830*)
Days to maturity					-0.6306** (-0.6686**)	-0.0591 (-0 0505)	-0 3195** (-0.5522**)	-0.1362 (-0 1523)	0.7471** (0.7619**)	-0.2940** (-0.3874**)	0.4853** (0.5253**)	-0.5250** (-0 5347**
Boll weight (g)						0 1397 (0.1683)	0.1870* (0 4351**)	0.0375 (0.0618)	-0.4562** (-0.4843**)	0.3148** (0 4430**)	-0.4059** (-0.4723**)	0 5827** (0.6211**)
Number of bolls/ Plant							0 0527 (0.2277*)	0.0115 (0 0138)	0.0784 (0.0805)	-0.1442 (-0 2128*)	0.1968* (0.2300*)	0 7152** (0.7809**)
Ginning percentage (%)								0.3043** (0.4602**)	-0.4084** (-0.6615**)	0.0662 (0.1689)	-0.2501** (-0.5168**)	0.3131** (0 5245**)
Micronaire value(µg/ inch)									-0.3603** (0.3817**)	0.1329 (0.2096*)	-0.1086 (-0.1207)	0.1272 (0.1392)
Fibre length (mm)										-0 3618** (-0.4956**)	0.4454** (0.4797**)	-0.3243** (-0 3299**)
Uniformity ratio											-0.3591** (-0 4567**)	0.0441 (0.0804)
Fibre strength (g/tex)												-0.2183* (-0.2355**)

*Significant at 5% level, **Significant at 1% level respectively; The values in the parenthesis are genotypic correlations

4.5.4 Plant height

Plant height registered significantly positive correlation with number of bolls per plant (0.2862/0.3687), fibre length (0.2298/0.2532) and fibre strength (0.2519/0.3120) at genotypic and phenotypic level and exhibited significant positive association with ginning percentage (0.2215) and seed cotton yield per plant (0.1830) at genotypic level.

4.5.5 Days to maturity

The trait days to maturity recorded significantly positive correlation with fibre length (0.7471/0.7619) and fibre strength (0.4853/0.5253) both at phenotypic and genotypic level, while it registered significant and negative association with boll weight (-0.6306/-0.6686), ginning percentage (-0.3195/-0.5522), uniformity ratio (-0.2940/-0.3874) and seed cotton yield per plant (-0.5250/-0.5347) both at phenotypic and genotypic level.

4.5.6 Boll weight

Boll weight showed significant and positive association with ginning percentage (0.1870/0.4351), uniformity ratio (0.3148/0.4430) both at phenotypic and genotypic level, while it exhibited significant and negative correlation with fibre length (-0.4562/-0.4843) both at phenotypic and genotypic level. Boll weight recorded (0.5827/0.6211) significantly positive correlation phenotypic at and genotypic level with seed cotton yield per plant.

4.5.7 Number of bolls per plant

Number of bolls per plant exhibited highly significant positive association with seed cotton yield per plant (0.7152/0.7809) both at phenotypic and genotypic level. Number of bolls per plant recorded significant positive association with fibre strength (0.1968/0.2300) at both at phenotypic and genotypic level.

4.5.8 Ginning percentage

The trait ginning percentage registered significant positive correlation with micronaire value (0.3043/0.4602) and seed cotton yield per plant (0.3131/0.5245) at phenotypic and genotypic level, whereas significant and negative correlation was found with fibre length (-0.4084/-0.6615) and fibre strength (-0.2501/-0.5168) both at phenotypic and genotypic level.

4.5.9 Micronaire value

Micronaire value registered highly significant negative (-0.3603) association at genotypic level and highly significant positive association (0.3817) at phenotypic level with fibre length. Micronaire value recorded negative association with fibre strength (-0.1086/-0.1207) at phenotypic and genotypic level.

4.5.10 Fibre length

The character fibre length showed significant negative association with uniformity ratio (-0.3618/-0.4956) and seed cotton yield per plant (-0.3243/-0.3299) both at phenotypic and genotypic level, while it exhibited significant and positive correlation with fibre strength (0.4454/ 0.4797) both at phenotypic and genotypic level.

4.5.11 Uniformity ratio

Uniformity ratio exhibited highly significant negative association with fibre strength (-0.3591/-0.4567) both at phenotypic and genotypic level.

4.5.12 Fibre strength

Fibre strength showed significant negative association (-0.2183/-0.2355) and highly significant negative association at both phenotypic and genotypic levels with seed cotton yield per plant.

4.5.13 Seed cotton yield per plant

Seed cotton yield per plant showed significant positive correlations with number of monopodia per plant (0.2589/0.5435), number of sympodia per plant (0.2710/0.3480), boll weight (0.5827/0.6211) number of bolls per plant (0.7152/0.7809) and ginning percentage (0.3131/0.5245) both at phenotypic and genotypic level and significant positive association with plant height (0.6211) at genotypic level, while it exhibited significant and negative correlation with days to 50% flowering (-0.3460/-0.3650), days to maturity (-0.5250/-0.5347), fibre length (-0.3243/-0.3299) and fibre strength (-0.2183/-0.2355) both at phenotypic and genotypic level. However, seed cotton yield per plant had no association with micronaire value and uniformity ratio.

4.6 PATH COEFFICIENT ANALYSIS

Based on the data recorded on twenty eight (28) hybrids and their eleven (11) parents. Phenotypic and genotypic correlations were worked out to determine direct and indirect effects of yield, yield contributing and quality characters on seed cotton yield per plant (Table 16).

The path coefficient analysis revealed that number of bolls per plant (0.6361), boll weight (0.2637), fibre length (0.1147), ginning percentage (0.0932), number of monopodia per plant (0.0781), micronaire value (0.0703) and number of sympodia per plant (0.0491) exhibited positive direct effects and uniformity ratio (-0.0764), plant height (-0.0285) and fibre strength (-0.0067) had recorded negative direct effects on seed cotton yield per plant at phenotypic level.

Ginning percentage (5.8228), fibre length (2.7254), number of bolls per plant (1.9121), uniformity ratio (1.9022), fibre strength (0.5227) and days to 50 % flowering (0.4551) exhibited positive direct effects and negative direct effect were exhibited by plant height (-0.9615), days to

Table16. Phenotypic and Genotypic path coefficients for yield contributing and fibre quality characters in cotton

Characters	Days to 50% flowering	No. of monopodia / plant	Number of sympodia/ plant	Plant height (cm)	Days to maturity	Boll weight (g)	Number of bolls/ plant	Ginning percentage (%)	Micronaire value (µg/ inch)	Fibre length (mm)	Uniformity ratio	Fibre strength (g/tex)	Seed cotton yield / plant (g)
Days to 50% flowering	**-0.2035 (0.4551)**	-0.0003 (-0.0409)	-0.0017 (-0.0172)	-0.0318 (0.0895)	0.0936 (0.2211)	0.1019 (-0 2413)	-0.0249 (0.0727)	0.0667 (-0.2548)	0.0191 (-0.0588)	-0 1068 (0.2592)	0.0718 (-0 2504)	-0 1263 (0 3351)	-0 3460 (-0.3650)
Number of monopodia/plant	0 0001 (0.2553)	**0.0781 (-2.8381)**	0 0013 (-0.5529)	0.0162 (-1.2066)	-0.0052 (0.4247)	0.0030 (-0.1081)	0.0197 (-1.5741)	0 0035 (-1.7834)	-0.0003 (-0.3268)	-0.0069 (0.5977)	-0.0021 (0.0303)	-0.0040 (-0.0460)	0.2589 (0.5435)
Number of sympodia/ plant	0.0004 (0.0553)	0.0008 (-0.2858)	**0.0491 (-1.4671)**	0.0147 (-0.6924)	-0.0025 (0 0932)	-0.0004 (-0.0328)	0 0144 (-0.5912)	0.0090 (-0.5956)	0.0037 (-0.0912)	0.0018 (-0 0838)	-0.0033 (0 2182)	-0.0025 (0 1166)	0.2710 (0.3480)
Plant height(cm)	-0.0045 (-0.1890)	-0.0059 (-0.4088)	-0.0085 (-0.4538)	**-0.0285 (-0.9615)**	-0.0024 (-0.0825)	0.0007 (0 0495)	-0.0082 (-0.3545)	-0.0038 (-0.2130)	0.0010 (0.0329)	-0.0066 (-0.2434)	0 0031 (0.1239)	-0 0072 (-0.3000)	0.1650 (0.1830)
Days to maturity	-0.1302 (-0.5790)	0.0190 (0.1783)	0.0142 (0.0757)	-0.0240 (-0.1022)	**-0.2830 (-1.1915)**	0.1785 (0.7966)	0.0167 (0.0601)	0.0904 (0.6580)	0 0385 (0.1814)	-0 2114 (-0 9078)	0.0832 (0.4616)	-0.1373 (-0.6259)	-0.5250 (-0 5347)
Boll weight (g)	-0.1321 (0 7327)	0 0102 (-0 0526)	-0.0020 (-0.0309)	-0.0065 (0.0711)	-0.1663 (0.9237)	**0.2637 (-1.3816)**	0.0368 (-0.2325)	0 0493 (-0.6012)	0.0099 (-0.0854)	-0.1203 (0.6692)	0.0830 (-0 6120)	-0 1070 (0.6525)	0.5827 (0 6211)
Number of bolls/ Plant	0.0778 (0 3055)	0 1607 (1.0605)	0.1865 (0.7705)	0.1820 (0.7050)	-0 0376 (-0 0965)	0.0889 (0 3218)	**0.6361 (1.9121)**	0.0336 (0.4353)	0.0073 (0 0263)	0.0499 (0.1540)	-0.00917 (-0.4070)	0.1252 (0.4397)	0 7152 (0.7809)
Ginning percentage (%)	-0.0305 (-3.2604)	0.0042 (3.6588)	0.0172 (2 3637)	0.0123 (1.2899)	-0.0298 (-3.2156)	0.0174 (2 5337)	0 0049 (1.3256)	**0.0932 (5.8228)**	0.0284 (2.6797)	-0.0381 (-3.8518)	0.0062 (0.9836)	-0 0233 (-3.0095)	0.3131 (0.5245)
Micronaire value(µg/ inch)	-0.0066 (0.1788)	-0.0003 (-0.1595)	-0.0053 (-0.0861)	-0.0026 (0.0474)	-0.0096 (0.2109)	0.0026 (-0.0856)	0.0008 (-0.0191)	0 0214 (-0.6373)	**0.0703 (-1.3849)**	-0.0253 (0.5286)	0 0093 (-0.2903)	-0.0076 (0.1672)	0.1272 (0.1392)
Fibre length (mm)	0 0602 (1.5525)	-0.0101 (-0.5739)	0.0043 (0 1556)	0.0263 (0 6900)	0.0857 (2.0764)	-0 0523 (-1 3200)	0 0090 (0.2195)	-0.0468 (-1.8028)	-0 0413 (-1 0402)	**0.1147 (2.7254)**	-0.0415 (-1.3507)	0.0511 (1.3075)	-0.3243 (-0.3299)
Uniformity ratio	0.0270 (-1 0468)	0.0020 (-0.0203)	0.0051 (-0 2829)	0.0084 (-0.2451)	0 0225 (-0.7369)	-0 0241 (0.8426)	0.0110 (-0.4048)	-0 0051 (0 3213)	-0.0102 (0.3988)	0.0277 (-0.9427)	**-0.0764 (1.9022)**	0.0274 (-0.8686)	0.0441 (0.0804)
Fibre strength (g/tex)	-0 0042 (1.1751)	0.0003 (0.0259)	0 0003 (-0.1268)	-0 0017 (0.4980)	-0.0033 (0 8383)	0.0027 (-0.7537)	-0.0013 (0 3670)	0.0017 (-0.8249)	0.0007 (-0 1927)	-0.0030 (0.7656)	0.0024 (-0.7288)	**-0.0067 (0.5227)**	-0.2183 (-0.2355)

Bold value are direct effect; The value in the parenthesis is genotypic correlation ; Phenotypic residual effect = 0.3803; Genotypic residual effect=0.6193 maturity (-1.1915), boll weight (-1.3816), micronaire value (-1.3849), number of sympodia per plant (-1.4671) and number of monopodia per plant (-2.8381) on seed cotton yield per plant at genotypic level.

Days to 50% flowering had shown positive effect on seed cotton yield per plant via days to maturity (0.0936/0.2211) and days to maturity had negative effect on seed cotton yield per plant via fibre length (-0.2114/-0.9078) both at phenotypic and genotypic.

Number of bolls per plant recorded positive effect on seed cotton yield per plant *viz.*, days to 50% flowering, number of monopodia per plant, plant height, boll weight, ginning percentage and fibre strength at genotypic and phenotypic level. Ginning percentage showed negative association with seed cotton yield per plant via fibre length (-0.0381/ -3.8518) at both the level.

4.7 GENERATION MEAN ANALYSIS

With a view to study the nature and mode of gene action for yield, yield components and quality characters, four crosses *viz.*, NH 545 x NH 452 (cross-1), NH 635 x PKV Rajat (cross-2), PH 1060 x Suvin (cross-3) and LRA 5166 x Suvin (cross-4) were selected on the basis of fibre quality, yield and yield components. The above mentioned four crosses are here referred as cross-1, cross-2, cross-3 and cross-4, respectively.

The analysis of variance of the four crosses for thirteen characters is presented in Appendix-1. The analysis of variance revealed that there were significant differences among the generations for various characters in all four crosses. Whenever the differences between different generation means were found to be non-significant on the basis of mean performance, further analysis was not done and if generation mean were found significant, the data were subjected to generation mean analysis to know the gene action controlling the traits.

4.7.1 Mean performance

The mean performance of six generation (P_1, P_2, F_1, F_2, BC_1 and BC_2) pertaining to four cross combinations for yield, yield component and quality characters is presented in Tables 17.1 to 17.13.

4.7.1.1 Days to 50% flowering

i) Cross- 1 (NH 545 x NH 452)

It is evident from the data presented in Table 17.1 that there were significant differences for mean to days to 50% flowering in parents and generations. The parent P_1 (66.33 days) was flowered earlier than parent P_2 (73.33 days) and mean value of F_1 (65.00 days) was on par with the parents P_1 (66.33 days), whereas mean value of F_2 68.33 days was recorded. The generation BC_1 (62.66 days) at flowered earlier than BC_2 (71.33 days).

ii) Cross-2 (NH 635 x PKV Rajat)

In this cross parent P_2 (71.33 days) was earlier in 50% flowering than P_1 (75.66 days). The mean value of F_1 (73.66 days) was on par with both the parents P_1 and P_2, while the mean values of segregating generation, F_2 (69.66 days) and BC_2 (69.33 days) were at par with each other and BC_2 generation was late in 50% flowering than BC_1.

iii) Cross- 3 (PH 1060 x Suvin)

The parent P_1 (74.83 days) flowered earlier than P_2 (83.65 days) for mean days to 50% flowering. The mean value of F_1 (81.00 days) and in segregating generations the mean value of F_2 (86.00 days) was higher than the back crosses BC_1 (78.60 days) and BC_2 (82.63 days).

iv) Cross- 4 (LRA 5166 x Suvin)

In P_1 (76.33 days) 50 % flowering was earlier than P_2 (81.62 days). F_1 (84.76 days) flowered late than the parents P_1 and P_2. The F_2 (80.10 days) mean value and back crosses BC_1 (73.70 days) and BC_2 (83.60 days) showed significant differences, while BC_1 (73.70 days) recorded significantly early flowering than BC_1, F_2 and F_1.

Table 17.1 Generation mean for days to 50% flowering

Cross No.	Cross	P_1	P_2	F_1	F_2	BC_1	BC_2	SE±	CD (5%)
1	NH 545 x NH 452	66.33	73.33	65.00	68.33	62.66	71.33	0.40	1.28
2	NH 635 x PKV Rajat	75.66	71.33	73.66	69.66	67.33	69.33	0.56	1.78
3	PH 1060 x Suvin	74.83	83.65	81.00	86.00	78.60	82.63	0.30	0.94
4	LRA 5166 x Suvin	76.33	81.62	84.76	80.10	73.70	83.60	0.44	1.40

Table 17.2 Generation mean for number of monopodia per plant

Cross No.	Cross	P_1	P_2	F_1	F_2	BC_1	BC_2	SE±	CD (5%)
1	NH 545 x NH 452	1.41	1.29	1.08	1.34	1.38	1.32	0.02	0.06
2	NH 635 x PKV Rajat	1.20	1.33	1.47	1.42	1.31	1.42	0.02	0.07
3	PH 1060 x Suvin	1.35	1.12	1.28	1.32	1.46	1.60	0.06	0.21
4	LRA 5166 x Suvin	1.41	1.29	1.08	1.34	1.38	1.32	0.02	0.06

Table 17.3 Generation mean for number of sympodia per plant

Cross No.	Cross	P_1	P_2	F_1	F_2	BC_1	BC_2	SE±	CD (5%)
1	NH 545 x NH 452	25.33	21.66	29.00	22.33	23.66	23.66	0.38	1.22
2	NH 635 xPKV Rajat	21.93	24.48	24.56	23.46	22.83	24.60	0.36	1.15
3	PH 1060 x Suvin	25.64	28.05	28.95	27.95	22.83	29.93	0.34	1.09
4	LRA 5166 x Suvin	23.98	26.24	24.32	27.47	22.27	27.54	0.46	1.46

Table 17.4 Generation mean for plant height (cm)

Cross No.	Cross	P_1	P_2	F_1	F_2	BC_1	BC_2	SE±	CD (5%)
1	NH 545 x NH 452	150.00	142.66	152.00	141.00	145.33	140.66	0.68	2.14
2	NH 635 x PKV Rajat	151.26	139.35	155.62	153.30	154.36	139.96	0.46	1.46
3	PH 1060 x Suvin	169.44	180.83	177.26	172.63	168.33	178.53	0.51	1.62
4	LRA 5166 x Suvin	157.28	181.00	174.32	164.36	160.93	183.59	0.54	1.71

4.7.1.2 Number of monopodia per plant

i) Cross-1 (NH 545 x NH 452)

Table 17.2 revealed that the parents P_1 (1.41) recorded high mean value over P_2 (1.29) and F_1 (1.08) recorded lower mean value than P_1 and P_2. In segregating generation, BC_2 (1.32) recorded higher mean value over BC_1 (1.38) and F_2 (1.24).

ii) Cross- 2 (NH 625 x PKV Rajat)

Parent P_2 (1.33) recorded significantly more number of monopodia per plant than P_1 (1.20). The mean value of F_1 (1.47) was significantly higher than P_1 and P_2. Among segregating generations, F_2 (1.42) and BC_2 exhibited same mean, where as it was higher than BC_1 (1.31).

iii) Cross- 3 (PH 1060 x Suvin)

Parent P_1 (1.35) recorded significant higher mean value than P_2 (1.12) for this trait. The mean value of F_1 (1.28) was significantly higher than of P_2, but recorded lower value than P_1. Among segregating generation, BC_2 (1.60) recorded higher mean than BC_1 (1.46) and F_2 (1.32).

iv) Cross- 4 (LRA- 5166 x Suvin)

Parent P_1 (1.56) recorded slightly higher number of monopodia in comparison to P_2 (1.43). F_1 (1.72) hybrids recorded the highest mean over all the generations P_1 (1.56), P_2 (1.43), F_2 (1.52), BC_1 (1.63) and BC_2 (1.31).

4.7.1.3 Number of sympodia per plant

i) Cross- 1 (NH 545 x NH 452)

It is evident from the data presented in Table 17.3, parent P_1 (25.33) recorded significantly more number of sympodia per plant than P_2 (21.66). F_1 (29.00) recorded highest mean number of sympodia. F_2 (22.33) recorded lower value as compared to BC_1 (23.66) and BC_2 (23.66).

ii) Cross- 2 (NH 635 x PKV Rajat)

The data revealed that there were significant differences for number of sympodia per plant in between parents. The parent P_2 (24.48) recorded more number of sympodia in comparison to P_1 (21.93) and it was at par with F_1 (24.56) while the value of BC_1 (22.83) and F_2 (23.46) were similar.

iii) Cross- 3 (PH 1060 x Suvin)

The parent P_2 (28.05) recorded higher number of sympodia than P_1 (25.64). F_1 (28.95) recorded higher number of sympodia per plant than parents P_1 and P_2. While, among the segregating generation, BC_2 (29.93) exhibited slightly higher value than BC_1 (22.83) and F_2 (27.95).

iv) Cross- 4 (LRA 5166 x Suvin)

The parent P_2 (26.24) recorded higher number of sympodia than P_1 (23.98). The mean value of F_1 (24.32) was significantly higher in case of P_1. F_2 (27.47) showed at par values with BC_2 (27.54), while BC_1 (22.27) recorded significantly lower value than BC_2 (27.54). Both back cross generations exhibited significant differences for this trait.

4.7.1.4 Plant height (cm)

i) Cross-1 (NH 545 x NH 452)

From the Table 17.4 it was observed that the parent P_1 (150.00 cm) recorded significantly higher value over P_2 (142.66 cm). The F_1 hybrid (152.00 cm) recorded significantly higher plant height over P_1, P_2, F_2, BC_1 and BC_2. Among segregating generations BC_1 (145.33 cm) exhibited higher mean values over F_2 (141.00 cm) and BC_2 (140.66 cm).

ii) Cross-2 (NH 635 x PKV Rajat)

Parent P_1 (151.26 cm) recorded significantly more plant height than P_2 (139.35 cm). The mean value of F_1 (155.62 cm) was significantly higher in case of P_2 (139.35 cm). Among the segregating generation, F_2 (153.30 cm) showed at par value with BC_1 (154.36 cm), while BC_2 (136.96 cm) recorded significantly lower value over both F_2 and BC_1.

iii) Cross-3 (PH 1060 x Suvin)

Parent P_2 (180.83 cm) recorded more plant high in comparison to P_1 (169.44 cm). The F_1 (177.26 cm) recorded less plant height than P_2 and recorded higher value than P_1 (169.44 cm), while among the segregating population, BC_2 (178.53 cm) exhibited slightly higher value than BC_1 (168.33 cm) and F_2 (172.63cm).

iv) Cross-4 (LRA 5166 x Suvin)

The parent P_2 (181.00 cm) had exhibited higher mean value for plant height than P_1 (157.28 cm). The F_1 (174.32 cm) also recorded higher value than P_1 parent. While, among the segregating populations, BC_2 (183.59 cm) recorded higher values than BC_1 (160.93 cm) and F_2 (164.36 cm).

4.7.1.5 Days to Maturity

i) Cross-1 (NH 545 x NH 452)

Parent P_1 (159.33 days) recorded significantly more number of days to maturity than P_2 (155.00 days). The mean value of F_1 (162.66 days) was significantly higher than P_2 and P_1. Among segregating generations, F_2 (156.66 days) exhibited higher values and at par value with BC_1 (154.33 days) and BC_2 (151.66 days) (Table 17.5.)

ii) Cross- 2 (NH 635 x PKV Rajat)

The parents P_1 (166.13 days) recorded higher days to maturity in comparison to P_2 (149.14 days) and F_1 (159.16 days). Among segregating generations, F_2 (159.43 days) recorded less days to maturity than BC_1 (163.73 days) and BC_2 (150.60 days).

Table 17.5 Generation mean for days to maturity

Cross No.	Cross	P_1	P_2	F_1	F_2	BC_1	BC_2	SE±	CD (5%)
1	NH 545 x NH 452	159.33	155.00	162.66	156.66	154.33	151.66	0.77	2.43
2	NH 635 x PKV Rajat	166.13	149.14	159.16	159.43	163.73	150.60	0.31	0.99
3	PH 1060 x Suvin	164.26	183.58	173.66	169.10	162.56	181.23	0.42	1.33
4	LRA 5166 x Suvin	147.11	182.65	176.12	171.17	152.23	180.74	0.45	1.42

Table 17.6 Generation mean for boll weight (g)

Cross No.	Cross	P_1	P_2	F_1	F_2	BC_1	BC_2	SE±	CD (5%)
1	NH 545 x NH 452	3.20	2.98	3.14	2.85	3.23	2.94	0.01	0.05
2	NH 635 x PKV Rajat	3.26	2.95	3.16	2.86	3.13	3.17	0.05	0.16
3	PH 1060 x Suvin	3.28	2.60	2.96	2.65	3.68	2.82	0.09	0.29
4	LRA 5166 x Suvin	3.20	2.98	3.14	2.85	3.23	2.94	0.01	0.05

Table 17.7 Generation mean for number of bolls per plant

Cross No.	Cross	P_1	P_2	F_1	F_2	BC_1	BC_2	SE±	CD (5%)
1	NH 545 x NH 452	31.66	26.66	33.33	30.00	33.66	28.33	0.45	1.43
2	NH 635 x PKV Rajat	31.97	27.74	33.73	36.79	33.76	34.96	0.66	2.10
3	PH 1060 x Suvin	32.10	46.63	43.15	43.52	35.70	41.54	0.969	3.05
4	LRA 5166 x Suvin	36.24	50.47	41.86	42.03	44.36	40.94	0.36	1.14

Table 17.8 Generation mean for ginning percentage (%)

Cross No.	Cross	P_1	P_2	F_1	F_2	BC_1	BC_2	SE±	CD (5%)
1	NH 545 x NH 452	38.60	37.53	39.73	38.00	37.96	34.40	0.38	1.20
2	NH 635 x PKV Rajat	36.75	38.40	40.20	36.02	39.20	36.36	0.55	1.75
3	PH 1060 xSuvin	37.69	33.32	35.17	36.40	35.11	34.31	0.27	0.87
4	LRA 5166 x Suvin	36.64	33.42	35.57	33.40	36.33	34.41	0.31	0.98

iii) Cross-3 (PH 1060 x Suvin)

The parent P_2 (183.58 days) exhibited higher mean value than P_1 (164.26 days). The F_1 (173.66 days) recorded higher mean value than P_1 (164.26 days) and lower value than P_2 (183.58 days). The BC_2 (181.23 days) recorded significant higher value than BC_1 (162.56 days) and F_2 (169.10 days).

iv) Cross- 4 (LRA 5166 x Suvin)

The parents P_2 (182.65 days) recorded higher days to maturity than P_1 (147.11 days) and F_1 (176.12 days). The mean values of F_2 (171.17 days) were more than P_1. Among segregating populations, BC_2 (180.74 days) recorded significantly more days to maturity over the F_2 (171.71 days) and BC_1 (152.23 days).

4.7.1.6 Boll weight (g)

i) Cross-1 (NH 545 x NH 452)

The parent P_1 (3.20 g) recorded significant higher mean value over P_2 (2.98 g). The F_1 (3.14 g) exhibited lower mean value over P_1 and higher mean value over P_2 (Table 17.6). Among the segregating generations, BC_1 (3.28 g), recorded higher mean value over BC_2 (2.94 g) and F_2 (2.85 g).

ii) Cross-2 (NH 635 x PKV Rajat)

The parent P_1 (3.26 g) recorded higher mean value over P_2 (2.95 g) and F_1 (3.16 g). Segregating generations, BC_1 (3.13 g) exhibited at par mean value over BC_2 (3.17 g). The F_2 (2.86 g) recorded lower mean value over BC_1 and BC_2.

iii) Cross-3 (PH 1060 x Suvin)

Significant differences were observed between parents and generations. The parent P_1 (3.28 g) exhibited higher boll weight over parent P_2 (2.60 g). The mean of F_1 (2.96 g) recorded lower mean value over P_1.

Among the segregating generations, BC_1 (3.68 g) recorded higher mean value over BC_2 (2.82 g) and F_2 (2.65 g).

iv) Cross-4 (LRA 5166 x Suvin)

The female, P_1 (3.20 g) recorded higher boll weight over P_2 (2.98 g). The F_1 (3.14 g) recorded higher mean value over P_2 (2.98 g) and lower mean value over P_1 (3.20 g). The segregating generations, BC_1 (3.23 g) recorded higher mean value over F_2 (2.85 g), and BC_2 (2.94 g).

4.7.1.7 Number of bolls per plant

i) Cross-1 (NH 545 x NH 452)

From the Table 17.7 it was observed that the parent P_1 (31.66) recorded significantly higher values over P_2 (26.66).The F_1 hybrid (33.53) recorded significantly higher number of bolls over P_1 and P_2. Among the segregating populations, BC_1 (33.66) recorded the highest mean values for number of bolls per plant over BC_2 (28.33) and F_2 (30.00).

ii) Cross-2 (NH 635 x PKV Rajat)

Mean of F_1 (33.73) exhibited significantly higher value over both the parents. While, the parent P_1 (31.97) and P_2 (27.74) differed significantly with each other. Among segregating generations, F_2 (36.79) recorded significantly more number of bolls per plant over the generations of parents BC_1 (33.76) and BC_2 (34.96).

iii) Cross-3 (PH 1060 x Suvin)

The parent P_2 (46.63) recorded significantly higher mean over P_1 (32.10). The F_1 hybrid (43.15) recorded lower mean value over P_2 and higher mean value over P_1. Among the segregating populations, F_2 (43.52) exhibited on par mean with BC_2 (41.45). BC_1 (35.70) recorded significantly less number of bolls per plant over BC_2, F_2 and F_1.

iv) **Cross-4 (LRA- 5166 x Suvin)**

The parent P_2 (50.47) recorded significantly higher mean value over P_1 (36.24) and F_1 (41.86). The BC_1 (44.36) recorded higher bolls per plant than BC_2 (40.94) and F_2 (42.03). The mean value of F_2 (42.03) recorded higher mean value over BC_2 and lower mean value than BC_1.

4.7.1.8 Ginning (%)

i) **Cross- 1 (NH 545 x NH 452)**

The data furnished in Table 17.8 revealed that the parent P_1 (38.60 %) recorded significantly higher value than of P_2 (37.53%), whereas the mean of F_1 (39.73%) was on par with P_1. Among segregating generations, F_2 (38.00%), BC_1 (37.96%) and BC_2 (34.40%) ginning percentage was lower than F_1 (39.73%).

ii) **Cross- 2 (NH 635 x PKV Rajat)**

In this cross parent P_2 (38.40%) exhibited more ginning percentage than parent P_1 (36.75%). The mean of F_1 hybrid (40.20%) was found at par with BC_1 (39.20%). Among the segregating generations, ginning percentage was at par in F_2 (36.02%) and BC_2 (36.36%). However, BC_1 generation found to be significantly superior over BC_2 and F_2 generations.

iii) **Cross- 3 (PH 1060 x Suvin)**

The parent P_1 (37.69%) recorded significantly higher values than that of P_2 (33.32%), whereas the mean of F_1 (35.17%) was higher than P_2. In segregating generations, F_2 (36.40%), BC_1 (35.11%) and BC_2 (34.31%) were at par with each other.

iv) **Cross- 4 (LRA 5166 x Suvin)**

In this cross parent P_1 (36.64%) significantly differed with parent P_2 (33.42%) and the mean of F_1 (35.57%) was found to be at par with P_1 (36.64%) and BC_1 (36.33%). The segregating generations, BC_1 (36.33%)

recorded higher values for ginning percentage over BC_2 (34.41%) and F_2 (33.40%).

4.7.1.9 Micronaire value (μg/inch)

i) Cross- 1 (NH 545 x NH 452)

From Table 17.9, it was observed that, in F_1 (3.44 μg/inch) micronaire value was less than both the parents P_1 (3.59 μg/inch) and P_2 (3.72 μg/inch). While, in F_2 micronaire value was higher (3.76 μg/inch) over BC_1 (3.54 μg/inch) and BC_2 (3.50 μg/inch).

ii) Cross- 2 (NH 635 x PKV Rajat)

There was significant differences between the parent P_1 (4.05 μg/inch) and P_2 (3.50 μg/inch) for micronaire value. The mean of F_1 (4.65 μg/inch) hybrid exhibited significantly higher value as compared to parent. Segregating generations, F_2 (3.60 μg/inch), BC_1 (3.74 μg/inch) and BC_2 (3.98 μg/inch) recorded lower average values as compared to P_1 parent.

iii) Cross- 3 (PH 1060 x Suvin)

Parent P_1 (3.29 μg/inch) exhibited significant differences with parent P_2 (3.80 μg/inch). The F_1 (3.25 μg/inch), F_2 (2.84 μg/inch), BC_1 (2.82 μg/inch) and BC_2 (3.46 μg/inch) recorded lower average values than P_2 parent.

iv) Cross- 4 (LRA 5166 x Suvin)

There were no significant differences between the parent P_1 (3.59 μg/inch) and P_2 (3.72 μg/inch). The mean of F_1 (3.44 μg/inch) hybrid exhibited significantly lower micronaire value as compared to both the parents, but in backcross generation, BC_2 (3.50 μg/inch) less micronaire value was noticed.

4.7.1.10 Uniformity ratio

i) Cross- 1 (NH 545 x NH 452)

Significant differences were not observed between the parents P_1 (45.10) and P_2 (45.20) for this character. The F_1 (46.67) recorded high mean value over both the parents. The generation, BC_1 (46.96) exhibited

Table 17.9 Generation mean for micronaire value (µg/inch)

Cross No.	Cross	P_1	P_2	F_1	F_2	BC_1	BC_2	SE±	CD (5%)
1	NH 545 x NH 452	3.59	3.72	3.44	3.76	3.54	3.50	0.05	0.15
2	NH 635 x PKV Rajat	4.05	3.50	4.65	3.60	3.74	3.98	0.14	0.44
3	PH 1060 x Suvin	3.29	3.80	3.25	2.84	2.82	3.46	0.07	0.23
4	LRA 5166 x Suvin	3.59	3.72	3.44	3.76	3.54	3.50	0.05	0.15

Table 17.10 Generation mean for uniformity ratio

Cross No.	Cross	P_1	P_2	F_1	F_2	BC_1	BC_2	SE±	CD (5%)
1	NH 545 x NH 452	45.10	45.20	46.67	45.43	46.96	45.44	0.26	0.84
2	NH 635 x PKV Rajat	46.18	47.31	49.10	45.63	46.76	48.38	0.35	1.11
3	PH 1060 x Suvin	46.67	45.36	48.20	45.52	45.38	47.63	0.13	0.41
4	LRA 5166 x Suvin	42.92	45.64	47.76	44.31	45.80	47.46	0.16	0.51

Table 17.11 Generation mean for fibre length (mm)

Cross No.	Cross	P_1	P_2	F_1	F_2	BC_1	BC_2	SE±	CD (5%)
1	NH 545 x NH 452	23.25	24.37	24.23	24.10	23.27	24.83	0.27	0.86
2	NH 635 x PKV Rajat	26.06	22.25	24.28	26.06	25.06	23.95	0.88	2.78
3	PH 1060 x Suvin	25.32	33.40	32.70	30.10	26.53	33.06	0.57	1.81
4	LRA 5166 x Suvin	24.15	32.54	31.20	29.51	25.76	32.56	0.38	1.21

high value over BC_2 (45.44) and F_2 (45.43) and at par value with F_1 (46.67) (Table 17.10).

ii) Cross- 2 (NH 635 x PKV Rajat)

No significant differences were observed between the parents P_1 (46.18) and P_2 (47.31). The F_1 (49.10) recorded high mean value over all the generations *viz.*, P_1 (46.18), P_2 (47.31), F_2 (45.63) and BC_1 (46.76). The mean value of F_1 (49.10) was at par with BC_2 (48.38) generation.

iii) Cross- 3 (PH 1060 x Suvin)

Significant differences were not observed between the parents P_1 (46.67) and P_2 (45.36). The F_1 (48.20) recorded the highest mean amont all the generations. In segregating gènerations, BC_2 (47.63) exhibited significant higher value over BC_1 (45.38) and F_2 (45.52).

iv) Cross-4 (LRA 5166 x Suvin)

Significant differences were observed for uniformity ratio among the generations. The F_1 (47.76) recorded high mean value over P_1 (42.92), P_2 (45.64), F_2 (44.31) and BC_1 (45.80). The mean value of F_1 (47.76) was at par with BC_2 (47.46) generation.

4.7.1.11 Fibre length (mm)

i) Cross-1 (NH 545 x NH 452)

From the Table 17.11, it was observed that no significant differences were observed among the generations for fibre length character. All the generations *viz.*, P_1 (21.47 mm), P_2 (22.50 mm), F_1 (23.06 mm), F_2 (21.30 mm), BC_1 (21.23 mm) and BC_2 (23.10 mm) exhibited at par values. The BC_2 recorded higher mean value over all the generations.

ii) Cross- 2 (NH 635 x PKV Rajat)

The parent P_1 (26.06 mm) recorded significantly higher value than that of P_2 (22.25 mm). The F_1 (24.28 mm) exhibited higher value than

P_2. Among the segregating generations, F_2 (26.06 mm) recorded significantly higher value than BC_1 (25.06 mm) and BC_2 (23.95 mm).

iii) Cross- 3 (PH 1060 x Suvin)

The parent P_2 (33.40 mm) recorded significantly higher values than that of P_1 (25.32 mm). The F_1 (32.70 mm) exhibited lower value than P_2. Among the segregating generations, BC_2 (33.06 mm) recorded significantly higher value than F_2 (30.10 mm) and BC_1 (26.53 mm). The mean value of P_2 (33.40 mm) exhibited at par nature with F_1 and BC_2.

iv) Cross- 4 (LRA 5166 x Suvin)

Parent P_1 (24.15 mm) and P_2 (32.54 mm) differed significantly; however, the mean of F_1 (31.20 mm) recorded lower mean value over P_2. Among segregating generations, BC_2 (32.56 mm) recorded significantly superior fibre length over BC_1 (25.76 mm) and F_2 (29.51 mm). The parent P_2 (32.54 mm) recorded at par mean value with BC_2 (32.56 mm).

4.7.1.12 Fibre strength (g/tex)

i) Cross-1 (NH 545 x NH 452)

Mean of F_1 (23.06 g/tex) exhibited higher fibre strength over both the parents P_1 (21. 47 g/tex) and P_2 (22.50)Table 17.12.The BC_2 (23.10 g/tex) recorded significantly higher value over BC_1 (21.23 g/tex) and F_2 (21.30 g/tex). The BC_2 (23.10 g/tex) exhibited at par mean value over F_1 (23.06 g/tex).

ii) Cross-2 (NH 635 x PKV Rajat)

Significant differences were not observed for fibre strength in the parents P_1 (24.15 g/tex) and P_2 (25.56 g/tex). The F_1 (23.42 g/tex) showed lower value than P_1 and P_2. Among the segregating generations, BC_1 (24.99 g/tex) exhibited higher mean value over F_2 (23.66 g/tex) and BC_2 (23.56 g/tex).

Table 17.12 Generation mean for fibre strength (g/tex)

Cross No.	Cross	P_1	P_2	F_1	F_2	BC_1	BC_2	SE±	CD (5%)
1	NH 545 x NH 452	21.47	22.50	23.06	21.30	21.23	23.10	0.15	0.49
2	NH 635 x PKV Rajat	24.15	25.56	23.42	23.66	24.99	23.56	0.19	0.59
3	PH 1060 x Suvin	25.32	26.61	27.86	26.66	25.98	24.85	0.19	0.59
4	LRA 5166 x Suvin	23.18	26.28	26.68	25.23	24.22	27.17	0.37	1.19

Table 17.13 Generation mean for seed cotton yield per plant (g)

Cross No.	Cross	P_1	P_2	F_1	F_2	BC_1	BC_2	SE±	CD (5%)
1	NH 545 x NH 452	79.36	80.30	96.90	97.00	91.73	86.63	2.56	8.09
2	NH 635 x PKV Rajat	82.73	76.06	94.40	95.98	98.46	96.56	0.38	1.20
3	PH 1060 x Suvin	91.28	83.94	86.10	83.30	89.48	86.76	0.41	1.31
4	LRA 5166 x Suvin	73.46	80.60	90.33	95.56	72.43	85.83	0.33	1.05

iii) Cross-3 (PH 1060 x Suvin)

The fibre strength in P_1 (25.32 g/tex) and P_2 (26.61 g/tex) was significant. Whereas in F_1 (27.86 g/tex) fibre strength was higher than F_2 (26.66 g/tex), BC_1 (25.98 g/tex) and BC_2 (24.85 g/tex).

iv) Cross-4 (LRA 5166 x Suvin)

The parent P_2 (26.28 g/tex) recorded significantly higher mean value over P_1 (23.18 g/tex). There were significant differences among F_2 (25.23 g/tex), BC_1 (24.22 g/tex) and BC_2 (27.17 g/tex). The BC_2 (27.17 g/tex) recorded at par mean value with P_2 (26.28 g/tex) and F_1 (26.68 g/tex).

4.7.1.13 Seed cotton yield per plant (g)

i) Cross- 1 (NH 545 x NH 452)

Significant differences among the parents P_1 (79.36 g) and P_2 (80.30 g) were not observed for seed cotton yield per plant Table 17.13. The mean of F_1 (96.90 g) was significantly superior over P_2 and P_1. The segregating generations, F_2 (97.00 g) recorded significantly higher mean values than BC_1 (91.73 g) and BC_2 (86.63 g).

ii) Cross- 2 (NH 635 x PKV Rajat)

The parent P_1 (82.73 g) recorded significantly higher yield compared to parent P_2 (76.06 g). The mean value of F_1 (94.40 g) was significant superior to both the parents. The segregating generation, BC_1 (98.46 g) exhibited higher mean value over BC_2 (96.36 g) and F_2 (95.98 g).

iii) Cross- 3 (PH 1060 x Suvin)

In this cross P_1 (91.28 g) recorded higher mean value over P_2 (83.94 g) and F_1 (86.10 g). Among the segregating generations, BC_1 (89.48 g), BC_2 (86.76 g) and F_2 (83.30 g) recorded less seed cotton yield than P_1 (91.28 g).

iv) Cross- 4 (LRA 5166 x Suvin)

The parent P_1 (73.46 g) recorded significantly high low value compared to P_2 (80.60 g). The mean of F_1 (90.33 g) was significantly superior to P_1 and P_2. In F_2 (95.56 g) seed cotton yield per plant was higher than parents, F_1, BC_1 and BC_2 generations.

4.7.2 Gene effects

Mean data on various characters recorded on different generations *viz.*, parents, F_1, F_2, BC_1 and BC_2 for four (4) cross combinations of cotton were subjected to joint scaling test. The weighted least square technique was employed under three (3) parameters (*viz.*, m, d and h) and six parameter model (*viz.*, m, d, h, i, j and l). First the data were subjected to three parameters model to test the adequacy of additive-dominance. Whenever, calculated χ^2 at 3 degrees of freedom was found to be significant, as it indicates the inadequacy of the additive- dominance model, then it was subjected to six parameter model, to know the non-significant parameters. Search was done for the best fit model scheme after eliminating non-significant parameters wherein χ^2 values become non-significant and all the tested parameters used in the model were found to be significant. The joint scaling test was found to be more efficient in detection of epistasis as compared to individual scaling tests, Ketata *et al.* (1976) had also concluded superiority of joint scaling test over simple scale in wheat.

The estimate of different genetic components of generation mean in terms of three and six parameter (best fit model) for thirteen (13) characters of four crosses in cotton are furnished in Table 18.1 to 18.13. The results are elaborated crosswise for thirteen (13) characters.

4.7.2.1 Days to 50% flowering

The scaling test results are presented in Table 18.1. The adequacy of additive-dominance model A, B, C and D scaling test were applied. It revealed that all the scaling tests for all the crosses were highly significant except scale A in cross 3 and scale B in cross 3 and 4 which indicated the three parameter model was not adequate to explain the genetic variation for this trait in these crosses.

Table 18.1. Scaling test, joint scaling test and estimates of m, d, h, i, j and l components by best fit model for days to 50% flowering

Parameter		Cross 1	Cross 2	Cross 3	Cross 4
		NH 545 x NH 452	**NH 635 x PKV Rajat**	**PH 1060 x Suvin**	**LRA 5166 x Suvin**
Scaling test	A	-6.004 ± 0.550 **	-14.672 ± 0.670 **	1.368 ± 0.596	-13.680 ± 0.988 **
	B	4.332 ± 0.644**	-6.336 ± 0.668 **	0.606 ± 0.487	0.972 ± 1.329
	C	3.664 ± 0.923**	-15.668 ± 0.967 **	23.522 ± 0.846 **	-6.880 ± 1.679 **
	D	2.668 ± 0.340*	2.670 ± 0.412 *	10.774 ± 0.258 **	2.914 ± 0.594 **
Joint Scaling test	m	70.912 ± 0.176**	67.972 ± 0.216 **	80.761 ± 0.134 **	79.310 ± 0.243 **
	d	-5.455 ± 0.162**	-0.230 ± 0.225	-3.026 ± 0.121 **	-4.414 ± 0.227 **
	h	-6.145 ± 0.353**	4.092 ± 0.341 **	7.791 ± 0.273 **	1.009 ± 0.499
	χ^2	**294.90 ****	**552.56 ****	**2397.45 ****	**314.76 ****
Best Fit Model	m	75.168 ± 0.713**	78.840 ± 0.894 **	100.793 ± 0.536 **	84.868 ± 1.216 **
	d	-3.500 ± 0.211**	2.168 ± 0.343 *	-4.413 ± 0.146 **	-2.574 ± 0.258 **
	h	-17.176 ± 1.957**	-31.520 ± 2.364**	-39.367 ± 1.577 **	-18.790 ± 3.633 **
	i	-5.336 ± 0.681**	-5.340 ± 0.825**	-21.548 ± 0.516 **	-5.828 ± 1.188 **
	j	-5.168 ± 0.342**	-4.168 ± 0.454**	0.381 ± 0.275	-7.326 ± 0.620 **
	l	7.008 ± 1.418**	26.348 ± 1.533**	19.574 ± 1.258 **	18.536 ± 2.810 **
Type of epitasis		Duplicate	Duplicate	Duplicate	Duplicate

The joint scaling test confirmed the result of individual scaling test with significant X^2 values, the 'm', 'd' and 'h' parameters of joint scaling test for all the crosses showed significance except 'd' for cross 2 and 'h' for cross 4.

The significant chi-square value and significant scales for cross 1, 2, 3 and 4 confirmed the result of Mather Scaling test, indicated the need for extending 3 parameter model to six parameter model for estimating epistatic components.

The estimates of best fit six parameter model indicated the significance of all the parameters i.e. 'm', 'd', 'h', ' i ' , 'j' and 'l' except cross 3, where in 'j' is non-significant indicating presence of additive, dominance and epistasis gene action and interaction in these crosses. The opposite signs of dominance 'h' and dominance x dominance effect 'l' recorded in crosses 1, 2, 3 and 4 indicate duplicate gene action.

4.7.2.2 Number of monopodia per plant

The scaling test result of monopodia per plant indicated that the scale C was significant in the cross 3, while scale A was non-significant in crosses 1, 2, 3 and 4, scale B was non-significant in crosses 1, 2, 3 and 4 and scale D was non-significant for cross 1, 2, 3 and 4 (Table 18.2).

In joint scaling test mean 'm' scale was non-significant in crosses 1, 2, 3 and 4, while 'd' and 'h' scale were also non-significant for all the crosses. The significant chi-square value and significant scale C for cross 3 confirmed the result of Mathers scaling test, indicating the need for extending three parameter model (additive-dominance) to six parameter model for estimating epistatic component.

Table 18.2. Scaling test, joint scaling test and estimates of m, d, h, i, j and l components by best fit model for number of monopodia per plant

Parameter		Cross 1	Cross 2	Cross 3	Cross 4
		NH 545 x NH 452	**NH 635 x PKV Rajat**	**PH 1060 x Suvin**	**LRA 5166 x Suvin**
Scaling test	A	0.272 ± 0.067	-0.062 ± 0.023	0.304 ± 0.087	0.038 ± 0.094
	B	0.272 ± 0.030	0.032 ± 0.071	0.816 ± 0.140	-0.472 ± 0.156
	C	1.288 ± 0.082	0.968 ± 0.046	1.956 ± 0.101 *	0.306 ± 0.191
	D	0.372 ± 0.023	0.508 ± 0.036	0.418 ± 0.079	0.370 ± 0.041
Joint Scaling test	m	1.482 ± 0.010	1.292 ± 0.007	1.412 ± 0.020	1.525 ± 0.044
	d	0.111 ± 0.009	-0.145 ± 0.006	0.183 ± 0.021	0.101 ± 0.027
	h	-0.260 ± 0.021	0.350 ± 0.015	0.349 ± 0.040	0.195 ± 0.086
	χ^2	**542.65 ****	**1207.74 ****	**429.96 ****	**82.49 ****
Best Fit Model	m	--	--	2.072 ± 0.160	--
	d	--	--	0.116 ± 0.024	--
	h	--	--	-0.508 ± 0.467	--
	i	--	--	-0.836 ± 0.158	--
	j	--	--	-0.256 ± 0.078	--
	l	--	--	-0.284 ± 0.315	--
Type of epitasis		--	--	Complementary	--

In six parameter model, for cross 3, additives component 'd' and dominant components 'h' were non-significant. In cross 3 additive x additive ('i'), additive x dominant ('j') and dominant x dominant ('l') type of interaction were non-significant. For this trait, 'h' and 'l' component had similar signs indicating complementary gene action for cross 3.

4.7.2.3 Number of sympodia per plant

The scaling test results showed that all tests were significant in most of the crosses, *viz.* 1, 3, and 4. The cross 2 was non-significant for scaling test A, B, C and D which indicated the three parameter model was not adequate to explain the genetic variation for this trait in this cross (Table 18.3).

The χ^2 value was significant for all the crosses confirmed the results of individual scaling tests. The 'm' parameter of joint scaling test for all the crosses showed significance, while 'd' significant for cross 3 and 'h' parameter was significant for cross 4. Due to significant of χ^2 values and significant scale in cross 1, 3 and 4 confirmed the results of Mather scaling test indicated the need of three parameters models was extended to Hayman (1958) six parameter model.

The estimates of best fit six parameter model indicated the significance of all the parameters mean (m) , additive (d), dominant (h), additive x additive (i), additive x dominance (j)' and dominance x dominance (l) except cross 1, where in 'd' and 'j' is non-significant, cross 2, where in 'd', 'i', 'j' and 'l' was non-significant and cross 3 and 4 in 'd' was non-significant.

Complimentary epistasis was recorded in cross 1 ('h' and 'l' with same signs) and duplicate epistasis was recorded in cross 3 and 4 (significant 'h' and 'l' components with opposite signs).

Table 18.3. Scaling test, joint scaling test and estimates of m, d, h, i, j and l components by best fit model for number of sympodia per plant

Parameter		Cross 1	Cross 2	Cross 3	Cross 4
		NH 545 x NH 452	**NH 635 x PKV Rajat**	**PH 1060 x Suvin**	**LRA 5166 x Suvin**
Scaling test	A	-7.004 ± 0.544 **	-0.836 ± 0.259	-8.930 ± 0.479 **	-13.554 ± 1.097 **
	B	-3.336 ± 0.534 **	0.160 ± 0.460	2.854 ± 0.6.21 *	4.512 ± 1.088 **
	C	-15.668 ± 0.826 **	-1.688 ± 0.728	10.584 ± 0.483 **	11.214 ± 1.412 **
	D	-2.664 ± 0.341 *	-0.506 ± 0.275	8.330 ± 0.3.93 **	5.128 ± 0.586 **
Joint Scaling test	m	22.687 ± 0.127 **	23.379 ± 0.101 **	28.081 ± 0.113 **	25.592 ± 0.218 **
	d	1.446 ± 0.121	-1.500 ± 0.095	-2.139 ± 0.138 *	-1.778 ± 0.214
	h	1.505 ± 0.271	0.736 ± 0.199	1.245 ± 0.150	3.394 ± 0.333 **
	χ^2	**400.45 ****	**18.349 ****	**1241.17 ****	**176.19 ****
Best Fit Model	m	18.170 ± 0.695 **	--	43.510 ± 0.801 **	35.275 ± 1.194 **
	d	1.834 ± 0.135	--	-1.208 ± 0.158	-1.229 ± 0.230
	h	5.818 ± 1.893 **	--	-37.294 ± 2.285 **	-20.253 ± 3.602 **
	i	5.328 ± 0.682 **	--	-16.660 ± 0.786 **	-10.256 ± 1.172 **
	j	-1.834 ± 0.301	--	-5.892 ± 0.389 **	-4.033 ± 0.618 **
	l	5.012 ± 1.358 **	--	22.736 ± 1.500 **	9.298 ± 2.693 **
Type of epitasis		Complimentary	--	Duplicate	Duplicate

4.7.2.4 Plant height

The scaling test result of plant height (Table 18.4) indicated that scale A was significant in crosses 1, 3 and 4 (except cross 2), scale B was significant in crosses 1, 2 and 4 (except cross 3), scale C was significant all four crosses, while scale D was significant in cross 1, 2 and 4 (except cross 3).

Joint scaling test 'm' scale was significant in all the crosses, 'd' scale was significant in all crosses, while 'h' scale was significant in crosses 1, 2 and 4 (except cross 3). The coefficient of joint scaling test and its χ^2 values were significant for all the crosses confirmed the results of Mather Scaling tests indicated the need for extending 3 parameter model to six parameter model for estimating epistatic component.

In six parameter model, mean (m) component of all crosses were significant, where as additive (d), dominant (h), additive x additive (i), additive x dominance (j)' and dominance x dominance (l) were significant for all crosses (except 'j' additive x dominance gene interaction was non-significant in cross 1).

Among significant 'h' and 'l' components estimated values had opposite signs indicated duplicate epistasis recorded in crosses 1, 2, 3 and 4.

4.7.2.5 Days to maturity

Table 18.5 revealed that results of scaling, joint scaling test and best fit model for estimation of components of variation.

The result of scaling test for days to maturity were observed significant for all crosses 1, 2, 3 and 4. The scale A, B, C and D scaling test were recorded significance indicating the presence of respective gene action.

Joint scaling test 'm' scale was significant in all the crosses, 'd' scale was significant in all crosses, while 'h' scale in 1 and 4 crosses were significant (except cross 2 and 3). The coefficient of joint scaling test

Table 18.4. Scaling test, joint scaling test and estimates of m, d, h, i, j and l components by best fit model for plant height

Parameter		Cross 1	Cross 2	Cross 3	Cross 4
		NH 545 x NH 452	**NH 635 x PKV Rajat**	**PH 1060 x Suvin**	**LRA 5166 x Suvin**
Scaling test	A	-11.336 ± 8.071 **	1.848 ± 0.486	-9.982 ± 0.707 **	-9.750 ± 1.454 **
	B	-13.316 ± 1.091 **	-15.076 ± 0.748 **	-1.036 ± 0.858	-11.858 ± 1.291 **
	C	-32.644 ± 1.706 **	11.340 ± 0.883 **	-14.214 ± 1.022 **	-29.472 ± 1.391 **
	D	-3.996 ± 0.487 **	12.284 ± 0.486 **	-1.598 ± 0.393	-15.790 ± 0.8.24 **
Joint Scaling test	m	143.851 ± 0.326 **	145.830 ± 0.179 **	172.608 ± 0.240 **	165.514 ± 0.309 **
	d	3.914 ± 0.262 **	7.554 ± 0.183 **	-7.589 ± 0.221 **	-12.959 ± 0.374 **
	h	-3.162 ± 0.674 **	9.993 ± 0.2847 **	0.391 ± 0.476	3.673 ± 0.562 **
	χ^2	**447.81 ****	**750.04 ****	**272.18 ****	**1561.67 ****
Best Fit Model	m	138.330 ± 1.055 **	169.878 ±1.000 **	171.909 ± 0.840 **	137.564 ± 1.732 **
	d	3.678 ± 0.403 **	5.958 ± 0.238 **	-5.727 ± 0.296 **	-11.865 ± 0.530 **
	h	-2.990 ± 3.034 **	-52.055 ± 2.620 **	-2.463 ± 2.499 *	70.450 ± 5.056 **
	i	7.992 ± 0.975 **	-24.568 ± 0.971 **	3.196 ± 0.786 **	31.580 ± 1.648 **
	j	0.990 ± 0.578	8.462 ± 0.429 **	-4.473 ± 0.479 **	-10.804 ± 0.940 **
	l	16.660 ± 2.381**	37.796± 1.679 **	7.822 ± 1.819 **	-33.688 ± 3.401 **
Type of epitasis		Duplicate	Duplicate	Duplicate	Duplicate

Table 18.5. Scaling test, joint scaling test and estimates of m, d, h, i, j and l components by best fit model for days to maturity

Parameter		Cross 1	Cross 2	Cross 3	Cross 4
		NH 545 x NH 452	**NH 635 x PKV Rajat**	**PH 1060 x Suvin**	**LRA 5166 x Suvin**
Scaling test	A	-13.312 ±1.051 **	2.164 ±0.546 *	-12.798 ± 0.320 **	-18.636 ± 1.121 **
	B	-14.336 ± 1.047 **	-7.090 ± 0.563 **	5.210 ± 0.817 **	2.412 ± 1.181 *
	C	22.992 ± 1.221**	4.142 ± 0.761 **	-18.788 ± 0.591 **	2.900 ± 1.634 **
	D	25.320 ± 0.860 **	4.534 ± 0.412 **	-5.600 ± 0.420 **	9.562 ± 0.524 **
Joint Scaling test	m	157.696 ± 0.222 **	157.668 ± 0.149 **	170.510± 0.141 **	165.682 ±0.362 **
	d	2.254 ± 0.239 *	9.543 ± 0.152 **	-11.128 ± 0.146 **	-22.213 ± 0.324 **
	h	5.248 ± 0.311 **	1.628 ±0.272	-0.478 ± 0.233	10.129 ± 0.723 **
	χ^2	**884.46 ****	**279.33 ****	**2099.10 ****	**573.08 ****
Best Fit Model	m	260.816 ± 1.739 **	166.695 ± 0.842 **	162.728 ± 0.860 **	183.894 ± 1.133 **
	d	2.176 ± 0.255 *	8.505 ± 0.173 **	-9.660 ± 0.185 **	-17.882 ± 0.430 **
	h	-123.440 ± 4.669 **	-31.521 ± 2.246 **	14.550 ± 2.467 **	-43.122 ± 3.391 **
	i	-50.640 ± 1.720 **	-9.068 ± 0.824 **	11.200± 0.840 **	-19.124 ± 1.048 **
	j	0.512 ± 0.730	4.627 ± 0.362 **	-9.004 ± 0.425 **	-10.524 ± 0.659 **
	l	78.288 ± 2.994 **	13.994 ± 1.481 **	-3.612 ± 8.642 **	35.348 ± 2.580 **
Type of epitasis		Duplicate	Duplicate	Duplicate	Duplicate

and its X^2 values were significant for cross 1, 2, 3 and 4 confirmed the results of Mather Scaling tests indicated the need for extending 3 parameters model to six parameter model for estimating epistatic component.

In six parameter model, mean of all crosses were significant, where as 'd' and 'h' components were also significant for all crosses. In crosses 1, 2, 3 and 4 additive x additive ('i'), dominant x dominant ('l') type of interaction recorded significant, while additive x dominant ('j') gene interaction was significant for crosses 2, 3 and 4 except cross 1.

Estimated values of 'h' and 'l' components had opposite signs, in crosses 1, 2, 3 and 4 indicate duplicate epistasis type of gene action.

4.7.2.6 Boll weight (g)

Table 18.6 revealed that results of scaling, joint scaling test and best fit model for estimation of components of variation. The scaling test result for boll weight indicated that scale A, B, C and D were non-significant in all crosses (except scale C for cross 3 recorded significant)

The joint scaling test 'm' scale was significant in 1, 2 and 3 crosses except cross 4, while additive 'd' and dominant 'h' scale were non-significant in all the crosses. The significant chi-square value and significant scale C for cross 3 confirmed the result of Mathers scaling test, indicating the need for extending three parameter model to six parameter model for estimating epistatic component.

The six parameter model used in cross 3, the 'm' component was non-significant, while 'd' component was significant. The epistatic interaction, additive x additive (i)' components was significant, while additive x dominance 'j' and dominance x dominance 'l' components were non-significant. The opposite signs were observed for component 'h' and 'l' indicating duplicate type of gene interaction.

Table 18.6. Scaling test, joint scaling test and estimates of m, d, h, i, j and l components by best fit model for Boll weight

Parameter		**Cross 1**	**Cross 2**	**Cross 3**	**Cross 4**
		NH 545 x NH 452	**NH 635 x PKV Rajat**	**PH 1060 x Suvin**	**LRA 5166 x Suvin**
Scaling test	A	0.118 ± 0.023	-0.172 ± 0.063	1.128 ± 0.168	0.186 ± 0.084
	B	-0.238 ± 0.020	0.224 ± 0.081	-1.688 ± 0.114	0.930 ± 0.139
	C	-1.60 ± 0.046	-1.088 ± 0.101	-2.964 ± 0.127 **	0.748 ± 0.192
	D	-0.470 ± 0.024	-0.570 ± 0.050	-1.202 ± 0.101	-0.184 ± 0.044
Joint Scaling test	m	3.060 ± 0.006 **	3.038 ± 0.018 **	3.383 ± 0.028 **	0.904 ± 0.029
	d	0.137 ± 0.005	0.113 ± 0.017	-0.360 ± 0.032	-0.062 ± 0.025
	h	0.011 ± 0.010	-0.020 ± 0.037	-0.824 ± 0.048	0.103 ± 0.055
	χ^2	**706.46 ****	**180.90 ****	**743.31 ****	**56.70 ****
Best Fit Model	m	--	--	1.416 ± 0.206	--
	d	--	--	-0.540 ± 0.034	--
	h	--	--	3.396 ± 0.589 **	--
	i	--	--	2.404 ± 0.203 **	--
	j	--	--	1.408 ± 0.099	--
	l	--	--	-1.844 ± 0.391	--
Type of epitasis		--	--	Duplicate	--

4.7.2.7 Number of bolls per plant

The scaling test A, B, C and D were significant in all the crosses, except A scale in cross 2, B scale in cross 3 and D scale in cross 1 which indicated the presence of epistasis interactions. Most of the coefficient of joint scaling test i.e. 'm', 'd' and 'h' were significant indicating significance of joint scaling test in all crosses. The result of both the individual scaling tests and joint scaling test provided evidence of epistasis interaction is governing the character (Table 18.7).

The crosses in which significance of scaling and joint scaling test requiring confirmation by using six parameter model to estimate component of genetic variance. The mean (m) value were significant for all crosses, while additive (d) component was significant for crosses 1, 3 and 4. The dominance (h) component was significant in crosses 1, 2, 3 and 4. In gene interactions additive x additive (i) was significant for the crosses 1, 2, 3 and 4, while additive x dominant (j) recorded significance for cross 1, 2 and 4. The dominant x dominant ('l') recorded significance in crosses 1, 3 and 4.

In cross 2 similar signs of 'h' and 'l' component were observed indicating complementary gene action. In cross 1, 3 and 4 signs of 'h' and 'l' were opposite which indicates duplicate inter-allelic interaction.

4.7.2.8 Ginning (%)

The scaling test A was significant for cross 1 and 3, B test was significant for cross 1 and 2. The C scale test showed significance in crosses 1, 2, 3 and 4, while D scale showed significance for 2, 3 and 4 (Table 18.8).

The joint scaling test 'm' scale was significant in all the crosses, 'd' scale was significant for cross 4, while 'h' scale was non-significant for all the crosses. The significant chi-square values and significant scales in crosses 1, 2, 3 and 4 confirmed the result of Mathers scaling test, indicating the need for extending three parameter model to six parameter model for estimating epistatic component.

Table 18.7. Scaling test, joint scaling test and estimates of m, d, h, i, j and l components by best fit model for number of boll per plant

Parameter		Cross 1	Cross 2	Cross 3	Cross 4
		NH 545 x NH 452	**NH 635 x PKV Rajat**	**PH 1060 x Suvin**	**LRA 5166 x Suvin**
Scaling test	A	2.332 ± 0.790 **	1.918 ± 0.946	-3.852 ± 0.632 **	10.682 ± 1.638 **
	B	-3.332 ± 0.782 **	8.464 ± 0.874 **	-7.00 ± 0.566	-10.452 ± 0.431 **
	C	-4.992 ± 0.718 **	19.990 ± 0.779 **	8.772 ± 1.520 **	9.746 ± 0.897 **
	D	-1.996 ± 0.578	4.804 ± 0.611 **	9.812 ± 0.776 **	4.758 ± 0.770 **
Joint Scaling test	m	28.827 ± 0.127 **	33.324 ± 0.182 **	38.990 ± 0.157 **	46.305 ± 0.177 **
	d	2.661 ± 0.134 **	4.652 ± 0.197 **	-7.068 ± 0.153 **	2.962 ± 0.223 **
	h	3.697 ± 0.241 **	3.600 ± 0.316 **	2.872 ± 0.295 *	-4.571 ± 0.212 **
	χ^2	**78.57 ****	**788.83 ****	**155.79 ****	**1074.74 ****
Best Fit Model	m	25.172 ± 1.164 **	39.467 ± 1.248 **	59.140 ± 1.561 **	52.849 ± 1.590 **
	d	2.500 ± 0.139 **	2.119 ± 0.250	-7.416 ± 0.171 **	-7.139 ± 0.399 **
	h	11.152 ± 3.307 **	-4.961 ± 3.631 **	-46.464 ± 3.511 **	-20.275 ± 4.694 **
	i	3.992 ± 1.156 **	-9.608 ± 1.223 **	-19.624 ± 1.552 **	-9.516 ± 1.540 **
	j	2.832 ± 0.537 **	-3.273 ± 0.626 **	1.574 ± 0.384	10.567 ± 0.845 **
	l	-2.992 ± 2.194 **	-0.774 ± 2.426	30.476 ± 2.050 **	9.286 ± 3.114 **
Type of epitasis		Duplicate	Complementary	Duplicate	Duplicate

Table 18.8 : Scaling test, joint scaling test and estimates of m, d, h, i, j and l components by best fit model for ginning percentage

Parameter		Cross 1	Cross 2	Cross 3	Cross 4
		NH 545 x NH 452	**NH 635 x PKV Rajat**	**PH 1060 x Suvin**	**LRA 5166 x Suvin**
Scaling test	A	-2.416 ± 0.275 *	1.370 ± 0.884	-2.424 ± 0.355 **	0.438 ± 0.628
	B	-4.472 ± 0.633 **	-5.864 ± 0.460 **	0.334 ± 0.350	-0.178 ± 0.830
	C	-3.616 ± 0.868 **	-11.458 ± 1.036 **	4.650 ± 0.621 **	-7.624 ± 0.949 **
	D	1.636 ± 0.492	-3.482 ± 0.577 **	3.370 ± 0.137 **	-3.942 ± 0.375 **
Joint Scaling test	m	37.430 ± 0.115 **	36.616 ± 0.160 **	35.335 ± 0.106 **	33.962 ± 0.219 **
	d	0.319 ± 0.112	0.058 ± 0.154	1.363 ± 0.078	2.601 ± 0.199 *
	h	1.482 ± 0.193	1.113 ± 0.311	0.289 ± 0.216	-0.571 ± 0.435
	χ^2	**115.03 ****	**223.81 ****	**714.11 ****	**198.19 ****
Best Fit Model	m	41.340 ± 0.993 **	30.611 ± 1.168 **	42.245 ± 0.297 **	27.150 ± 0.794 **
	d	0.536 ± 0.131	-0.825 ± 0.177	2.185 ± 0.115 **	1.614 ± 0.264
	h	-11.760 ± 2.424 **	12.059 ± 3.039 **	-16.105 ± 0.848 **	16.572 ± 2.366 **
	i	-3.272 ± 0.984 **	6.964 ± 1.155 **	-6.740 ± 0.274 **	7.884 ± 0.749 **
	j	1.024 ± 0.330	3.617 ± 0.456 **	-1.379 ± 0.156	0.308 ± 0.446
	l	10.160 ± 1.489 **	-2.470 ± 1.975 **	8.830 ± 0.751 **	-8.144 ± 1.722 **
Type of epitasis		Duplicate	Duplicate	Duplicate	Duplicate

The six parameter model, component 'm' was significant in all the crosses (crosses 1, 2, 3 and 4), while 'd' components was significant in cross 3 and 'h' components were significant in cross 1, 2, 3 and 4. The additive x additive ('i') and dominant x dominant ('l') type of interaction recorded significant in all crosses, while additive x dominant ('j') gene interaction was significant for cross 2. The crosses 1, 2, 3 and 4 recorded significant 'h' and 'l' components with opposite signs indicated duplicate epistasis.

4.7.2.9 Micronaire value (µg/inch)

The scaling test result of micronaire value indicated that scale A, B and D were non-significant for all the crosses. The C scale test showed significance in crosses 2 and 3 (Table 18.9).

The joint scaling test 'm' scale was significant in all the crosses, while 'd' and 'h' scale were non-significant for all crosses. The significant chi-square value and significant scale for crosses 2 and 3 confirmed the result of Mathers scaling test, indicating the need for extending three parameter model to six parameter model for estimating epistatic component.

In six parameter model, the mean 'm' component was significant in 2 and 3 crosses. While additive 'd' components and dominant 'h' component was non-significant in cross 2 and 3. For the cross 2 the value of 'h' and 'l' components were with similar signs indicating complementary gene action, whereas in cross 3 the signs of 'h' and 'l' components were opposite indicating duplicate gene action.

Table 18.9. Scaling test, joint scaling test and estimates of m, d, h, i, j and l components by best fit model for micronaire value

Parameter		Cross 1	Cross 2	Cross 3	Cross 4
		NH 545 x NH 452	**NH 635 x PKV Rajat**	**PH 1060 x Suvin**	**LRA 5166 x Suvin**
Scaling test	A	0.056 ± 0.099	-1.220 ± 0.122	-0.904 ± 0.109	-0.134 ± 0.134
	B	-0.162 ± 0.131	-0.184 ± 0.169	-0.140 ± 0.078	1.164 ± 0.073
	C	0.846 ± 0.090	-2.464 ± 0.210 *	-2.244 ± 0.0108 *	-1.330 ± 0.116
	D	0.476 ± 0.087	-0.530 ± 0.061	-0.600 ± 0.057	-1.180 ± 0.062
Joint Scaling test	m	3.726 ± 0.017 **	4.061 ± 0.028 **	3.037 ± 0.026 **	3.104 ± 0.027 **
	d	-0.010 ± 0.017	-0.125 ± 0.024	-0.619 ± 0.028	-0.803 ± 0.032
	h	0.239 ± 0.024	-0.395 ± 0.067	-0.097 ± 0.045	-0.203 ± 0.044
	χ^2	**94.26 ****	**622.42 ****	**573.80 ****	**736.52 ****
Best Fit Model	m	--	2.720 ± 0.145 *	2.350 ± 0.120 *	--
	d	--	0.272 ± 0.079	-0.258 ± 0.037	--
	h	--	1.588 ± 0.416	1.058 ± 0.344	--
	i	--	1.060 ± 0.122	1.200 ± 0.0114	--
	j	--	-0.518 ± 0.094	-0.382 ± 0.064	--
	l	--	0.344 ± 0.296	-0.156 ± 0.232	--
Type of epitasis		--	Complementary	Duplicate	--

4.7.2.10 Uniformity ratio

In scaling test result of scale A was significant in the cross 1 and 3 and B test was non-significant for all crosses. The C scale test showed significance in crosses 2, 3 and 4, while 'D' scale showed significance for cross 2 and 4 (Table 18.10).

The joint scaling test 'm' scale was significant in all the crosses and 'd' scale was non-significant for all the crosses, while 'h' scale was significant only for cross 3. The significant chi-square value and scaling test for all crosses confirmed the result of Mathers scaling test, indicating the need for extending three parameter model (additive-dominance) to six parameter model for estimating epistatic components.

In six parameter model, mean (m) of all crosses were significant. and (d) components was non significant for all crosses. Whereas, 'h' component was significant for all crosses. In all crosses, additive x additive (i) type of interaction recorded significant, while additive x dominant (j) type of interaction recorded significant for cross 3 and dominant x dominant (l) type of interaction recorded significant for cross 1, 2 and 4. The estimated values of 'h' and 'l' components had opposite signs indicated that crosses 1, 2, 3 and 4 showed duplicate epistasis.

4.7.2.11 Fibre length (mm)

The scaling test result of fibre length indicated that scale A was significant in the crosses 3 and 4 and B scale was significant only for cross 2. The C scale test showed significance in crosses 2 and 3, while D scale showed significance for cross 2 and 3 (Table 18.11).

The joint scaling test 'm' scale was significant in all the crosses 'd' scale was significant for crosses 2, 3 and 4, while 'h' scale was significant for cross 3 and 4. The significant chi-square values and significant scales confirmed the result of Mathers scaling test, indicating the

Table 18.10. Scaling test, joint scaling test and estimates of m, d, h, i, j and l components by best fit model for uniformity ratio

Parameter		Cross 1	Cross 2	Cross 3	Cross 4
		NH 545 x NH 452	**NH 635 x PKV Rajat**	**PH 1060 x Suvin**	**LRA 5166 x Suvin**
Scaling test	A	2.176 ± 0.147 *	-1.760 ± 0.632	-4.122 ± 0.217 **	0.904 ± 0.639
	B	-0.996 ± 0.465	0.354 ± 0.467	1.694 ± 0.243	1.512 ± 0.821
	C	-1.900 ± 0.550	-9.142 ± 0.741 **	-6.364 ± 0.269 **	-6.336 ± 0.838 **
	D	-1.540 ± 0.226	-3.868 ± 0.338 **	-1.968 ± 0.183	-4.626 ± 0.439 **
Joint Scaling test	m	44.949 ± 0.098 **	46.233 ± 0.125 **	45.033 ± 0.052 **	43.816 ± 0.140 **
	d	1.111 ± 0.101	-1.057 ± 0.120	-0.198 ± 0.056	-0.901 ± 0.140
	h	1.838 ± 0.112	0.424 ± 0.259	2.850 ± 0.074 *	1.615 ± 0.287
	χ^2	**255.55 ****	**291.11 ****	**812.38 ****	**164.62 ****
Best Fit Model	m	42.062 ± 0.495 **	39.009 ± 0.690 **	42.084 ± 0.371 **	35.032 ± 0.893 **
	d	-0.62 ± 0.202	-0.565 ± 0.134	0.658 ± 0.065	-1.356 ± 0.160
	h	8.870 ± 1.242 **	16.421 ± 1.968 **	7.632 ± 0.001 **	24.404 ± 2.645 **
	i	3.080 ± 0.452 **	7.736 ± 0.677 **	3.936 ± 0.366 **	9.252 ± 0.878 **
	j	1.586 ± 0.242	-1.057 ± 0.328	-2.908 ± 1.160 *	-0.304 ± 0.451
	l	-4.260 ± 0.766 **	-6.330 ± 1.406 **	-1.508 ± 0.644	-11.868 ± 1.882 **
Type of epitasis		Duplicate	Duplicate	Duplicate	Duplicate

Table 18.11. Scaling test, joint scaling test and estimates of m, d, h, i, j and l components by best fit model for fibre length

Parameter		Cross 1	Cross 2	Cross 3	Cross 4
		NH 545 x NH 452	**NH 635 x PKV Rajat**	**PH 1060 x Suvin**	**LRA 5166 x Suvin**
Scaling test	A	-0.936 ± 0.467	-0.172 ± 0.250	-4.964 ± 0.255 **	-3.816 ± 0.397 **
	B	1.060 ± 0.445	-4.628 ± 0.355 **	0.028 ± 0.502	1.380 ± 0.791
	C	0.312 ± 0.893	10.188 ± 1.548 **	2.316 ± 0.830 *	-1.024 ± 0.657
	D	0.094 ± 0.227	7.494 ± 0.772 **	3.626 ± 0.479 **	0.706 ± 0.336
Joint Scaling test	m	23.891 ± 0.083 **	23.394 ± 0.099 **	28.874 ± 0.077 **	28.113 ± 0.152 **
	d	-0.862 ± 0.071	2.766 ± 0.094 *	-4.625 ± 0.078 **	-6.472 ± 0.142 **
	h	0.530 ± 0.192	0.495 ± 0.163	3.517 ± 0.109 **	2.689 ± 0.288 **
	χ^2	**41.01**	**242.90 ****	**409.98 ****	**123.85 ****
Best Fit Model	m	--	39.148 ± 1.548 **	36.412 ± 0.962 **	29.758 ± 0.725 **
	d	--	1.908 ± 0.119	-4.040 ± 0.084 **	-4.194 ± 0.271 **
	h	--	-34.656 ± 3.190 **	-16.092 ± 2.266 **	-2.406 ± 2.158 *
	i	--	-14.988 ± 1.543 **	-7.252 ± 0.959 **	-1.412 ± 0.672
	j	--	2.228 ± 0.199 *	-2.496 ± 0.277 *	-2.598 ± 0.426 *
	l	--	19.788 ± 1.674 **	12.188 ± 1.342 **	3.848 ± 1.469 **
Type of epitasis		--	Duplicate	Duplicate	Duplicate

need for extending three parameter model (additive-dominance) to six parameter model for estimating epistatic component.

In six parameter model mean 'm' of all crosses were significant. Whereas 'd' component was significant for crosses 3 and 4, while 'h' component was significant for crosses 2, 3 and 4. In crosses 2 and 3 additive x additive (i) recorded significant while, additive x dominant (j) and dominant x dominant (l) type of interaction recorded significant for cross 2, 3 and 4.

Among the significant 'h' and 'l' components estimated values had opposite signs indicated duplicate epistatic type gene interaction for crosses 2, 3 and 4.

4.7.2.12 Fibre strength (g/tex)

In scaling test A scale was found to be significant for cross 2, while test B scale recorded significant for cross 3. The scale C was significant in cross 1, while D scale was significant in cross 3 (Table 18.12).

The joint scaling test 'm' scale was significant in all the crosses. While 'd' and 'h' scale was non-significant for all the crosses. The significant chi-square values and significant scales confirmed the result of Mathers scaling test, indicating the need for extending three parameters model to six parameter model for estimating epistatic component.

The six parameter model was used in crosses 1, 2 and 3. In these crosses 'm' component was significant in all crosses. While'd' component was non-significant in all crosses and 'h' component was significant in crosses 1, 2 and 3. In cross 1 and 3 additive x additive (i), while additive x dominant (j) gene interaction was non-significant for cross 1, 2 and 3. The dominant x dominant (l) type of interaction recorded significant for cross 2 and 3.

Table 18.12. Scaling test, joint scaling test and estimates of m, d, h, i, j and l components by best fit model for fibre strength

Parameter		Cross 1	Cross 2	Cross 3	Cross 4
		NH 545 x NH 452	**NH 635 x PKV Rajat**	**PH 1060 x Suvin**	**LRA 5166 x Suvin**
Scaling test	A	-2.072 ± 0.272	2.196 ± 0.601 *	-1.216 ± 0.216	-1.378 ± 0.898
	B	0.636 ± 0.220	-1.854 ± 0.266	-4.776 ± 0.365 **	1.320 ± 0.915
	C	-4.900 ± 0.363 **	-1.702 ± 0.538	-1.028 ± 0.362	-1.842 ± 0.798
	D	-1.732 ± 0.199	-1.022 ± 0.359	2.482 ± 0.207 *	-0.892 ± 0.579
Joint Scaling test	m	21.449 ± 0.070 **	24.701 ± 0.094 **	25.755 ± 0.067 **	24.288 ± 0.198 **
	d	-0.979 ± 0.072	0.589 ± 0.094	-0.550 ± 0.066	-1.830 ± 0.253
	h	1.284 ± 0.111	-1.778 ± 0.165	1.521 ± 0.133	2.116 ± 0.350
	χ^2	**245.77 ****	**72.32 ****	**194.17 ****	**11.76 ****
Best Fit Model	m	18.522 ± 0.407 **	22.713 ± 0.725 **	30.930 ± 0.400 **	--
	d	-0.514 ± 0.085	-0.805 ± 0.104	-0.646 ± 0.095	--
	h	6.570 ± 1.045 **	3.101 ± 1.980 **	-14.018 ± 1.172 **	--
	i	3.464 ± 0.398 **	2.044 ± 0.717	-4.964 ± 0.413 **	--
	j	-1.354 ± 0.163	2.025 ± 0.313	1.780 ± 0.192	--
	l	-2.028 ± 0.664	-2.386 ± 1.298 *	10.956 ± 0.796 **	--
Type of epitasis		Duplicate	Duplicate	Duplicate	--

Among dominant 'h' and dominant x dominant 'l' components estimated values had opposite signs recorded for cross 1, 2 and 3 indicated that presence of duplicate epistasis.

4.7.2.13 Seed cotton yield per plant (g)

The scaling test A, B, C and D were significant in all the crosses, except A scale in cross 3, B scale in cross 4 and D scale in cross 3 which indicated the presence of epistatic interactions (Table 18.13).

The joint scaling test i.e. 'm', 'd' and 'h' were significant in all crosses except component 'd' in cross 2 and 3. Significant chi-square values and significant scales for all the crosses confirmed the result of Mathers scaling test, indicating the need for extending three parameters model (additive-dominance) to six parameter model for estimating epistatic component. The results of both, the individual scaling tests and joint scaling test provided evidence of epistatic interaction in governing this character.

The crosses in which significance of scaling tests and joint scaling test confirmed to use six parameter model to estimate component of genetic variance. The mean 'm' gene effects were significant for all crosses, similarly additive component 'd' was significant for crosses 1, 2, 3 and 4. The dominant component 'h' was significant in all crosses.

In gene interactions additive x additive (i) was significant for crosses 1, 2, 3 and 4, while additive x dominance (j) was significant for the cross 4. The dominant x dominant (l) recorded significance in crosses 1, 2, 3 and 4.

In all crosses dominant (h) and dominant x dominant (l) were recorded opposite signs, hence, crosses 1, 2, 3 and 4 were exhibited duplicate epistatic interaction.

Table 18.13. Scaling test, joint scaling test and estimates of m, d, h, i, j and l components by best fit model for seed cotton yield per plant (g)

Parameter		Cross 1	Cross 2	Cross 3	Cross 4
		NH 545 x NH 452	**NH 635 x PKV Rajat**	**PH 1060 x Suvin**	**LRA 5166 x Suvin**
Scaling test	A	-6.144 ± 1.062 **	19.804 ± 0.825 **	1.922 ± 0.627	-18.990 ± 0.888 **
	B	-3.976 ± 1.446 **	22.668 ± 0.459 **	3.496 ± 0.529 **	0.424 ± 1.085
	C	21.152 ± 1.192 **	36.348 ± 0.642 **	-14.222 ± 0.931 **	47.482 ± 0.935 **
	D	15.636 ± 0.902 **	-3.062 ± 0.440 **	-0.820 ± 0.267	33.024 ± 0.590 **
Joint Scaling test	m	88.711 ± 0.266 **	85.035 ± 0.124 **	86.813 ± 0.178 **	87.435 ± 0.232 **
	d	6.120 ± 0.299 **	-1.884 ± 0.124	2.016 ± 0.147	-8.393 ± 0.273 **
	h	9.920 ± 0.428 **	18.934 ± 0.260 **	-4.883 ± 0.308 **	14.172 ± 0.455 **
	χ^2	**532.95 ****	**3564.00 ****	**1645.67 ****	**6209.09 ****
Best Fit Model	m	117.756 ± 1.836 **	73.276 ± 0.895 **	67.971 ± 0.568 **	143.109 ± 1.222 **
	d	6.184 ± 0.343 **	3.332 ± 0.165 **	3.671 ± 0.197 **	-3.539 ± 0.313 **
	h	-62.208 ± 5.209 **	69.720 ± 2.604 **	43.187 ± 1.665 **	-137.391 ± 3.652 **
	i	-31.272 ± 1.803 **	6.124 ± 0.879 **	19.640 ± 0.533 **	-66.048 ± 1.181 **
	j	-1.084 ± 0.876	-1.432 ± 0.444	0.787 ± 0.308	-9.707 ± 0.661 **
	l	41.392 ± 3.437 **	-48.596 ± 1.768 **	-25.058 ± 1.329 **	84.614 ± 2.507 **
Type of epitasis		Duplicate	Duplicate	Duplicate	Duplicate

Discussion

CHAPTER-V

DISCUSSION

Plant breeders aim is to find superior genotypes from the available gene pool or from genetically heterogeneous population. However, selection is a difficult task as phenotypic expression is altering mind not only by a genotype but also by the environment. Critical assessment of the material with which the breeder is working becomes necessary. Studies based on bio-metrical background provide a precise genetic phenomenon to a plant breeder for genetic interpretation of material under investigation.

In the manifestation of hybrid vigour, the combining ability plays vital role. An evaluation of the inbred lines for the genetic potential in this regard is necessarily for indentifying suitable parents for hybrid combinations. Further information on the combining ability and its effects enables the breeder to classify the selected parents.

Cotton is a major crop in which heterosis is being exploited for higher seed cotton yield and its component characters including fibre properties. For improvement of seed cotton yield and its component characters,. it is necessary to have selection of good parents and subsequent adoption of proper breeding methods are the prime steps in any crop improvement programme. Estimation of combining ability effects helps us to discriminate poor general combiners so that appropriate parental lines can be used to produce superior hybrids. One of the techniques which is widely used to generate the information about the gene action governing expression of various yield and quality attributes is the line x tester design. This method permits estimation of additive and non-additive components of heritable variance besides other genetic properties of parental lines.

Expression of the characters is often influenced by non-allelic interactions in association with additive or dominant gene effects. Generation mean analysis is a powerful statistical procedure used for detection of epistasis by raising several generations of a single cross simultaneously. Further, as the generation mean analysis is based on first order statistics (means), the error is inherently smaller in the estimates. If the joint Scaling test is employed, the precession of estimates increases and fitness of model is known so that, the order of interaction whether diagonal or higher order can be established.

In view of importance explained above, the present investigation was carried out and results of the present study are discussed below under the following headings.

5.1 Genetic variability

5.2 Combining ability studies

5.3 Heterosis

5.4 Correlations

5.5 Path analysis

5.6 Generation mean analysis

5.1 GENETIC VARIABILITY

The success of any breeding programme depends on the spectrum of genetic variability present in the population. A wider spectrum of variability will enhance the chances of selecting desired genotypes. In the presence of high amount of genetic advance helps breeder to exercise selection on desired characters to achieve the objective quickly. Therefore, for improvement of target trait of any crop, it is necessary to have full information on the variability, heritability and genetic advance (Burton, 1952 and Swarup and Chaugale, 1962).

In present investigation genotypic and phenotypic coefficients of variability were low for days to 50% flowering. These results are an agreement with the finding of Bavaji *et al.* (1989), Siddiqui (1996), Sumathi and Nadarajan (1996), Murthy (1997), Sangeetha (1998), Narisireddy and Ratnakumari (2004a), Kale *et al.* (2006), Preetha and Raveendran (2007), Sundas *et al.* (2010), Kancherla (2011), Kulkarni *et al.* (2011) and Mendez-Natera *et al.* (2012).

High heritability coupled with low genetic advance was observed for days to 50 % flowering revealing the preponderance of non-additive gene action governing the inheritance of this trait. Similar finding were reported by Patil and Chopde (1983), Jagtap and Kolhe (1987), Jagtap and Mehetre (1998), Sangeetha (1998), Preetha and Raveendran (2007) and Kancherla (2011).

Low heritability coupled with low genetic advance was observed in case of number of monopodia per plant, the results are in agreement with finding of Ahmed *et al.* (2006) and Kancherla (2011), however the estimates of PCV and GCV was low. Similar findings were reported by Singh *et al.* (1978a), Gite *et al.* (2007), Kancherla (2011)and Kulkarni *et al.* (2011).

The estimates of PCV and GCV were moderate for number of sympodia per plant. Similar results were reported by Naidu and Katarki (1968), Khorgade and Ekbote (1981), Murthy (1997), Sangeetha (1998), Rao and Reddy (2001), Kale *et al.* (2006), Gite *et al.* (2007), Singh *et al.* (2009), Soomro *et al.* (2010), Kancherla (2011) and Kulkarni *et al.* (2011).

High heritability and low genetic advance observed for number of sympodia per plant revealed the predominant role of non-additive gene action in the inheritance of this trait. Similar finding were reported by Singh *et al.* (1978a), Doss and Kadambavanasundaram (1993), Ahmed *et al.* (2006), Kale *et al.* (2006) and Kancherla (2011).

The estimates of PCV and GCV were low for plant height in present investigation. Similar results were reported by Kale *et al.* (2006), Singh *et al.* (2009), Khan *et al.* (2009), Soomro *et al.* (2010), Sabir *et al.* (2010) and Kulkarni *et al.* (2011). High heritability coupled with low genetic advance was observed in plant height, it revealing the preponderance of non-additive gene action. Similar finding were reported by Kausik and Kapoor (2006) and Bindupriya (2008).

The PCV and GCV were low for days to maturity in present study. Similar results were reported by Pandey *et al.* (2002), Kale *et al.* (2006) and Sundas *et al.* (2010). High heritability coupled with low genetic advance is recorded for days to maturity. Similar finding were reported by Bindupriya (2008) and Kulkarni *et al.* (2011).

The estimate of PCV and GCV were low for boll weight. Similar results were reported by Dhanda *et al.* (1987), Boder *et al.* (1988), Krishnarao and Mary (1990), Rajarathinum *et al.* (1993), Singh *et al.* (1994), Sumathi and Nadarajan (1996), Jagtap and Mehetre (1998), Rao and Reddy (2001), Ahmad *et al.* (2003), Narisireddy and Ratnakumari (2004a), Kale *et al.* (2006), Preetha and Raveendran (2007), Khan *et al.* (2009), Singh *et al.* (2009), Patnaik and Sial (2009) and Lal and Singh (2012).

An estimate of high heritability and high genetic advance was recorded for boll weight indicating the role of additive gene action governing the inheritance of this trait. Singh *et al.* (1987a), Krishnarao and Mary (1990), Tiwari *et al.* (1992), Rajarathinam *et al.* (1993), Chhabra *et al.* (1995), Rokadia *et al.* (1996), Sumathi and Nadarajan (1996), Jagtap and Mehetre (1998), Sangeetha (1998), Valarmathi and Jehangir (1998a), Rao and Reddy (2001), Narisireddy and Ratnakumari (2004a) and Kancherla (2011) reported high heritability coupled with high genetic advance for this trait.

Moderate estimates of PCV and GCV were observed for number of bolls per plant. These findings are in agreement with the finding of Singh *et al.* (1978a), Dhanda *et al.* (1987), Singh *et al.* (1987a), Krishnarao and Mary (1990), Singh *et al.* (1994), Murty *et al.* (1995), Rokadia *et al.* (1996), Sumathi and Nadarajan (1996), Murthy (1997), Jagtap and Mehetre (1998), Murty *et al.* (1999), Rao and Reddy (2001), Ahmad *et al.* (2003), Baloch (2004), Kausik and Kapoor (2006), Murty and Chamundeswari (2006), Preetha and Raveendran (2007), Singh *et al.* (2009), Sabir *et al.* (2010) and Kancherla (2011).

The high heritability coupled with high genetic advance observed in number of bolls per plant in present study indicating the influence of additive gene action. Krishnarao and Mary (1990), Tiwari *et al.* (1992), Rajarathinam *et al.* (1993), Singh *et al.* (1994), Chhabra *et al.* (1995) , Sumathi and Nadarajan (1996), Murthy (1997), Jagtap and Mehetre (1998), Valarmathi and Jehangir (1998a), Rao and Reddy (2001), Ahmed *et al.* (2006), Preetha and Raveendran (2007), Kumari *et al.* (2010) and Kancherla (2011) reported high heritability coupled with high genetic advance for this trait.

Low estimates of PCV and GCV were observed for ginning percentage in present study. These results are in agreement with the findings of Dhonda *et al.* (1987), Singh *et al.* (1987a), Bavaji *et al.* (1989), Krishnarao and Mary (1990), Sumathi and Nadarajan (1996), Murthy (1997), Jagtap and Mehetre (1998), Rao and Reddy (2001), Pandey *et al.* (2002), Ahmad *et al.* (2003), Kale *et al.* (2006), Preetha and Raveendran (2007) and Kancherla (2011).

The high heritability and low genetic advance was observed for ginning percentage indicated that this trait controlled by non-additive gene action. These results are in agreement with the finding of Doss and Kadambavanasundaram (1993), Singh *et al.* (1994), Chhabra *et al.* (1995), Sumathi and Nadarajan (1996), Jagtap and Mehetre (1998), Shankarapandian *et al.* (1998), Rao and Reddy (2001) and Kancherla (2011).

Moderate estimate of PCV and GCV were recorded in the present study for micronaire value. Similar results were reported by Krishnarao and Mary (1990), Nadarajan and Sreerangaswamy (1990), Rajarathinam *et al.* (1993), Sangeetha (1998), Kumar *et al.* (2000) and Kancherla (2011).

High heritability coupled with high genetic advance was observed for micronaire value indicating the presence of additive gene action. Similar findings were reported by Krishnarao and Mary (1990), Nadarajan and Sreerangaswamy (1990), Avtar *et al.* (1993), Rajarathinam *et al.* (1993), Rao and Reddy (2001) and Kancherla (2011).

The estimate of PCV and GCV were moderate for fibre length. Similar results were reported by Baloch (2004), Kale *et al.* (2006), Ali *et al.* (2009) and Sabir *et al.* (2010). In present study, additive gene action due to high heritability coupled with high genetic advance was observed for this trait. Similar result was reported by Baloch *et al.* (2004).

Low estimates of PCV and GCV were observed for uniformity ratio. Similar findings were by Preetha and Raveendran (2007) and Kancherla (2011). In present study reported moderate heritability coupled with low genetic advance was noticed for this trait. These findings are in agreement with Baloch (2004), Preetha and Raveendran (2007) and Kancherla (2011).

The estimate of PCV and GCV were low for fibre strength. Similar results were reported by Rajarathinam *et al.* (1993), Sangeetha (1998), Kumar *et al.* (2000), Rao and Reddy (2001), Preetha and Raveendran (2007), Akhtar *et al.* (2008), Ali *et al.* (2009), Kulkarni *et al.* (2011) and Kancherla (2011). High heritability and moderate genetic advance was recorded for this trait. Similar results for this trait were reported by Avtar *et al.* (1993), Valarmathi and Jehangir (1998a) and Kancherla (2011).

The estimate of PCV and GCV were moderate for seed cotton yield per plant. These findings are agreement with the result reported by Rajarathinam *et al.* (1993), Singh *et al.* (1994), Murty *et al.* (1995), Sumathi and Nadarajan (1996), Murthy (1997), Jagtap and Mehetre (1998), Ahuja and Tuteja (2000), Rao and Reddy (2001), Ahmad *et al.* (2003), Baloch (2004), Kumari and Chamundeshwari (2005), Murthy and Chamundeshwari (2005), Kausik and Kapoor (2006), Preetha and Raveendran (2007), Khan *et al.* (2009), Singh *et al.* (2009), Patnaik and Sial (2009), Patnaik and Sial (2010), Kancherla (2011) and Lal and Singh (2012).

The high heritability coupled with high genetic advance was observed for seed cotton yield per plant indicating the preponderance of additive gene action. These finding are in agreement with the results reported by Singh *et al.* (1994), Murthy *et al.* (1995), Sumathi and Nadarajan (1996), Jagtap and Mehetre (1998), Sankarapandian *et al.* (1998), Ahuja and Tuteja (2000), Rao and Reddy (2001), Baloch (2004), Kumari and Chamunreshwari (2005), Ahmed *et al.* (2006), Kale *et al.* (2006), Preetha and Raveendran (2007) and Kumari *et al.* (2010) and Kancherla (2011).

The estimate of PCV and GCV were moderate for seed cotton yield per plot, while high heritability and high genetic advance was recorded for this trait.

The moderate estimate of PCV and GCV for seed cotton yield quintal per ha was recorded. Similar results were reported by Patnaik and Sial (2009), Khan *et al.* (2009) and Patnaik and Sial (2010). High heritability and high genetic advance for this trait was reported in present study. Similar findings were reported by Patnaik and Sial (2009) and Patnaik and Sial (2010).

5.2 Combining ability studies

The performance of parents in hybrid combinations can be tested by combining ability analysis which also characterizes the nature and magnitude of gene action involved in the expression of quantitative traits. The main objective of this study is to identify parents with better potential to transmit desirable characters to the progeny and to identify the better specific crosses for fibre quality, yield and yield components. The analysis of quantitative inheritance was also an equally important objective to gain knowledge regarding the nature and magnitude of gene action for appropriate and efficient breeding procedure.

Information regarding nature of gene action will be highly helpful in the development of efficient breeding programme. General combining ability is attributed to additive and additive x additive gene action, which is fixable in nature. On the other hand specific combining ability is attributed to non-additive gene action which may be due to dominance or epistasis and is non-fixable in nature. The presence of non-additive genetic variance is the primary justification for initiating the hybrid breeding programme (Cockerhan, 1961). Combining ability analysis therefore was done to generate information on GCA effects of parents and SCA effects of crosses which would help in selection of better parents and cross combinations for their further use in hybrid breeding programme. This will also provide the information regarding the type and magnitude of gene action, which will help in choice of the breeding method to be applied for the improvement of the desired traits.

5.2.1 Analysis of variance and mean

The analysis of variance for combining ability revealed significant mean squares due to parents and crosses for all the characters (except for number of monopodia per plant) indicating the presence of sufficient variability in the experimental material. The mean performance of parents differed from that of crosses as evident from the significance of parents vs. crosses source variation for all characters (except for number of monopodia per plant, boll weight, micronaire value, seed cotton yield per plot and seed cotton yield quintal per ha) which indicated the role of non-additive genetic variation. Further, the mean sum of squares attributed to the male and female parents of hybrids provide a measure of general combining ability and the interaction between the male and female parents provide a measure of specific combining ability (Rojas, 1951).

Significant differences for most of the characters were observed within parents and crosses. In lines, significant differences were observed for number of monopodia per plant, plant height, number of bolls per plant, micronaire value, seed cotton yield per plant, seed cotton yield per plot and seed cotton yield quintal per ha. While in testers, significant differences were recorded for days to 50% flowering, days to maturity, boll weight, ginning percentage, fibre length, uniformity ratio, fibre strength, seed cotton yield per plant, seed cotton yield per plot and seed cotton yield quintal per ha. (except for number of monopodia per plant, number of sympodia per plant, plant height, number of bolls per plant and micronaire value). In line x tester significant differences were noted for all the characters (except for number of monopodia per plant and ginning percentage). However, in crosses significant differences were also observed for parents and crosses for all the traits studied, except for number of monopodia per plant, boll weight, micronaire value, seed cotton yield per plot and seed cotton yield quintal per ha (Table 10).

Above results suggests the presence of enough variability in the experimental material. In general, hybrids were early in maturity and high yielding compared to the parents, which is desirable and may be exploited for development of high yielding hybrids. The crosses involving parental lines NH 545 and PH 1060 were having early maturity, while crosses with the tester Suvin were late in maturity. Further, the crosses with PH 1076 and NH 615 recorded higher number of bolls per plant. The lines LRA 5166, PH 1076 and PH 1060 recorded better performance for fiber length and fiber strength, whereas the crosses involving the lines PH 1076 and NH 615 recorded maximum seed cotton yield per plant.

5.2.2 Analysis of variance and variance components

The nature of gene action in controlling the expression of characters can be confirmed by the comparison of magnitude of GCA and SCA variance components. The general as well as specific combining ability variances were found to be important for all the traits studied indicating the role of both fixable and non-fixable variances in the expression of all these traits (Table 9). There was a wide variation for yield and fibre quality characteristics studied among parents and F_1 combinations. This suggests that the relative magnitude of GCA and SCA variance indicated the preponderance of non-additive gene action for controlling the traits.

The estimates of SCA variances were greater than GCA variance for days to 50% flowering indicating the preponderance of non-additive gene action governing this trait. Similar results were also reported by Jagtap and Kolhe (1987), Jagtap (1994), Narisireddy and Satyanarayana (2004), Muthu *et al.* (2005), Subramanian *et al.* (2005), Ahuja and Dhayal (2007), Preetha and Raveendran (2008) and Kancherla (2011).

The variance due to SCA was higher than GCA for number of monopodia per plant indicating the importance of non-additive gene action in controlling this trait. These results are in accordance with Bhandari (1980), Rao (1982), Laxman and Ganesh (2003), Narisireddy and Satyanarayana (2004), Ahuja and Dhayal (2007) and Kancherla (2011).

Estimates of variance due to SCA were higher than GCA for number of sympodia per plant showing the importance of non-additive gene action.

Similar findings were reported by Surana *et al.* (1996), Murthy and Ranganathacharyulu (1998), Valarmathia and Jehangir (1998b), Punitha *et al.* (1999b), Laxman and Ganesh (2003), Iqbal *et al.* (2003a), Narisireddy and Satyanarayana (2004), Ahuja and Dhayal (2007), Preethe and Ravindran (2008) and Ravikumar *et al.* (2010) and Kancherla (2011).

Non-additive gene action plays important role in controlling the plant height and such traits controlled by dominant gene. Similar results were also reported by Nirania *et al.* (1992), Koodalingam and Ramligamm (1992), Krishnarao (1998), Gul-Hassan *et al.* (1999) and Zia-Ul-Islam *et al.* (2001). For days to maturity, non-additive gene action played significant role in present study. Similar result were reported by Ahuja and Dhayal (2007).

The variance due to SCA was higher than GCA for boll weight indicating the importance of non-additive gene action in controlling this trait. These result are in accordance with Rao (1982), Duhoon *et al.* (1984), Jagtap and Kolhe (1987), Patil *et al.* (1990), Shanti and Selvaraj (1995), Tuteja *et al.* (1996), Murthy and Ranganathacharyulu (1998), Punitha *et al.* (1999b), Subhan *et al.* (2003), Muthu *et al.* (2005), Subramanian *et al.* (2005), Ahuja and Dhayal (2007), Ilyas *et al.* (2007), Ravikumar *et al.* (2010) and Kancherla (2011).

Non-additive gene action was responsible for controlling the number of bolls per plant. Similar result were also reported by Patil *et al.* (1990), Verma *et al.* (1991), Jagtap (1994), Shanthi and Selvaraj (1995), Rathore *et al.* (1996), Hassans *et al.* (1999), Soomro *et al.* (2000), Iqbal *et al.* (2003a), Saravanan *et al.* (2003), Rauf *et al.* (2006), Ahuja and Dhayal (2007) , Ravikumar *et al.* (2010) and Kancherla (2011).

The component of variance due to SCA was higher than GCA for ginning percentage suggesting the role of non-additive gene action for this trait. These results are in accordance with Rao (1982), Jagtap and Kolhe (1987), Singh *et al.* (1988), Kalsy *et al.* (1994), Tuteja *et al.* (1996), Valarmathi and Jehangir (1998b), Subramanian *et al.* (2005), Preetha and Raveendran (2008), Ravikumar *et al.* (2010) and Kancherla (2011).

The predominant role of non-additive gene action was noted in the inheritance of micronaire value. Similar results were also observed by Rajan *et al.* (1999), Cheatham *et al.* (2003), Pushpam and Raveendran (2005), Ahuja and Dhayal (2007), Ilyas *et al.* (2007), Basal *et al.* (2009), Saravanam *et al.* (2010), Ravikumar *et al.* (2010) and Kancherla (2011).

In present investigation non-additive type of gene action were observed for fibre length. These results are supported by Mane and Bhatade (1992), Patel *et al.* (1997) and Gul-Hasan *et al.* (1999).

The components of variance due to SCA were higher than GCA for uniformity ratio suggesting the role of non-additive gene action for this trait. Similar results were also reported by Rajan *et al.* (1999), Pushpam and Raveendran (2005), Ahuja and Dhayal (2007), Preetha and Raveendran (2008), Basal *et al.* (2009), Emine and Oktay (2010) and Kancherla (2011).

For fibre strength, preponderance of non-additive gene action were found. These results are accordance with Valarmathi and Jehangir (1998b), Rajan *et al.* (1999), Pushpam and Raveendran (2005); Ahuja and Dhayal (2007), Ilyas *et al.* (2007), Emine and Oktay (2010), Ravikumar *et al.* (2010), Saravaran *et al.* (2010) and Kancherla (2011).

In the presnt study predominant role of non-additive gene action was observed for seed cotton yield per plant. These result are supported by Bhatade *et al.* (1992), Shanti and Selvaraj (1993), Jagtap (1994), Tuteja *et al.* (1996), Mandloi *et al.* (1998), Punitha *et al.* (1999b), Soomro *et al.* (2000), Islam *et al.* (2001), Subhan *et al.* (2003), Iqbal *et al.* (2003a), Muthu *et al.* (2005), Ahuja and Dhayal (2007), Saravaran *et al.* (2010), Ravikumar *et al.* (2010) and Kancherla (2011).

Non-additive gene action played a significant role in controlling seed cotton yield per plot. Estimates of variance due to SCA were higher than GCA for seed cotton yield quintal per ha.

The presence of non-additive gene action suggests the possibility of improvement through hybridization.

5.2.3 Estimation of general and specific combining ability effects

General combining ability (GCA) is the ability of a parent to produce superior progeny with other lines which helps the plant breeder in the selection of desirable parents that can be utilized in hybridization program. Whereas specific combining ability (SCA) effects are the deviations in the performance of two parents in a particular hybrid combination. Hence, parents with highest GCA effects would be more desirable for certain traits associated with yield, whereas, for earliness low GCA parents were desirable. Specific combining ability effects are useful to identify the best hybrid combination in array of crosses.

5.2.3.1 General combining ability effects

The GCA effects recorded for eleven parents (7 lines and 4 testers) for fifteen characters indicated that the line NH 545 with negatively significant GCA effects was good combiner, where as NH 615 and NH 630 which exhibited significant positive effects are considered as poor general combiners for earliness character.

Favorable genes for number of monopodia per plant, predominantly contributed by the line NH 615 and PH 1076. Line NH 630 recorded negative significant and found to be poor combiner.

The lines PH 1076 and NH 545 exhibited to be good general combiner for number of sympodia per plant and having positive significant GCA effect. Lines PH 1076, PH 1060 and LRA 5166 exhibited positive significant GCA effects and good general combiner for plant height. While, lines NH 615, NH 630 and NH 635 exhibited poor combining ability by recording significant negative GCA effects for plant height.

The lines NH 615, PH 1060 and PH 1076 recorded significant negative GCA effects are considered as good general combiner for earliness. For boll weight character, the lines PH 1060 and LRA 5166 recorded significant positive GCA effects showing them good combiner.

For number of bolls per plant, the lines PH 1076 and NH 615 exhibited highest *per se* performance and also found good general combiner in positive direction.

As regards the fibre quality, the parent PH 1060 was observed to be good combiner and negative GCA effect for micronaire value. The lines NH 545, NH 630 and NH 635 recorded positive GCA effects and undesirable for micronaire values. For fibre length, lines PH 1060 and LRA 5166 exhibited positive significant values and good combines for fiber quality.

For uniformity ratio, the line NH 545 showed positive GCA effects and to be good combiner for this trait .The line LRA 5166 exhibited significant positive and good general combining ability for fibre strength.

The lines, PH 1076 and NH 615 exhibited highest *per se* performance and observed to be good general combiner by exhibiting highest positive GCA effect for seed cotton yield per plant, seed cotton yield per plot.

Among the testers, NH 452 (*G. hirsutum*) was the best general combiner for number of sympodia per plant, days to maturity, days to 50% flowering, boll weight, ginning percentage, uniformity ratio, seed cotton yield per plant and seed cotton yield per plot and found poor combiner for fibre strength.

The tester, NH 625 (*G. hirsutum*) possesses favorable genes for days to 50% flowering, days to maturity, boll weight, ginning percentage, uniformity ratio and seed cotton yield per plant and unfavorable genes for number of sympodia per plant, micronaire value and fibre strength.

The tester, PKV Rajat (*G.hirsutum*) was best general combiner for days to maturity, boll weight, number of bolls per plant, fibre strength, seed cotton yield per plant and seed cotton yield per plot, but was found to be poor combiner for micronaire value and fibre length.

The tester, Suvin (*G. barbadense*) possessed favorable gene for fibre quality traits, micronaire value, fibre length and fibre strength, whereas it exhibited unfavorable genes for days to 50% flowering, days to maturity, boll weight, ginning percentage, uniformity ratio, seed cotton yield per plant and seed cotton yield per plot, it exhibited low *per se* performance and as well as poor combining ability for these traits.

It was observed in some instances that the lines and testers with good mean performance are not necessarily being good general combiners and vice-versa. Thus the association between *per se* performance and GCA effects was evident in the present study indicating that the effectiveness of choice of parents based on *per se* performance alone was not appropriate but based on consistent and significant GCA effects are important. Similar findings were also reported by (Marani, 1967).

It was also observed that in some instances *per se* performance of parents for some traits in general were related to their GCA effects, Murthy and Ranganathacharyula (1998) reported similar finding. Thus if a trait is unidirectionally controlled by a set of alleles and additive effects are important, the choice of parents based on *per se* performance may be effective. It can be concluded that, among the lines PH 1076 (*G.hirsutum*) was proved to be good combiner for seed cotton yield per plant and its yield contributing traits like number of monopodia per plant, number of sympodia per plant, plant height, days to maturity, number of boll per plant and fibre length, whereas the genotype NH 615 (*G.hirsutum*) was found to posses favorable alleles for cotton yield per plant and its contributing traits like number of monopodia per plant, number of bolls per plant and days to maturity.

Chawla and Gupta (1982) stated that parents with high mean performance as well as high GCA effects produce transgessive sergeants in the F_2 as well as in later generations.

5.2.3.2 Specific combining ability effects

Significant SCA effects were observed for seed cotton yield per plant and its component traits, whereas for fibre quality few crosses had recorded significant SCA effects.

Generally for the trait days to 50% flowering, earliness is the desirable, the crosses with negative SCA effects should be used for improving the trait. The intra and interspecific crosses NH 545 x NH 452, LRA 5166 x NH 625 and NH 615 x Suvin recorded highly significant negative SCA effects in desired direction involving parents (*G. hirsutum* x *G. hirsutum*) and (*G. hirsutum* x *G. barbadance*). Superiority of a (*G. hirsutum* x *G. hirsutum*) combination might be due to concentration and interaction between favorable gene contributions by the parents. Non-additive gene action played a significant role in governing the trait, so breeding methods which were designed for population improvement such as recurrent selection would be helpful in developing early maturing genotypes.

For number of monopodia per plant, none of crosses recorded significant SCA effects, where parents having poor combining ability. Expression of good potential in hybrid combination by the poor combiners through accumulation of favourable allells might be the reason to produce promising specific combiner in desired directions (Ilyas, 2007).

Significant SCA effects were noticed in four crosses for the trait number of sympodia per plant in desired direction. The intraspecific crosses PH 1060 x PKV Rajat (*G. hirsutum* x *G. hirsutum*), PH 1076 x PKV Rajat (*G. hirsutum* x *G. hirsutum*) and LRA 5166 x NH 452 (*G. hirsutum* x *G. hirsutum*) and interspecific cross NH 615 x Suvin (*G. hirsutum* x *G. barbadance*) exhibited significant SCA effects in desired direction. The cross NH 630 x NH 625 (*G. hirsutum* x *G. hirsutum)* showed significant and positive SCA effect for plant height.

For days to maturity, the intraspecific crosses NH 630 x NH 625 (*G. hirsutum* x *G. hirsutum*), NH 635 x NH 625 (*G. hirsutum* x *G. hirsutum*), PH 1060 x PKV Rajat (*G. hirsutum* x *G. hirsutum*), PH 1076 x NH 452 (*G. hirsutum* x *G. hirsutum*), PH 1076 x NH 625 (*G. hirsutum* x *G. hirsutum*) and PH 1076 x PKV Rajat (*G. hirsutum* x *G. hirsutum*) and interspecific crosses NH 545 x Suvin (*G. hirsutum* x *G. barbadence*), NH 635 x Suvin (*G. hirsutum* x *G. barbadence*) and LRA 5166 x Suvin (*G. hirsutum* x *G. barbadence*) exhibited negative and significant SCA effects for this trait.

For boll weight, the crosses NH 630 x PKV Rajat (*G. hirsutum* x *G.hirsutum*), PH 1076 x NH 452 (*G. hirsutum* x *G. hirsutum*), PH 1076 x PKV Rajat (*G. hirsutum* x *G. hirsutum*) and LRA 5166 x Suvin (*G. hirsutum* x *G.barbadence*) showed the positive SCA effects. The high SCA effects in all the above crosses were either due to combination of parents involved which further substantiate the operation of non-additive gene action for this trait.

The intraspecific crosses, PH 1076 x PKV Rajat (*G. hirsutum* x *G. hirsutum*), NH 615 x PKV Rajat (*G. hirsutum* x *G. hirsutum*), NH 630 x NH 452 (*G. hirsutum* x *G. hirsutum*), PH 1060 x NH 625 (*G. hirsutum* x *G. hirsutum*) and PH 1060 x PKV Rajat (*G. hirsutum* x *G. hirsutum*) and interspecific crosses NH 630 x Suvin (*G. hirsutum* x *G. barbadence*) and LRA 5166 x Suvin (*G. hirsutum* x

G. barbadence) showed highest positive and significant SCA effects for number of bolls per plant. The superiority of interspecific combinations (*G. hirsutum* x *G. barbadence*) may due to the presence of genetic diversity among the parents and there could be some complementation indicating importance of non-additive gene effects reported by Singh and Chatrath (1997) and Rauf *et al.* (2006).

For the micronaire value, interspecific crosses, NH 545 x Suvin (*G. hirsutum* x *G. barbadence*), NH 615 x Suvin (*G. hirsutum* x *G. barbadence*) and PH 1060 x Suvin (*G. hirsutum* x *G. barbadence*) and intraspecific crosses NH 635 x NH 452, NH 635 x NH 625, PH 1060 x NH 452, PH 1076 x NH 452, NH 615 x PKV Rajat, PH 1076 x PKV Rajat and LRA 5166 x PKV Rajat showed significant and positive SCA effects.

For fibre length, the interspecific crosses NH 630 x Suvin (*G. hirsutum* x *G. barbadence*), PH 1060 x Suvin (*G. hirsutum* x *G. barbadence*), LRA 5166 x Suvin (*G. hirsutum* x *G. barbadence*) and PH 1076 x Suvin (*G. hirsutum* x *G. barbadence*) and intraspecific crosses NH 545 x NH 625, NH 615 x NH 625, NH 615 x PKV Rajat, NH 635 x NH 452, NH 635 x NH 625, NH 635 x PKV Rajat, PH 1060 x NH 625, PH 1076 x NH 452 and LRA 5166 x PKV Rajat showed significant positive and SCA effects.

For uniformity ratio, no any of cross recorded the significant and positive SCA effects, whereas for fibre strength, intraspecific crosses NH 545 x PKV Rajat, NH 635 x NH 452 and NH 635 x NH 625 and one interspecific cross NH-1060 x Suvin (*G. hirsutum* x *G. barbadence*) exhibited significant positive SCA effects.

The highest SCA effects for seed cotton yield per plant were observed in intraspecific crosses NH 545 x NH 452, NH 615 x PKV Rajat, NH 630 x NH 452, NH 635 x NH 625, PH 1060 x NH 625, PH 1060 x PKV Rajat, PH 1076 x NH 452 and PH 1076 x PKV Rajat and interspecific crosses NH 630 x

Suvin (*G. hirsutum* x *G. barbadence*) and LRA 5166 x Suvin (*G. hirsutum* x *G. barbadence*). The three intraspecific crosses *viz.,* PH 1076 x PKV Rajat, NH 615 x PKV Rajat and PH 1076 x NH 452 recorded highest *per se* performance and significant SCA effects.

For seed cotton yield per plot and seed cotton yield quintal per ha, the crosses NH 615 x PKV Rajat, PH 1060 x PKV Rajat, PH 1076 x PKV Rajat and LRA 5166 x Suvin (*G. hirsutum* x *G. barbadence*) exhibited significant SCA effects in desired direction.

The intraspecific cross PH 1076 x PKV Rajat exhibited significant and positive SCA effects in desired direction for important yield contributing traits *viz.,* number of sympodia per plant, boll weight, number of bolls per plant, micronaire value, seed cotton yield per plant, seed cotton yield per plot and seed cotton yield quintal per ha.

The intraspecific cross NH 615 x PKV Rajat recorded significant positive SCA effect for days to 50% flowering, number of bolls, micronaire value, fibre length, seed cotton yield per plant, seed cotton yield per plot and seed cotton yield in quintal per ha indicating the definite possibility of exploiting these cross combinations for yield improvement through heterosis breeding. Interestingly, these two cross combinations exhibited good uniformity ratio, fibre strength and ginning percentage quality traits.

Also interspcific cross LRA 5166 x Suvin recorded significant SCA effect for fibre quality and yield characters such as days to maturity, boll weight, number of bolls per plant, micronaire value, fibre length and seed cotton yield per plant. Hybrids superior with fibre quality traits are not good for seed cotton yield and vice versa. Similar findings were also reported by Khan and Idris (1995), Gul-Hassan *et al.* (1999) and Ahuja and Dhayal (2007). This suggested that high yielding hybrids with acceptable levels of quality traits should be considered.

A comparison of five best cross combinations for various characters is presented in Table 19. The perusal of GCA effects of different characters in present investigation revealed SCA effects and *per se* performance of the crosses were not closely related, which indicates that the hybrids with high *per se* performance need not be the once with high SCA effects and vice versa. But for the characters, days to 50% flowering (desirable in negative direction), number of sympodia per plant, days to maturity, boll weight, number of bolls per plant, micronaire value, fibre length, fibre strength, seed cotton yield per plant, seed cotton yield per plot and seed cotton yield quintal per ha. had high correlation between the SCA effects and *per se* performance of the F_1 crosses was observed, which signifies the contribution of non-additive gene effects in the inheritance of these traits. So the cross combinations may be selected either on the basis of SCA or mean performance or in combination. Rauf *et al.* (2006) observed correlation between SCA effects and *per se* performance of F_1 crosses for seed cotton yield and number of sympodial branches.

High SCA effects were observed for different inter and intraspecific crosses for the most of characters. The cross NH 545 x NH 452 for days to 50% flowering, NH 615 x NH 452 for number of monopodia per plant, PH 1076 x PKV Rajat for number of sympodia per plant, PH 1060 x PKV Rajat for days to maturity, PH 1076 x NH 452 for boll weight, PH 1076 x PKV Rajat for number of bolls per plant, PH 1060 x NH 625 for ginning percentage, NH 545 x Suvin for micronaire value, LRA 5166 x Suvin (*G. hirsutum* x *G. barbadence*) for fibre length, NH 545 x NH 625 for uniformity ratio, LRA 5166 x Suvin (*G. hirsutum* x *G. barbadence*) for fibre strength and PH 1076 x PKV Rajat for seed cotton yield per plant, seed cotton yield per plot and seed cotton quintal per ha were recorded highest SCA effect.

Table 19. Performance of five superior crosses for different characters in cotton

Sr. No.	Crosses	*Per se* perfor-mance	SCA effect	Parent-I		Parent-II		Heterosis over (%)			
				Per se	GCA effect	*Per se*	GCA effect	MP	BP	SH-I (NHH 44)	SH-2 (DCH 32)
1	**Days to 50% flowering**										
	NH 545 x NH 452	68.66	-2.952**	67.00	-2.429**	72.33	-2.048**	1.44	-5.07**	1.48	-8.44**
	NH 545 x NH 625	71.66	0.095	67.00	-2.429**	74.00	-2.095**	1.65	-3.15*	5.91**	-4.44**
	LRA 5166 x NH 625	72.00	-1.655*	74.33	-0.345	74.00	-2.095**	-2.95*	-3.14*	6.40**	-4.00**
	PH 1076 x NH 452	73.00	-0.702	75.00	-0.345	72.33	-2.048**	-0.90	-2.67	7.88**	-2.67
	PH 1060 x NH 625	73.66	-0.405	77.33	0.071	74.00	2.095**	-2.64*	-4.74**	8.87**	-1.78
2	**Number of monopodia per plant**										
	NH 615 x NH 452	1.86	0.143	1.40	0.219**	1.26	0.048	40.00**	33.33**	27.27*	55.56**
	NH 615 x NH 625	1.80	0.067	1.40	0.219**	1.20	0.058	38.46**	28.57*	22.73	50.00**
	PH 1076 x Suvin	1.73	0.189	1.40	0.144*	1.46	-0.056	20.93	18.18	18.18	44.44*
	PH 1076 x NH 452	1.66	0.018	1.40	0.144*	1.26	0.040	25.00*	19.05	13.64	38.89*
	NH 615 x PKV Rajat	1.63	0.010	1.40	0.219**	1.20	-0.051	25.64	16.67	11.36	36.11*
3	**Number of sympodia per plant**										
	PH 1076 x PKV Rajat	28.26	2.576*	24.66	1.950**	23.06	0.139	18.44**	14.69*	24.13**	22.16**
	LRA 5166 x NH 452	27.59	4.296**	22.53	-1.293*	25.66	0.992**	14.51**	7.52	21.19**	19.27**
	PH 1076 x NH 452	27.40	0.863	24.66	1.956**	25.66	0.992**	8.90	6.78	20.35**	18.44
	PH 1060 x PKV Rajat	27.02	2.646**	23.06	0.640	23.06	0.139	17.17**	17.17**	18.68**	16.80
	NH 545 x Suvin	26.90	1.796	22.33	1.627**	26.26	-0.118	10.92*	2.44	18.16**	16.28**

Table 19. Contd...

Sr. No.	Crosses	*Per se* performance	SCA effect	Parent-I		Parent-II		Heterosis over (%)			
				Per se	GCA effect	*Per se*	GCA effect	MP	BP	SH-1 (NHH 44)	SH-2 (DCH 32)
4	**Plant height (cm)**										
	PH 1076 x PKV Rajat	162.40	2.989	167.13	11.192**	123.26	0.611	11.85**	-2.83	19.65**	21.25**
	PH 1076 x PKV Rajat	160.46	3.264	145.86	8.983**	123.26	0.611	19.25**	10.01**	18.22**	19.81**
	PH 1076 x NH 452	158.60	-0.035	167.13	11.192**	136.26	-0.165	4.55	-5.11*	16.85**	18.42**
	PH 1076 x Suvin	158.46	0.817	145.86	8.983**	166.00	1.058	1.62	-4.54	16.75**	18.32**
	PH 1076 x NH 452	158.16	1.740	145.86	8.983**	136.26	-0.165	12.12**	8.43**	16.53**	18.09**
5	**Days to maturity**										
	PH 1060 x PKV Rajat	146.66	-4.988**	148.33	-3.679**	150.33	-8.762**	-1.79**	-2.44**	-9.09**	-10.57**
	PH 1076 x PKV -Rajat	150.66	-2.071**	152.33	-2.595**	150.33	-8.762**	-0.44	-1.09	-6.61**	-8.13**
	PH 1076 x NH 452	154.33	-3.786**	152.33	-2.595**	163.66	-3.381**	-2.32**	-5.70**	-4.34**	-5.89**
	NH 615 x PKV -Rajat	154.66	0.679	147.33	-1.345**	150.33	-8.762**	3.95**	2.88**	-4.13**	-5.69**
	PH 1060 x NH 452	156.33	-0.0702	148.33	-3.679**	163.66	-3.381**	0.21	-4.48**	-3.10**	-4.67**
6	**Boll weight (g)**										
	PH 1076 x NH 452	3.28	1.127**	3.12	0.003	2.98	0.171**	7.54**	5.13	4.13	9.33**
	PH 1060 x NH 625	3.24	0.077	3.10	0.073**	3.05	0.111**	5.37*	4.52	2.86	8.00**
	LRA 5166 x NH 452	3.22	0.077	3.16	0.063*	2.98	0.171**	4.89*	1.90	2.22	7.33**
	NH 635 x NH 452	3.21	0.065	2.94	-0.002	2.98	0.171**	8.56**	7.83**	2.01	7.11**
	PH 1076 x PKV Rajat	3.20	0.161**	3.12	0.003	3.05	0.057	3.73	2.56	1.59	6.67**

Table 19. Contd...

Sr. No.	Crosses	*Per se* performance	SCA effect	Parent-I		Parent-II		Heterosis over (%)			
				Per se	GCA effect	*Per se*	GCA effect	MP	BP	SH-1 (NHH 44)	SH-2 (DCH 32)
7	**Number of bolls per plant**										
	PH 1076 x PKV Rajat	34.72	3.850**	25.50	3.850**	24.34	0.937**	39.33**	36.16**	49.78**	59.66**
	NH 615 x PKV Rajat	32.84	2.860**	23.34	2.860**	24.34	0.937**	37.73**	34.92**	41.67**	51.01**
	PH 1076 x NH 452	30.90	3.850**	25.50	3.850**	24.72	-0.084	23.06**	21.18*	33.30**	42.09**
	LRA 5166 x Suvin	30.70	0.437	25.84	0.437	29.26	-0.378	9.76**	4.92	32.44**	41.17**
	PH 1060 x PKV Rajat	29.42	-1.119**	25.84	-1.119**	24.34	0.937**	17.28**	13.88**	26.95**	35.32**
8	**Ginning Percentage(%)**										
	PH 1060 x NH 625	42.05	0.586	37.34	0.586	40.16	1.550*	8.15	4.70	21.73**	20.01**
	NH 630 x NH 625	41.73	-0.837	33.35	-0.837	40.16	1.550*	13.53*	3.91	20.81**	19.10**
	PH 1076 x PKV Rajat	41.70	0.536	38.34	0.636	40.16	1.550*	6.24	3.83	20.72**	19.01**
	NH 630 x NH 452	41.43	0.636	38.34	0.636	38.06	-0.124	8.46	8.06	19.94**	18.24**
	NH 630 x NH 452	41.30	-0.837	33.35	-0.837	39.98	1.403*	12.65*	3.31	19.58**	17.88**
9	**Micronaire value (µg/inch)**										
	PH 1060 x Suvin	2.99	0.226*	3.60	-0.864**	3.87	-0.409**	-19.84**	-22.63*	-16.60**	12.38**
	LRA 5166 x Suvin	3.04	-0.689**	3.30	0.094	3.87	-0.409**	-15.24	-21.51**	-15.40**	14.00**
	PH 1060 x NH 625	3.04	-0.433**	3.60	-0.864**	4.42	0.293**	-24.25**	-31.27**	-15.46**	14.00*
	PH 1060 x PKV Rajat	3.08	-0.221*	3.60	-0.864**	3.96	0.121**	-18.63**	-22.35**	-14.29**	15.50**
	PH 1076 x Suvin	3.19	-0.531**	4.63	0.093	3.87	-0.409**	-24.81**	-30.96**	-11.04**	19.88**
10	**Fibre length(mm)**										
	LRA 5166 x Suvin	32.46	2.027**	24.93	0.932**	33.62	4.489**	10.90**	-3.43**	31.71**	7.56**
	PH 1076 x Suvin	31.51	0.740**	23.16	1.270**	33.62	4.489**	11.00**	-6.26**	27.86**	4.42**
	PH 1060 x Suvin	30.70	1.340**	23.06	-0.147	33.62	4.489**	8.31**	-8.69**	24.54**	1.71
	NH 630 x Suvin	30.41	1.107**	24.25	-0.197	33.62	4.489**	5.12**	-9.53**	23.39**	0.77
	NH 615 x Suvin	28.75	0.186	23.91	-0.943**	33.62	4.489**	-0.06	-14.49**	16.63**	-4.75**

Table 19. Contd...

Sr. No.	Crosses	*Per se* performance	SCA effect	Parent-I		Parent-II		Heterosis over (%)			
				Per se	GCA effect	*Per se*	GCA effect	MP	BP	SH-1 (NHH 44)	SH-2 (DCH 32)
11	**Uniformity ratio**										
	NH 545 x NH 625	48.73	0.498	45.96	1.818**	49.36	0.977**	2.24	-1.28	0.48	15.58**
	NH 545 x PKV Rajat	48.36	1.277	45.96	1.818**	47.83	-0.169	3.13	1.11	-0.27	14.71**
	PH 1060 x NH 452	47.53	1.033	45.96	0.302	45.93	0.759*	3.45	3.14	-1.99	12.74**
	NH 615 x NH 625	46.83	1.392	47.56	-0.975*	49.36	0.977**	-3.37	-5.13*	-3.44	11.08**
	LRA 5166 x NH 625	46.73	0.490	47.40	-0.173	49.36	0.977**	-3.41	-5.33*	-3.64	10.84**
12	**Fibre Strength (g/tex)**										
	LRA 5166 x Suvin	27.50	0.134	25.60	1.090**	26.36	2.203**	5.8499	4.30	32.70**	24.70**
	PH 1060 x Suvin	27.46	1.371**	21.53	-0.186	26.36	2.203**	14.58**	4.15	32.51**	24.54**
	PH 1076 x Suvin	26.76	0.740	22.30	-0.249	26.36	2.203**	10.00**	1.52	29.16**	21.39**
	NH 615 x Suvin	26.12	-0.464	22.33	0.312	26.36	2.203**	7.28**	-0.92	26.06**	18.47**
	NH 545 x Suvin	26.02	0.048	20.27	-0.300	26.36	2.203**	11.58**	-1.30	25.58**	18.02**
13	**Seed cotton yield per plant (g)**										
	PH 1076 x PKV Rajat	109.33	13.978**	78.00	12.428**	72.35	6.542**	45.43**	40.17**	38.60**	54.33**
	NH 615 x PKV Rajat	99.87	7.455**	68.75	9.490**	72.35	6.542**	41.56**	38.04**	26.61**	40.98**
	PH 1076 x NH 452	97.29	4.298**	78.00	12.428**	73.47	4.182**	28.46**	24.73**	23.34**	37.34**
	NH 615 x NH 452	88.88	-1.175	68.75	9.490**	73.47	4.182**	24.99**	20.97**	12.68**	25.47**
	NH 615 x NH 625	87.37	-0.247	68.75	9.490	67.75	1.745**	28.01**	27.08**	10.76**	23.33**

*, ** indicated significant 5 and 1% level, respectively.

The ideal specific combination should be one where high magnitude of SCA in addition to high GCA in both or at least in one of the parents is present. Similar results were reported by earlier workers, Mane and Bhatade (1992), Goudar *et al.* (1996), Patel *et al.* (1997), Krishnarao (1998), Gul-Hassan *et al.* (1999), Pavasia *et al.* (1999a), Murthy and Rangnathacharyulu (1999), Zia-Ul-Islam *et al.* (2001), Laxman and Ganesh (2003), Narisireddy and Satyanarayana (2004), Neelima *et al.* (2004), Rauf *et al.* (2006) and Kancherla (2011).

Intraspecific crosses produced superior cross combinations with high SCA effects which might be due to mutual cancellation of the contribution by different yield components, so both additive and non-additive variances should be considered for successful breeding programme. Similar results were observed by Patel *et al.* (1997), Murthy and Ranganathacharyulu (1998) and Murthy and Ranganathacharyulu (1999), whereas high SCA effects resulted due to average x average general combiners may excepted to throw high yielding segregants in later generations and could be exploited for isolating superior genotypes (Bhatade *et al.,* 1992). The crosses involving both good combiners are excepted to release desirable segregates in the subsequent generations (Gururajan and Basu, 1992). However parents with high x high GCA effects were reported by Goudar *et al.* (1996), Narisireddy and Satyanarayana (2004) and De Aguiar *et al.* (2007).

5.3 HETEROSIS

Heterosis is defined as the increased vigour of F_1 over parental mean and is gènetic expression of beneficial effects of hybridization. Heterosis is a universal phenomenon which occurs both in self and cross pollinated species. The magnitude of heterosis provides a basis for genetic diversity and a guide to the choice of parents for developing superior F_1 hybrids, so as to exploit hybrid vigour and/or for building better gene pools to be employed in population improvement.

Heterosis in cotton was reported in both intra and interspecific crosses (Turner, 1953, Miller and Maroni, 1963, Al Rawi and Kohel, 1969, Davis and Palomo, 1980, Basabag and Gencer, 2000, Wei *et al.*, 2002, Yuna *et al.*, 2002, Zhang and Zhu, 2002, Wu *et al.*, 2004). Intraspecific hybrids (*G. hirsutum* x *G. barbadense*) have great yield and quality potential for the commercial production of cotton. Their yields are similar to *G. hirsutum* L. and also fiber properties (length, fitness and strength) similar to *G. barbadense* L. Davis (1978), Clark *et al.* (1998) stated that intraspecific hybrid cotton have better performance compared to varieties for fiber yield, ginning efficiency, fiber length, fiber fitness and fiber uniformity. However, these interspecific hybrids exhibit several undesirable traits like overly vigorous vegetative growth, late maturation, low fiber uniformity and led to produce high properties of impurities, neps and mots (Hughs and Lalor, 1986).

Hybrid cotton is an optimistic approach for significant improvement in genetic potential for yield and fiber quality traits. For commercial exploitation of heterosis in cotton, the pre-requisites are identification of parents which show good heterosis on crossing and production of hybrids with low cost. The work on heterosis has been reviewed from time to time on various quality, yield and yield components in cotton by many workers *viz.*, Dovairaj (1968), Al-Rawi and Kohel (1969), Baker and Verhalen (1975) and Singh *et al.* (1987b). The aim of heterosis analysis is to find out the best combination of parents for their prospects for future use in hybrid breeding programme.

In the present investigation, heterosis was measured over mid parent, better parent and standard checks (NHH 44 and DCH 32) for fibre quality, yield and yield components. A high level of heterosis in desired direction was observed in several hybrids for various characters (Table 20).

1. Days to 50% flowering

Significant negative heterosis over mid parent and better parent was recorded in three and fourteen crosses, respectively. The cross LRA 5166 x NH 625 exhibited significant negative heterosis over mid parent and cross PH 1060 x Suvin (*G.hirsutum* x *G. barbadense*) recorded significant negative heterosis over better parent. The best performing hybrid NH 545 x NH 452 showed significant and negative heterotic performance over DCH 32. Significant negative heterosis for earliness was also reported by Baker and Verhalen (1975), Sangwan and Yadava (1986), Siddiqui and Patil (1994), Basha (1997), Rajput *et al.* (1997), Kumaresan *et al.* (1999) Potdukhe (2002), Natera *et al.* (2007), Ganapathy and Nadarajan (2008), Deosarkar *et al.* (2009) and Kancherla (2011).

While, negative heterosis over better parent was reported by Potdukhe (2001), Natera *et al.* (2007), Siddiqui and Patil (1994), Rajput *et al.* (1997), Ganapathy and Nadarajan (2008), Deosarkar *et al.* (2009) andKancherla (2011). Significant heterosis over commercial checks were reported by Rajput *et al.* (1997), Muthu *et al.* (2005), Giri *et al.* (2006), Hemadia (2006), Deosarkar *et al.* (2009) and Kancherla (2011).

2. Number of monopodia per plant

Four and two crosses exhibited significant positive heterosis over mid and better parent for number of monopodia per plant respectively, whereas one and five crosses rewarded significant positive heterosis over standard hybrid

Table 20. Number of crosses with significant desirable heterosis in cotton

Sr. No.	Character	SCA effect	Significant heterosis in the desired direction over			
			Mid parent	Better parent	SH (NHH 44)	SH (DCH 32)
1	Days to 50% flowering	3	3	14	0	3
2	Number of monopodia per plant	0	4	2	1	5
3	Number of sympodia per plant	4	4	2	6	3
4	Plant height	1	13	6	17	18
5	Days to maturity	9	6	21	10	13
6	Boll weight	4	11	5	1	11
7	Number of bolls per plant	7	10	6	17	21
8	Ginning percentage	0	2	0	19	17
9	Micronaire value	11	9	7	17	28
10	Fibre length	13	10	4	10	2
11	Uniformity ratio	0	0	0	0	20
12	Fibre strength	4	10	1	25	19
13	Seed cotton yield per plant	10	13	8	9	17
14	Seed cotton yield per plot	4	7	6	3	9
15	Seed cotton yield qtl./ ha.	4	7	6	4	8

NHH 44 and DCH 32. An intraspecific cross, NH 615 x NH 452 was found to exhibit the highest significant positive heterosis over mid parent, heterosbetiosis and checks NHH 44 and DCH 32. Similar results over mid parent was reported by Singh and Singh (1982), Singh and Kalsy (1983), Gencer and Kaynak (1994), Basha (1997), Potdukhe (2001), Maisuria *et al.* (2006) and Deosarkar *et al.* (2009)

Significant positive heterosis over better parent was reported by Basha (1997), Doss and Kadambavanasundaram (1997), Ahuja and Tuteja (2000), Potdukhe (2001), Deva *et al.* (2002), Kharde *et al.* (2004), Maisuria *et al.* (2006), Deosarkar *et al.* (2009). Significant positive heterosis over commercial check for this trait was reported by Tuteja *et al.* (1993), Muthu *et al.* (2005), Giri *et al.* (2006), Maisuria *et al.* (2006), Deosarkar *et al.* (2009), Tuteja *et al.* (2011) and Kumar *et al.* (2013).

3. Number of sympodia per plant

The range of mid parent and heterobetiosis for this trait were from -15.20 to 18.44 per cent, and -21.06 to 17.17 per cent, whereas the range of heterosis over NHH 44 and DCH 32 was from -15.10 to 26.13 per cent and from -16.44 to 22.16 per cent respectively. The cross PH 1076 x PKV Rajat had shown significantly positive heterosis over mid parent as well as on two checks. The cross PH 1060 x PKV Rajat exhibited significant positive heterosis over better parent.

These results are in agreement with mid parent those of Khadi *et al.* (1993), Gencer and Kaynak (1994), Basha (1997), Babar *et al.* (2001), Panhwar *et al.* (2002), Potdukhe (2002), Maisuria *et al.* (2006), Natera *et al.* (2007), Ganpathy and Nadarajan (2008), Deosarkar *et al.* (2009) and Kancherla (2011).

The positive and significant heterobetiosis was given by Potdukhe (2001), Deva *et al.* (2002), Kharde *et al.* (2004), Maisuria *et al.* (2006), Natera *et* *al.* (2007), Ganapathy and Nadarjana (2008), Deosarkar *et al.* (2009) and Kancherla (2011) and standard heterosis for this trait was reported by Tuteja *et al.* (1993), Babar *et al.* (2001), Muthu *et al.* (2005), Maisuria *et al.* (2006), Deosarkar *et al.* (2009), Kancherla (2011) and Tuteja *et al.* (2013).

4. Plant height (cm)

Positive heterosis is desirable for this character for seed cotton yield. The heterosis ranged from -9.05 to 19.25 per cent, from -17.79 to 10.01 per cent, from -2.26 to 18.22 per cent and from -0.95 to 21.25 per cent over mid parent, better parent and over checks NHH 44 and DCH 32. The intraspecific cross PH 1060 x PKV Rajat exhibited the highest positive significant heterosis over mid and better parent. Most promising cross PH 1076 x PKV Rajat showed highly significant heterosis over two checks.

Similarly, positive heterosis over mid parent for plant height has been reported by Potdukhe (2002), and Ganapathy and Nadarajan (2008), whereas over better parent reported by Nirania *et al.* (1992), Pavasia *et al.* (1999), Ahuja and Tuteja (2000), Deva *et al.* (2002), Kharde *et al.* (2004) and Ganapathy and Nadarajan (2008). Significant and positive heterosis over commercial check reported by Tuteja *et al.* (1993), Bhatade and Rajeshwar (1994), Muthu *et al.* (2005), Giri *et al.* (2006) and Kumar *et al.* (2013).

5. Days to maturity

The relative heterosis ranged from -2.40 (NH 635 x NH 625) to 9.59 per cent (PH 1076 x Suvin). Heterobeltiosis ranged from -6.14 (NH 545 x Suvin) to 2.88 per cent (NH 615 x PKV Rajat). For standard heterosis the values varied from -9.09 (PH 1060 x PKV Rajat) to 14.46 per cent (PH 1076 x Suvin) over check NHH 44 and from -10.57% (PH 1060 x PKV Rajat) to 12.6 per cent (PH 1076 x Suvin) over check DCH 32.

Negative heterosis is desirable for days to maturity. The crosses NH 635 x NH 625 and NH 545 x Suvin recorded significant negative heterosis over mid parent and better parent. The cross PH 1060 x PKV Rajat showed highly significant heterosis over checks NHH 44 and DCH 32. Significant heterosis for this trait was also noticed by Deosarkar *et al.* (2009).

6. Boll weight (g)

Boll weight is a key component which contributes to seed cotton yield. Hybrids with high boll weight are desirable. The range of heterosis was from -16.85 to 22.30 per cent, from -27.04 to 7.83 per cent, from -26.35 to 7.94 per cent and from -22.67 to 13.33 per cent over mid parent, better parent, NHH 44 and DCH 32.

The cross NH 635 x NH 452 recorded significant and positive heterosis over better parent. The hybrid LRA 5166 x Suvin had recorded significant heterosis for boll weight over mid parent, checks NHH 44 and DCH 32. Positive heterosis over mid parent for boll weight was reported by Babar *et al.* (2001), Panhwar *et al.* (2002), Soomro and Baloch (2005), Maisuria *et al.* (2006), Natera *et al.* (2007), Deosarkar *et al.* (2009) and Kancherla (2011).

Positive and significant heterosis over better parent were also reported by Ahuja and Tuteja (2000), Solangi *et al.* (2001), Solangi *et al.* (2002), Ramlingam and Ponnusamy (2003), Kharde *et al.* (2004), Maisuria *et al.* (2006), Natera *et al.* (2007) Deosarkar *et al.* (2009) and Kancherla (2011). Similar findings over commercial checks were reported by Giri *et al.* (2006), Verma *et al.* (2006), Kancherla (2011), Kumar *et al.* (2013) and Tuteja *et al.* (2013).

7. Number of bolls per plant

Bolls per plant is a key component which contributes to seed cotton yield. The range of heterosis was form -16.89 to 39.33 per cent, from -20.44 to

36.16 per cent, from -10.79 to 49.78 per cent and from -1.04 to 42.09 per cent over mid parent, better parent, commercial checks NHH 44 and DCH 32.

The hybrids PH 1076 x PKV Rajat and NH 615 x PKV Rajat had recorded significant positive heterosis over mid parent, better parent, NHH 44 and DCH 32. Positive heterosis for these trait over mid parent has been reported by Ahmad *et al.* (2002), Solangi *et al.* (2002), Ramlingam and Ponnusamy (2003), Deshpande and Baig (2004), Soomro and Baloch (2005), Maisuria *et al.* (2006), Ganapathy and Nadarajan (2008), Pole *et al.* (2008), Deosarkar *et al.* (2009) and Kancherla (2011).

Similar result over better parent were reported by Ahuja and Tuteja (2000), Babar *et al.* (2001), Ahmad *et al.* (2002), Ramlingam and Ponnusamy (2003), Maisuria *et al.* (2006), Pole *et al.* (2008), Ganapathy and Nadarajan (2008), Deosarkar *et al.* (2009) and Kancherla (2011).

The significant heterosis over standard checks were also reported by Bhatade and Rajeshwar (1994), Rajkumari *et al.* (1996), Meshram *et al.* (1998), Babar *et al.* (2001), Soomro and Baloch (2005), Maisuria *et al.* (2006), Muthu *et al.* (2005), Gumber *et al.* (2006), Giri *et al.* (2006), Deosarkar *et al.* (2009), Tuteja *et al.* (2011), Kancherla (2011), Kumar *et al.* (2013) and Tuteja *et al.* (2013).

8. Ginning percentage

Nineteen and seventeen crosses recorded significant and positive heterosis over NHH 44 and DCH 32. An intraspecific cross, NH 630 x NH 625 recorded highest significant positive value over mid parent. The hybrid PH 1076 x NH 625 recorded the highest positive significant heterosis followed by NH 630 x NH 625 over standard checks NHH 44 and DCH 32. These results are in accordance with over mid parent reported by Patel *et al.* (1996), Basha (1997), Patel *et al.* (1998), Solangi *et al.* (2001), Solangi *et al.* (2002), Ganapathy *et al.* (2005), Tutaja *et al.* (2005b), Maisuria *et al.* (2006) and Kancherla (2011).

Whereas, heterosis over standard check was given by Singh *et al.* (2003) and Kancherla (2011).

9. Micronaire value (µg/inch)

The heterosis ranged from -24.81 (PH 1076 x Suvin) to 29.08 per cent (LRA 5166 x PKV Rajat) over mid parent and from-31.27 (PH 1060 x NH 452) to 20.69 per cent (NH 545 x Suvin) over better parent.

Heterosis in negative direction is desirable for this trait. The cross PH 1076 x Suvin was found superior as it showed the highest negative heterosis over mid parent. The cross PH 1060 x NH 625 exhibited negative heterosis over better parent and the cross PH 1060 x Suvin recorded significant and negative heterosis over check NHH 44.

Similar negative significant over mid parent were reported by Prakash (1982), Gencer and Kaynak (1994), Jain (1996), Punitha *et al.* (1999a), Natera *et al.* (2007) and Kancherla (2011). Heterosis in negative direction over better parent was reported by Gencer and Kaynak (1994), Doss and Kadambavanasundaram (1997), Punitha *et al.* (1999a), Natera *et al.* (2007) and (2011)Kancherla and significant over commercial check was reported by Punitha *et al.* (1999a), Tuteja *et al.* (2005) and Kancherla (2011).

10. Fibre length (mm)

The range of heterosis over mid parent ranged from -15.40 to 20.76 per cent and over better parent it varied between -24.35 to 18.18 per cent. For standard heterosis, the range varied from -18.46 and -33.44 per cent (PH 1060 x PKV Rajat) to 31.71 % and 7.56 per cent (LRA 5166 x Suvin) over standard check NHH 44 and DCH 32.

The cross PH 1076 x NH 452 registered significant positive heterosis over mid parent and cross PH 1076 x NH 452 showed highly significant positive heterosis over better parent. The interspecific cross LRA 5166 x Suvin recorded highest significant positive heterosis followed by PH 1076 x Suvin over checks NHH 44 and DCH 32. Significant positive heterosis over mid parent were also reported by Jain (1996), Ahuja and Tuteja (2000) and over commercial check was given by Jain (1996), Kumar *et al.* (2003), Tuteja *et al.* (2011) and Tuteja *et al.* (2013).

11. Uniformity ratio

The distribution of heterosis for uniformity ratio the range varied from -13.93 to 3.45 per cent, from -14.86 to 3.41 per cent, from -16.49 to 0.84 per cent and from -3.94 to 15.58 per cent for relative heterosis, heterobeltiosis, standard checks NHH 44 and DCH 32.

None of cross recorded significant positive heterosis over mid parent, better parent and standard check NHH 44 and twenty one crosses exceeded significantly over standard check DCH 32. The cross NH 545 x NH 625 showed significant positive heterosis over check DCH 32. Standard heterosis for uniformity ratio were also reported by Patnaik *et al.* (2004), Tuteja *et al.* (2005) and Kancherla (2011).

12. Fibre strength (g/tex)

Ten, one, twenty five and nineteen crosses recorded significant positive heterosis over mid parent, better parent, over NHH 44 and DCH 32 respectively. Highest mid parental positive heterosis was observed in PH 1060 x Suvin and NH 545 x Suvin. The cross NH 615 x NH 452 exhibited significant positive heterosis over better parent. The interspecific cross LRA 5166 x Suvin recorded the highest significant heterosis over checks NHH 44 and DCH 32.

Significant positive heterosis over mid parent were also reported by Prakash (1982), Jain (1996), Punitha *et al.* (1999a), Khan (2002) and Kancherla (2011) and significant over better parent given by Punitha *et al.* (1999a), Khan

(2002) and Kancherla (2011). Similar results over commercial check in accordance with Kancherla (2011).

13. Seed cotton yield per plant (g)

For seed cotton yield, the mid parental heterosis ranged from -22.55 (NH 545 x Suvin) to 45.43 per cent (PH 1076 x PKV Rajat). The intraspecific hybrids PH 1076 x PKV Rajat, NH 615 x PKV Rajat and PH 1076 x NH 452 recorded the highest significant positive heterosis over mid parent, better parent and checks NHH 44 and DCH 32.

Significant positive heterosis over mid parent were also noticed by Patel *et al.* (1996), Tuteja *et al.* (1996), Basha (1997), Siruguppa and Parameswarappa (1998), Kajjidoni *et al.* (1999), Babar *et al.* (2001), Ahmad *et al.* (2002), Solangi *et al.* (2002), Deshpande and Baig (2004), Soomro and Baloch (2005), Tutaja *et al.* (2005b), Soomro *et al.* (2006), Natera *et al.* (2007), Pole *et al.* (2008), Deosarkar *et al.* (2009), Kancherla (2011) and Kaushik and Kapoor (2013).

Significant positive heterosis over better parent were reported by Basha (1997), Kajjidoni *et al.* (1999), Babar *et al.* (2001), Ahmad *et al.* (2002), Maisuria *et al.* (2006), Natera *et al.* (2007), Ganapathy and Nadarajan (2008), Deosarkar *et al.* (2009), Patel *et al.* (2009), Kancherla (2011) and Kaushik and Kapoor (2013).

The significant positive heterosis over standard check were noticed by Ahmad *et al.* (2002), Kumar *et al.* (2003), Muthu *et al.* (2005), Giri *et al.* (2006), Maisuria *et al.* (2006), Tuteja *et al.* (2006), Natera *et al.* (2007), Deosarakar *et al.* (2009), Patel *et al.* (2009), Kancherla (2011), Kumar *et al.* (2013) and Tuteja *et al.* (2013).

14. **Seed cotton yield per plot (g)**

For seed cotton yield, the mid parental heterosis ranged from -22.55 (NH 635 x Suvin) to 45.44 per cent (PH 1076 x PKV Rajat). The estimates of heterobeltiosis for seed cotton yield per plot ranged from -28.69 (NH 635 x Suvin) to 40.17 per cent (PH 1076 x PKV Rajat). Seven and six crosses recorded positive heterosis over mid parent and better parent. The intraspecific hybrid PH 1076 x PKV -Rajat exhibited highest significant positive heterosis over mid parent. While three and nine recorded significant positively significant over check NHH 44 and DCH 32. The cross PH 1076 x PKV Rajat recorded highest positive heterosis followed by NH 615 x PKV Rajat and PH 1076 x NH 452 over checks NHH 44 and DCH 32.

15. **Seed cotton yield qtl./ha**

Out of twenty eight crosses, seven, six, four and eight crosses recorded positive heterosis over mid parent, better parent, standard checks NHH 44 and DCH 32 respectively. The intraspecific hybrid PH 1076 x PKV Rajat and NH 615 x PKV Rajat exhibited highest significant positive heterosis over mid parent, better parent, checks NHH 44 and DCH 32. Similar significant positive heterosis over standard check was reported by Tuteja *et al.* (2013).

5.4 CORRELATIONS

Selection may not lead to desired genetic gain, if it has unfavorable association with other yield attributes. Knowledge on the association between yield and yield component traits is, essential in any crop improvement programme for efficient selection. Yield is a complex character, which is highly influenced by the environment, hence, selection based on yield alone may limit the improvement, whereas the yield component characters are less complex in inheritance and influenced by the environment to a lesser extent. Thus, effective improvement in yield may be brought about through selection of yield component characters show association among themselves and also with yield. Several workers reported conflicting relationship among different yield components. So the present study was carried out utilizing parents and F_1s to understand the associations between inter and intra specific cross. Genotypic correlations in general are higher than phenotypic correlations. This may be due to relative stability of genotype as majority of them have been subjected to certain amount of selection (Johnson *et al.,* 1955).

In the present study, correlation coefficients were worked out for 11 parents and 28 hybrids derived from line x testers (7 x 4) programme. An overview of correlation studies indicated that, number of bolls per plant showed significant positive association with yield, whereas fibre strength exhibited significant negative association with yield.

The significant positive association of number of monopodia per plant and number of sympodia per plant with seed cotton yield per plant obtained in the present study. Number of bolls per plant showed significant and positive association with seed cotton yield. Contrary finding of significant and positive association with seed cotton yield per plant were also given by Rao *et al.* (2001), Kaushik *et al.* (2003), Iqbal *et al.* (2003b), Ahuja *et al.* (2004), Naveed *et al.* (2004), Muthu *et al.* (2004), Nariasireddy and Ratnakumari (2004b), Rauf *et al.* (2004), Kaushik *et al.* (2005), Iqbal *et al.* (2006), Annapurve *et al.* (2007), Preetha and Raveendran (2007), Patnaik and Sial (2010), Kancherla (2011) and Lal and Singh (2012).

Positive significant association of boll weight at genotypic and phenotypic level with seed cotton yield per plant was noticed in the present study. These results are in agreement with Sangwan and Yadava (1987), Singh *et al.* (1987a), Krishnarao and Mary (1990), Larik *et al.* (1999), Afiah and Ghoneim

(2000), Ahmad and Azhar (2000), Satange *et al.* (2000), Iqbal *et al.* (2003b), Muthu *et al.* (2004), Preetha and Raveendran (2007) and Kancherla (2011).

Ginning percentage showed significant positive association with seed cotton yield. The present findings are supported by Singh *et al.* (1987a), Hussain *et al.* (2000), Iqbal *et al.* (2003b), Ahuja *et al.* (2004), Muthu *et al.* (2004), and Preetha and Raveendran (2007).

Negative and significant association between fiber strength with seed cotton yield per plant was observed. Such finding were reported by Rajarathinam *et al.* (1993), Shanti and Selvaraj (1994) and Kancherla (2011).

In the present study, number of sympodia per plant exhibited significant and positive association with number of bolls per plant and ginning percentage. Similar results were observed by Chimanshette *et al.* (1990), Shanti and Selvaraj (1993), Kowsalya and Reveendran (1996), Larik *et al.* (1999), Rao *et al.* (2001), Iqbal *et al.* (2003b), Muthu *et al.* (2004), Muthuswamy and Vivekanandan (2004) Iqbal *et al.* (2006) and Kancherla (2011).

Boll weight has significant and positive association with ginning percentage and uniformity ratio and positive and non-significant with micronaire value. Ginning percentage had significant positive association with microniare value. Similar finding were reported by Muthu *et al.* (2004). Significant negative association of uniformity ratio with fibre strength was noted in the present study. Similar finding were supported by Preetha and Raveendran (2007) and Kancherla (2011).

The character, micronaire value exhibited negative association with fibre strength. Such results confirmed with the results of Krishnarao and Mary (1990), Preetha and Raveendran (2007) and Kancherla (2011).

The character fibre strength exhibited significant and negative association with seed cotton yield. These results ware confirmed with the results of Sangeetha (1998), Rao *et al.* (2001) and Kancherla (2011).

Seed cotton yield per plant showed significant positive correlation with number of monopodia per plant, number of sympodia per plant, boll weight, number of bolls per plant, plant height and ginning percentage. These finding are in agreement with Gite *et al.* (2006), Kaushik and Kapoor (2006), Murthy and Chamundeshwari (2006), Singh *et al.* (2009), Khan *et al.* (2009), Kancherla (2011), Mendez-Natera *et al.* (2012) and Rajamani *et al.* (2013).

5.5 PATH ANALYSIS

Number of monopodia per plant, number of sympodia per plant, number of bolls per plant and ginning percentage were found to have maximum direct positive effect on seed cotton yield per plant. These results are in agreement with the results reported by Hussain *et al.* (2000), Ahmad and Azhar (2000), Baloch *et al.* (2001), Rao *et al.* (2001), Kaushik *et al.* (2003), Pandey *et al.* (2003), Iqbal *et al.* (2003b), Ahuja *et al.* (2004), Muthu *et al.* (2004), Narisireddy and Ratnakumari (2004b), Rauf *et al.* (2004), Kaushik *et al.* (2005), Iqbal *et al.* (2006), Gite *et al.* (2006), Preetha and Raveendran (2007) and Rajamani *et al.* (2013).

The number of bolls per plant had highest positive direct effect on seed cotton yield per plant followed by boll weight. Similar results reported by Singh *et al.* (2009) and Kancherla (2011).

In the present study, number of bolls per plant exhibited indirect effect on seed cotton yield per plant via number of sympodia. These results are in agreement with Kowsalya and Raveendram (1996), Iqbal *et al.* (2003b), Kancherla (2011) and Lal and Singh (2012).

The number of sympodia per plant had exhibited positive indirect effect on seed cotton yield via number of bolls per plant. Similar findings were reported by Patnaik and Sial (2010) and Kancherla (2011).

Among the fibre quality traits, fibre length showed negative indirect effect on seed cotton yield via., ginning percentage, micronaire value and uniformity ratio, while ginning percentage exhibited indirect positive effect via., number of sympodia per plant, boll weight, number of bolls per plant, micronaire value and uniformity ratio on seed cotton yield per plant. Similar results were reported by Sangeetha (1998) and Kancherla (2011).

5.6 GENERATION MEAN ANALYSIS

Generation mean analysis is often used to estimate components of mean (additive and dominance effects and non-allelic interaction) of individual traits. Mather (1949) introduced tests for epistasis, through scaling test, which was further elaborated by Cavalli (1952). Hayman (1958) described the procedure for partitioning of generation mean in to six parameters *viz.,* mean (m), additive (d), dominance (h), additive x additive (i), additive x dominance (j) and dominance x dominance (l) gene effects. Gamble (1962) proposed a model partitioning the estimation of additive, dominance and epistasis effects from six generations *viz.,* P_1, P_2, F_1, F_2, BC_1 and BC_2 of a cross. This model is considered to be perfect fit and is not materially different from the proposed by Hayman and Mather (1955).

Generation mean analysis was carried out with six generations of four cross combinations, for fibre quality, yield and its components. The epistasis has been revealed from the results of joint scaling test with least square technique of the mean data of different characters.

It was observed that simple additive dominance model (three parameters) was found to be inadequate for the characters studied which was evident from significance of χ^2 values and significant scales. As all the thirteen characters studied exhibited lack of good fit for simple additive-dominance model, the data were subjected to six parameter model of joint scaling test to know the non-significant parameters.

Search was made for best fit model and tested at χ^2 (6-p) degrees of freedom.

For days to 50 % flowering, the additive dominance model was tested by the joint scaling test which was inadequate for the character in the crosses. The additive, dominant and interactions were observed in crosses. The estimates of gene effects revealed that dominance effect was more pronounced and in desirable direction for the inheritance of 50% flowering. Opposite signs of 'h' and 'l' component in all crosses indicate duplicate type of epistasis for days to 50% flowering. Similar results were also reported by Mehetre *et al.* (2003), Ismail (2007) and Kancherla (2011).

Regarding number of monopodia per plant, the scaling test recorded non-significant scales for three crosses 1, 2 and 4 except cross 3 which indicated the absence of non-allelic gene interaction in crosses 1, 2 and 4. In joint scaling test, additive component and dominant component was recorded non-significant. For this trait dominant 'h' and dominant x dominant 'l' component had similar signs indicating complementary gene action. Similar results were also reported by Mehetre *et al.* (2003).

For number of sympodia per plant, the significant additive (d) gene action was present in cross 3 and significant dominance (h) gene effect was observed cross 4 in joint scaling test. In best fit model, additive (d) component were found non-significant and dominant (h) component was found significant. Similarly, the dominant x dominant (l) gene action was found significant. The opposite signs of (h) and (l) component recorded for the cross 3 and 4 indicate duplicate gene action, while complimentary epistasis for cross 1 ('h' and 'l' components with same signs) was recorded. The present findings are supported by Rajendrakumar and Raveendran (1999), Ahmed and Mehra (2000), Iqbal and Nadeem (2003), Mehetre *et al.* (2003), Singh *et al.* (2005) and Kancherla (2011).

Additive as well as dominance effects were important for inheritance of plant height. In present investigation plant height had significant individual scaling test and joint scaling test in all four crosses indicating presence of non-allelic gene interactions. In joint Scaling test, additive (d) component and dominance (h) component were significant. The X^2 value was found significant indicating the presence of epistasis. The digenic interactions additive x additive (i), additive x dominance (j) and dominance x dominance (l) gene action was found significant in cross 1, 2, 3 and 4 which indicated expression of plant height was governed by additive (d), dominance (h), additive x additive (i), additive x dominance (j) and dominance x dominance (l) gene action. Opposite signs of dominance (h) and dominance x dominance (l) revealed that existence of duplicate gene interaction for plant height. As per the results the character had shown preponderance for additive as well as dominance gene action so it suggests that the character governed by additive component could be improved through selection, while in other cases selection in later generations of segregating population would be meaningful. The existence of significant scaling test, joint scaling test inferred presence of additive, dominance and digenic interactions. These results in are agreement with Mehetre *et al.* (2003) and Kancherla (2011).

For days to maturity, the additive as well as dominant gene effects were significant for this trait. In joint scaling test, dominance (h) component was recorded significant in two crosses. The chi-square value was found to be significant indicating the presence of epistasis or linkage. The estimates of six parameter model showed that, additive (d) and dominance (h) gene action was found significant for days to maturity in cross 1, 2, 3 and 4. The epistasis interaction was found significant which indicated expression of days to maturity was governed by additive (d), dominance (h), additive x additive (i), additive x dominance (j) and dominance x dominance (l) gene action in various crosses. Similar results in agreement with Mehetre *et al.* (2003).

Opposite signs of dominance (h) and dominance x dominance (l) revealed that existence of duplicate gene interaction in crosses 1, 2, 3 and 4 for days to maturity. Thus, it suggests that the character governed by additive component could be improved through selection. While in other cases selection in later generations of segregating population would be meaningful. Similar findings were also reported by Ahmed and Mehra (2000) and Kancherla (2011).

Boll weight was predominantly under the control of dominance effects. Among the crosses studied, none of the scale showed significant effect except scale C in cross 3. In best fit model, dominant component (h) and additive x additive (i) recorded significant for cross 3. Opposite signs of 'h' and 'l' in the cross 3 indicated duplicate type of epistasis. Similar results were reported by Reedy *et al.* (2002), Mehetre *et al.* (2003), Singh *et al.* (2005), Singh (2010) and Nidagundi *et al.* (2012).

For number of bolls per plant, the crosses 1, 2, 3 and 4 were found to be best fit for six parameter model. In the present investigation bolls per plant had significant individual scaling test and joint scaling test in all crosses indicating presence of non-allelic gene interactions except cross 1 in scale D, cross 2 in scale A and cross 3 in scale B.

The estimates of six parameter model showed that, additive (d), dominance (h), additive x additive (i), additive x dominance (j) and dominance x dominance (l) components exhibited significant in cross 1, 2, 3 and 4. In cross 1, 3 and 4, dominance component (h) exhibited greater magnitude and possessed opposite signs to that of dominance x dominance (l) component indicating the prevalence of duplicate type of epistasis. Similar duplicate type of epistasis were reported by Reddy *et al.* (2002), Mehetre *et al.* (2003), Singh *et al.* (2010) and Kancherla (2011).

In case of ginning percentage scales were significant indicated presence of non-allelic gene interaction. The estimates of six parameter model showed, additive gene action was found significant for ginning percentage in cross 3. While, predominance of dominance gene action was found in cross 1, 2, 3 and 4. The digenic interaction, additive x additive (i), in cross 1, 2, 3 and 4. Whereas additive x dominance (j), in cross 2. The dominance x dominance (l) gene action was found significant in all crosses. Opposite signs of dominance (h) and dominance x dominance (l) revealed that existence of duplicate gene interaction in crosses 1, 2, 3 and 4 for ginning percentage. So it suggests that the character governed by additive component could be improved through selection while in other cases selection in later generations of segregating population would be meaningful. Similar findings were noticed by Raveendran (199), Mehetre *et al.* (2003), Singh *et al.* (2005) and Kancherla (2011).

For micronaire value, additive as well as dominant effects were important. Among the crosses studied, in crosses 2 and 3 recorded significance for scale C, the significant scales for micronaire value indicating adequacy of additive dominance model. As the scaling test results were non-significant, Jinks and Jones (1958) three parameter model was used for estimation of component of genetic variation i.e. mean (m), additive [d] and dominance [h]. In best fit model, the mean (m) recorded significant whereas, other components were found non significant for crosses 2 and 3. Hence, this traits recorded complementary (h and l components with similar signs) and duplicate (h and l component with opposite signs) gene interaction for micronaire value. Similar finding were recorded by Mehetre *et al.* (2003).

In case of uniformity ratio, the significant individual scaling test for all the crosses and joint scaling test significant in cross 3. The X^2 values were found significant in all the crosses indicating presence of non-allelic gene interactions. The estimates of six parameter model showed that, the additive gene action was found non-significant for uniformity ratio in all four crosses which indicated expression of uniformity ratio was governed by dominance, additive x additive and dominance x dominance gene action in various respective crosses. Opposite signs of dominance (h) and dominance x dominance (l) revealed that existence of duplicate gene interaction in cross 1, 2, 3 and 4 for uniformity ratio. Duplicate gene interaction in uniformity ratio were also reported by Nadarajan and Sreerangaswamy (1992) and Phogat and Singh (2000).

For fibre length, scaling test and joint scaling test were found significant for crosses 2, 3 and 4 with significant X^2 values indicating presence on non allelic gene interactions in above crosses. The estimates of six parameter model which indicated expression of fibre length as governed by additive, dominance, additive x additive, additive x dominance and dominance x dominance gene action in respective crosses. The 'h' and 'l' components with apposite signs indicate duplicate gene action for fibre length. For fibre length duplicate epistasis were reported by Mehetre *et al.* (2003) and Kancherla (2011).

For fibre strength scaling tests were found significant for crosses 1, 2 and 3 with significant X^2 values indicating presence of non allelic interaction. The estimates of six parameter model showed dominance (h) component was found significant in crosses 1, 2 and 3. The opposite signs of dominance (h) and dominance x dominance (l) revealed that existence of duplicate gene interaction in crosses 1, 2 and 3 for fibre strength. Similar results for fibre strength were reported by Phogat and Singh (2000), Singh *et al.* (2005), Bhatti *et al.* (2006) and Kancherla (2011).

For seed cotton yield per plant, scaling tests, joint scale in test and χ^2 values were found significant for all the crosses indicating presence of non-allelic interactions. The best fit model showed that additive (d), dominance (h) additive x additive (i) and dominance x dominance (l) were found significant for in all the crosses. The opposite signs of dominance (h) and dominance x dominance (l) revealed that existence of duplicate gene interaction in cross 1, 2, 3 and 4: Thus, it suggests that the character governed by additive component could be improved through selection. While in other cases selection in later generations of segregating population would be meaningful. For seed cotton yield per plant, duplicate epistatic were also reported by several workers., Pillai and Amirthadvarathinam (1997), Rajendrakumar and Raveendran (1999), Ahmmed and Mehra (2000), Phogat and Singh (2000), Reddy *et al.* (2002), Iqbal and Nadeem (2003), Mehetre *et al.* (2003) Singh *et al.* (2005), Ismail (2007), Singh *et al.* (2010), Kancherla (2011) and Nidagundi *et al.* (2012).

In the present investigation, a considerable variation in the relative magnitude of different genetic parameters *viz.,* m, [d], [h], [i], [j] and [l] was observed from cross to cross for the same character, it may be described to the presence of variable frequency of genes with opposing and reinforcing effects in the parents involved in the crosses (Mather and Jinks, 1982, Hallauer and Miranda, 1989).

In the present study, magnitude of [d] was relatively small to that of other gene effects. This indicates that additive gene is playing a miner contribution to the inheritance of seed cotton yield and fibre quality traits. The material used in present investigation was derived from single cross. In majority of the characters, the dominance gene action is playing a major role as compared to additive gene action. It suggests that selection of high yielding genotypes would be postponed till later generations where dominance effect would have diminished.

The importance of dominance gene effects was indicated not only by its significance and relative magnitude but also by its signs positive dominance gene effects suggest its enhancing effects on the performance of different traits.

In the present study epistasis interaction were observed for the characters *viz.,* days to 50% flowering (cross 1, 2, 3 and 4, number of sympodia per plant (crosses 3 and 4), plant height (crosses 1, 2, 3 and 4), days to maturity (crosses 1, 2, 3 and 4), boll weight (cross 3), number of bolls per plant (crosses 1, 3 and 4), ginning percentage (crosses 1, 2, 3 and 4), uniformity ratio (crosses 1, 2, 3 and 4), micronaire value (cross 3), fibre length (crosses 2, 3 and 4), fibre strength (crosses 1, 2 and 3) and seed cotton yield per plant (crosses 1, 2, 3 and 4), were influenced by dominance (h), dominance x dominance (l) type of gene interaction in one cross or other (Table 21). Similar results reported by earlier workers Rajendrakumar and Raveendran (1999) for sympodia per plant, number of bolls per plant, boll weight and seed cotton yield per plant, Ahmmed and Mehra (2000) for number of bolls per plant and boll weight. Bhatti *et al.* (2006) for fibre strength and micronaire value. Kancherla (2011) for days to 50% flowering, number of sympodia per plant, number of bolls per plant, ginning percentage, uniformity ratio, micronaire value, fibre strength and seed cotton yield per plant, Such type of duplicate type of gene action will pose hindrance to a plant breeder while attempting selection in long run.

In the complementary type of gene action particularly [i] and [l] reinforce the effect of dominance, while in the duplicate type of interaction, they oppose the effect of the dominance component. For this reason, Jinks and Jones (1958) suggested that heterosis in likely to be expressed with greater magnitude in crosses, where complementary type of interaction was observed, while it may not

Table 21. Direction of dominance gene (h) and dominance x dominance (l) for various characters in 4 crosses of cotton.

Sr. No.	Characters	Gene action	Cross 1 to 4			
			1	2	3	4
1	Days to 50% flowering	(h)	-	-	-	-
		(l)	+	+	+	+
2	Number of monopodia per plant	(h)	0	0	0	0
		(l)	0	0	0	0
3	Number of sympodia per plant	(h)	+	+	-	-
		(l)	+	0	+	+
4	Plant height	(h)	-	-	-	+
		(l)	+	+	+	-
5	Days to maturity	(h)	-	-	+	-
		(l)	+	+	-	+
6	Boll weight	(h)	0	+	+	0
		(l)	0	0	0	0
7	Number of bolls per plant	(h)	+	-	-	-
		(l)	-	0	+	+
8	Ginning percentage	(h)	-	+	-	+
		(l)	+	-	+	-
9	Micronaire value	(h)	-	0	0	+
		(l)	0	0	0	0
10	Fibre length	(h)	0	-	-	-
		(l)	0	+	+	+
11	Uniformity ratio	(h)	+	+	+	+
		(l)	-	-	0	-
12	Fibre strength	(h)	+	+	-	+
		(l)	0	-	+	0
13	Seed cotton yield per plant	(h)	-	+	+	-
		(l)	+	-	-	+

+ = Significant positive direction
- = Significant negative direction
0 = Non-significant effect

be observed at all crosses showing duplicate type of interaction. In present investigation, number of monopodia per plant (cross 3), number of sympodia per plant (cross 1) and number of bolls per plant (cross 2) exhibited complementary type of epistasis. Similar findings were also reported by Mehetre *et al.* (2003), Ismail (2007) and Kancherla (2011).

The significance of additive x additive (i) components indicates the preponderance of additivity over non-additivity. In such cases, in a particular cross to improve the trait pedigree method will be rewarding such gene effects were noticed in certain crosses for various traits in the present study *viz.,* days to 50% flowering (cross 1, 2, 3 and 4), number of sympodia per plant (cross 1, 3 and 4), plant height (cross 1, 2, 3 and 4), days to maturity (cross 1, 2, 3 and 4), boll weight (cross 3), number of bolls per plant (cross 1, 2, 3 and 4), ginning percentage (cross 1, 2, 3 and 4), uniformity ratio (cross 1, 2, 3 and 4), fibre length (cross 2 and 3), fibre strength (cross 1 and 3) and seed cotton yield per plant (cross 1, 2, 3 and 4) and these interactions would enhance the isolation of superior recombination's from the segregating generations.

The epistatic component of additive x dominance (j) gene effects were found to be of considerable importance and observed in certain crosses for days to 50% flowering (cross 1, 2, 3 and 4), number of sympodia per plant (cross 3 and 4), plant height (cross 2, 3 and 4), days to maturity (cross 2, 3 and 4), number of bolls per plant (cross 1, 2 and 4), ginning percentage (cross 2), uniformity ratio (cross 3), fibre length (cross 2, 3 and 4) and seed cotton yield per plant (cross 4). These findings are in agreement with the earlier findings of Rajendrakumar and Raveendran (1999), Ahmmed and Mehra (2000), Iqbal and Nadeem 2003, Bhatti *et al.* (2006), Ismail (2007) and Kancherla (2011).

In present study, the magnitude of dominance effect was higher than additive effect for all the characters except number of monopodia per plant, boll weight and micronaire value indicating the possibility of heterosis breeding for improvement of those traits.

The presence of dominance and epistatic effects for different traits in all the crosses would slow down the progress of selection. Hence, suggested the use of intermating of selections followed by visual selection in early segregating generations, which would simultaneously exploit both type of gene effects. Further, this approach is likely to break some undesirable linkages resulting in the establishment of rare useful recombination.

5.7 PERFORMANCE OF FIVE BEST CROSSES

The performance of five best crosses based on *per se* performance of seed cotton yield are presented in Table 22. The best five crosses were PH 1076 x PKV Rajat, NH 615 x PKV Rajat, PH 1076 x NH 452, NH 615 x NH 452 and NH 615 x NH 625. Theses crosses also exhibited significant heerosis in desired direction for various traits.

The cross PH 1076 x PKV Rajat exhibited highest *per se* performance, SCA effect and significant heterosis in desired direction for seed cotton yield and fiber properties. This cross registered significant SCA effects for eight out of fifteen characters. Among the five best cross combinations, PH 1076 x PKV Rajat showed the highest magnitude of standard heterosis (39.02 and 53.34%) over NHH 44 and DCH 32. Also the cross NH 615 x PKV Rajat recorded better *per se* performance, SCA effect and significant heterosis (26.96 and 40.97%) over NHH 44 and DCH 32. This cross recorded significant SCA effect for seven out of fifteen traits.

Among the crosses PH 1076 x NH 452, NH 615 x NH 452 and NH 615 x NH 625 registered well *per se* performance and significant heterosis for seed cotton yield and fibre quality parameters.

Table 22. *Per se* performance, GCA effects of parents, SCA effects of crosses and heterosis for seed cotton yield

Sr. No.	Crosses	*Per se* performance (g)	Seed cotton yield/plot (g)	Seed cotton yield kg/ha	GCA		SCA	Heterosis (%)			
					P-I	P-II		MP	BP	SH-I (NHH 44)	SH-II (DCH 32)
1.	PH 1076 x PKV Rajat	109.33	1968.00	2733.33	313.202**	167.238**	345.845**	45.49**	40.19**	39.02**	54.34**
2.	NH 615 x PKV Rajat	99.87	1797.66	2496.66	239.619**	345.845**	182.762*	41.61**	38.12**	26.98**	40.97**
3.	PH 1076 x NH 452	97.29	1751.33	2432.33	313.202**	106.953**	105.131	28.75**	24.76**	23.71**	37.36**
4.	NH 615 x NH 452	88.88	1600.00	2221.66	239.619**	106.953**	31.953	25.27**	21.49**	12.99**	25.45**
5.	NH 615 x NH 625	87.37	1572.66	2184.00	239.619**	28.048	9.286	28.01**	27.10**	11.08	23.32**

*,** indicated significant at 5 and 1% level, respectively.

Summary and Conclusions

CHAPTER-VI

SUMMARY AND CONCLUSION

The present investigation entitled "Studies on heterosis, combining ability and gene action for fibre characters, yield and its components in intra and interspecific hybrids of upland cotton (*Gossypium sp.*) was undertaken to estimate genetic parameters like combining ability, heterosis, heritability, correlation and path coefficients on fibre quality, yield and yield contributing characters. Further, through generation mean analysis the nature and magnitude of gene effects were also investigated.

Twenty eight (28) crosses were obtained by seven (7) lines and four (4) testers in L x T design to know the combining ability, gene action and heterosis for fibre quality, yield and yield component traits. Variability, heritability, genetic advance as per cent of mean, correlations and path matrix were worked out for the traits *viz.,* days to 50% flowering, number of monopodia per plant, number of sympodia per plant, plant height, days to maturity, boll weight, number of bolls per plant, ginning percentage, micronaire value, fibre length, uniformity ratio, fibre strength, seed cotton yield per plant, seed cotton yield per plot and seed cotton yield quintal per ha.

The partitioning the gene effects through generation mean analysis was carried out in six (6) generations of four (4) inter and intraspecific cross combinations (NH 545 x NH 452; NH 635 x PKV Rajat; PH 1060 x Suvin and LRA 5166 x Suvin). Joint scaling test of Cavelli (1952) and best fit model of Mather and Jinks (1982) were adopted to trace out precise estimates, magnitude and direction of genetic parameters *viz.,* m, (d), (h), (i), (j) and (l).

Analysis of variance revealed significant differences among the genotypes for various characters studied indicating the presence of ample variation for effective selection. High PCV and GCV were recorded for micronaire value, seed cotton yield per plant and seed cotton yield per plot and moderate were observed for number of bolls per plant and fiber length. High PCV and GCV were recorded in majority of character indicated that most of characters controlled by genetically and highly sensitive to environment. High heritability estimates coupled with high genetic advance were observed for fiber length, micronaire value and seed cotton yield per plant. This indicate there is chance for improvement in character through seleciton.

Combining ability revealed significant differences for most of the characters within parents and crosses. In lines, significant differences were observed for number of monopodia per plant, plant height, number of bolls per plant, micronaire value, seed cotton yield per plant, seed cotton yield per plot and seed cotton yield quintal per ha., where in testers significant differences were recorded for days to 50% flowering, days to maturity, boll weight, ginning percentage, fibre length, uniformity ratio, fibre strength, seed cotton yield per plant, seed cotton yield per plot and seed cotton yield quintal per ha. (except for number of monopodia per plant, number of sympodia per plant, plant height, number of bolls per plant and micronaire value). In line x tester significant differences were noted for all the characters (except for number of monopodia per plant and ginning percentage). However, in parent vs crosses significant differences were observed for all the traits studied, except for number of monopodia per plant, boll weight, micronaire value, seed cotton yield per plot and seed cotton yield quintal per ha.

The preponderance of non-additive gene action in all the characters studied which may be exploits by hybrid development programmes.

Among the lines, PH 1076 and among the testers, PKV Rajat was identified as best general combiners for yield, which was also good combiner for one or other fibre quality characters. The crosses involving the lines NH 545, PH 1076 and LRA 5166 were identified as best combiners for earliness. Based on these parental lines hybrid NH 545 x NH 452, NH 615 x

Suvin and LRA 5166 x NH 625 were identified as early hybrids. Based on SCA effects, the intraspecific crosses, PH 1076 x PKV Rajat, NH 615 x PKV Rajat and PH 1076 x NH 452 were identified as best specific combiner for yield and fibre traits. For fibre quality traits, both inter and intraspecific cross combinations i.e., LRA 5166 x Suvin, NH 635 x PKV Rajat and PH 1076 x Suvin recorded significant negative SCA effect for micronaire value and LRA 5166 x Suvin, PH 1076 x Suvin and PH 1060 x Suvin exhibited for fibre length and NH 635 x NH 625, NH 635 x NH 452, PH 1060 x Suvin and NH 545 x PKV Rajat exhibited positive SCA effects for fibre strength.

Significant heterosis in desired direction was observed in many crosses for various traits under study. The intraspecific hybrid PH 1076 x PKV Rajat exhibited the highest significant positive heterosis followed by NH 615 x PKV Rajat and PH 1076 x NH 452 over mid parent value. The estimates of heterobeltiosis for seed cotton yield per plant the cross PH 1076 x PKV Rajat registered highest positive significant heterosis followed by NH 615 x PKV Rajat and NH 615 x NH 625 over better parent. The cross PH 1076 x PKV Rajat recorded highest positive significant heterosis followed by NH 615 x PKV Rajat and PH 1076 x NH 452 over check NHH 44 and DCH 32 respectively. It is concluded that intraspecific crosses PH 1076 x PKV Rajat, NH 615 x PKV Rajat and PH 1076 x NH 452 were identified as promising hybrids for seed cotton yield and fibre quality characters. Interspecific hybrids LRA 5166 x Suvin, NH 615 x Suvin and PH 1076 x Suvin showed the better fibre quality and seed cotton yield.

The significant positive association of number of monopodia per plant, number of sympodia per plant, boll weight, number of bolls per plant, ginning percentage with seed cotton yield per plant was noticed at phynotypic and genotypic level. Boll weight has significant and positive association with ginning percentage and uniformity ratio. Significant negative association of uniformity ratio was recorded with fibre strength.

Path coefficient analysis revealed that number of bolls per plant, ginning percentage and fibre length were found to have maximum direct positive effects on seed cotton yield per plant and number of bolls per plant exhibited indirect effect on seed cotton yield per plant via number of sympodia, fibre length, number of monopodia per plant and plant height. Among the fibre quality traits, fibre length showed negative indirect effect on yield via ginning percentage, micronaire value and uniformity ratio, while ginning percentage exhibited indirect positive effect via number of sympodia per plant, boll weight, number of bolls per plant, micronaire value and uniformity ratio on seed cotton yield per plant. Path coefficient analysis revealed that bolls per plant, ginning percentage and fibre length should be given more emphasis in cotton yield improvement programme.

Estimates of gene effects through joint scaling test of three and six parameter model in four crosses for thirteen characters were investigated. It was noticed that simple additive dominance model exhibited lack of good fit for all the traits indicating the role of non-allelic interactions. In the present study epistatic interactions were observed for the major characters, *viz.*, number of sympodia per plant (duplicate type in crosses 3 and 4 while, complementary type in cross 1), plant height (duplicate type in crosses 1, 2, 3 and 4), days to maturity (duplicate type for crosses 1, 2, 3 and 4), boll weight (duplicate type for cross 3), number of bolls per plant (duplicate type for crosses 1, 3 and 4 and complementary type for cross 2), ginning percentage, uniformity ratio and seed cotton yield per plant (duplicate type for crosses 1, 2, 3 and 4), fibre length (duplicate type for crosses 2, 3 and 4) and fibre strength (duplicate type for crosses 1, 2 and 3).

Three and six parameter model schemes for same trait in different crosses were noticed in the present investigation. It was due to different parents involved with variable gene frequency with opposing and reinforcing gene effects. The magnitude of (h) was high to that of other gene effects.

A perusal of generation mean analysis indicated that non-allelic interactions and epistasis is the integral part of genetic architecture of the material used in experiment and breeder cannot ignore it. Hence, it can be stated that, to break the linkage between gene constellations reciprocal recurrent selection or diallel selective mating systems are the breeding strategies proposed for the improvement of yield and yield attributes in cotton.

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Appendix

Appendix – I

Analysis of variance of six generations for thirteen characters in four crosses of cotton

Sr. No.	Source	d.f	Mean Square			
			Cross- I	Cross- II	Cross- III	Cross- IV
1.	Days to 50% flowering					
	Replication	2	1.16	1.16	0.66	0.17
	Generation	5	47.83**	28.10**	47.06**	54.86**
	Error	10	0.50	0.96	0.27	0.59
2.	Number of monopodia per plant					
	Replication	2	0.00	0.00	0.01	0.00
	Generation	5	0.06**	0.06**	0.15**	0.07**
	Error	10	0.00	0.00	0.01	0.00
3.	Number of sympodia per plant					
	Replication	2	0.38	0.04	0.15	0.38
	Generation	5	20.85**	3.66**	25.61**	13.47**
	Error	10	0.45	0.40	0.36	0.64
4.	Plant height					
	Replication	2	5.05	0.96	0.85	0.40
	Generation	5	68.32**	162.54**	78.66**	559.78**
	Error	10	1.38	0.64	0.79	0.88
5.	Days to maturity					
	Replication	2	2.72	1.04	0.52	0.07
	Generation	5	86.88**	141.37**	227.10**	682.38**
	Error	10	178	0.29	0.54	0.61
6.	Boll weight					
	Replication	2	0.00	0.00	0.05	0.00
	Generation	5	0.06**	0.06**	1.21**	0.15**
	Error	10	0.00	0.00	0.02	0.00
7.	Number of bolls per plant					
	Replication	2	1.55	0.45	1.70	0.06
	Generation	5	23.38**	28.76**	91.36**	67.74**
	Error	10	0.62	1.33	2.81	0.39
8.	Ginning percentage					
	Replication	2	0.05	0.42	0.01	0.01

Sr. No.	Source	d.f	Mean Square			
			Cross- I	Cross- II	Cross- III	Cross- IV
	Generation	5	3.68**	8.63**	7.11**	6.13**
	Error	10	0.43	0.93	0.22	0.29
9.	Micronaire value					
	Replication	2	0.01	0.01	0.00	0.00
	Generation	5	0.04**	0.51**	0.42**	0.47**
	Error	10	0.00	0.05	0.01	0.00
10.	Fibre length					
	Replication	2	0.81	2.23	0.09	0.01
	Generation	5	1.18*	15.09**	38.19**	38.25**
	Error	10	0.22	2.35	0.99	0.44
11.	Uniformity ratio					
	Replication	2	0.36	0.12	0.09	0.10
	Generation	5	1.93.**	5.21**	4.62**	10.18**
	Error	10	0.21	0.37	0.05	0.08
12.	Fibre strength					
	Replication	2	0.22	0.22	0.14	0.76
	Generation	5	2.32**	2.25**	3.47**	7.12**
	Error	10	0.07	0.10	0.10	0.42
13.	Seed cotton yield per plant					
	Replication	2	7.02	0.57	0.09	0.35
	Generation	5	184.35**	248.38**	28.94**	256.68**
	Error	10	19.81	0.44	0.52	0.33

*,** indicated significant at 5 and 1 per cent, respectively.

APPENDIX-II

Weekly weather data during crop growth period for the year 2012-13 at Parbhani

MW	Period	Rainfall (mm)	R.D.	Temperature °C		Humidity (%)		EVP (mm)	BSS (hrs.)	W. V. (km/h)
				Max.	Min.	AM	PM			
27	02-08 July	37.3	2.0	33.0	23.4	83	62	4.5	6.1	6.1
28	09-15 July	27.2	3.0	33.0	23.2	87	55	4.5	5.0	5.0
29	16-22 July	134.9	6.0	30.3	23.1	93	69	2.9	4.7	4.7
30	23-29 July	21.0	4.0	30.0	23.4	88	70	1.8	6.8	6.8
31	30-05 Aug	18.9	2.0	31.1	22.8	89	59	3.0	7.1	7.1
32	06-12 Aug	5.9	0.0	31.2	22.7	88	61	3.3	6.2	6.2
33	13-19 Aug	4.8	1.0	31.0	21.5	86	65	5.1	4.7	4.7
34	20-26 Aug	35.4	3.0	31.1	22.2	92	60	4.1	4.3	4.3
35	27-02 Sept	40.6	3.0	31.7	23.0	90	67	4.6	3.7	3.7
36	03-09 Sep	108.4	5.0	30.2	22.3	95	72	4.0	4.3	4.3
37	10-16 Sep	28.4	1.0	31.2	22.1	90	62	5.2	5.5	3.9
38	17-23 Sep	61.9	3.0	30.8	22.2	90	68	4.4	6.0	3.9
39	24-30 Sep	21.8	2.0	32.1	21.6	91	58	4.3	7.8	3.2
40	01-07 Oct.	49.0	2.0	30.4	22.8	89	68	4.1	3.3	3.6
41	08-14 Oct.	0.0	0.0	33.3	18.6	82	38	5.1	9.3	2.0
42	15-21 Oct.	0.0	0.0	33.9	15.6	73	26	5.8	10.1	3.2
43	22-28 Oct.	0.0	0.0	32.2	19.1	69	36	5.2	6.7	4.0
44	29-04 Nov.	3.2	0.0	30.7	17.4	78	43	5.1	7.4	4.8
45	05-11 Nov.	1.0	0.0	31.2	16.7	80	38	3.9	8.2	2.2
46	12-18 Nov.	0.0	0.0	30.6	12.5	72	25	4.8	8.6	3.2
47	19-25 Nov.	0.0	0.0	30.4	28.5	74	34	5.5	9.8	2.7
48	26-02 Dec.	0.0	0.0	31.9	16.4	80	39	4.2	7.6	2.4
49	03-09 Dec.	0.0	0.0	31.2	14.6	67	35	5.1	9.6	3.4
50	10-16 Dec.	0.0	0.0	32.8	15.3	67	33	4.8	9.7	2.2
51	17-23 Dec.	0.0	0.0	30.2	11.6	75	29	4.9	8.8	4.0
52	24-31 Dec.	0.0	0.0	29.1	9.2	70	29	4.9	9.3	3.5
50	10-16 Dec.	0.5	0.0	28.4	12.2	80	41	3.3	9.0	3.0
51	17-23 Dec.	0.0	0.0	28.0	5.8	74	24	3.9	10.2	2.8
52	24-31 Dec.	0.0	0.0	29.1	11.2	71	39	3.9	9.7	2.7
1	01-07 Jan.	1.0	0.0	31.9	14.3	73	32	5.1	8.4	2.8
2	08-14 Jan.	0.0	0.0	29.4	10.3	76	27	4.7	8.4	3.0
Total		601.2	38							

Conted...

Weekly weather data during crop growth period for the year 2013-14 at Parbhani

MW	Period	Rainfall (mm)	R.D.	Temperature °C		Humidity (%)		EVP (mm)	BSS (hrs.)	W. V. (km/h)
				Max.	Min.	AM	PM			
25	18-24 June	24.0	1.0	33.3	23.0	85	61	5.4	6.0	7.1
26	25-01 July	41.8	3.0	30.1	22.5	85	64	4.7	2.9	6.6
27	02-08 July	80.1	4.0	32.1	22.6	92	62	5.1	5.4	5.9
28	09-15 July	96.4	4.0	29.2	22.7	90	79	3.4	2.2	4.5
29	16-22 July	154.0	5.0	26.7	22.0	93	84	2.9	0.8	5.7
30	23-29 July	50.5	2.0	28.6	22.6	86	65	3.7	2.5	5.3
31	30-05 Aug	77.5	3.0	28.3	21.8	91	75	3.5	2.8	6.5
32	06-12 Aug	19.7	2.0	29.8	22.5	89	67	4.6	3.2	4.6
33	13-19 Aug	59.8	4.0	30.5	22.7	91	65	3.6	4.3	4.3
34	20-26 Aug	9.3	2.0	28.5	21.7	89	71	4.3	1.5	7.2
35	27-02 Sept	0.0	0.0	31.0	22.9	82	59	4.6	5.5	3.9
36	03-09 Sep	29.8	1.0	33.1	22.6	85	61	5.9	8.1	4.3
37	10-16 Sep	84.5	5.0	31.6	22.2	92	63	3.2	6.1	2.8
38	17-23 Sep	150.6	5.0	30.5	22.4	93	67	3.9	3.6	4.3
39	24-30 Sep	0.0	0.0	32.2	22.0	86	53	5.0	8.0	3.7
40	01-07 Oct.	40.8	4.0	31.5	22.8	89	64	4.8	5.8	3.4
41	08-14 Oct.	66.2	5.0	30.7	21.7	93	70	4.4	6.1	3.0
42	15-21 Oct.	0.0	0.0	32.5	19.5	83	46	5.2	8.5	2.3
43	22-28 Oct.	8.3	2.0	30.8	21.2	85	56	4.2	6.1	5.1
44	29-04 Nov.	0.0	0.0	31.7	15.0	78	37	5.1	9.2	2.3
45	05-11 Nov.	0.0	0.0	30.4	13.3	71	36	5.2	8.8	2.9
46	12-18 Nov.	0.0	0.0	29.2	12.1	79	35	4.9	7.9	3.8
47	19-25 Nov.	14.0	2.0	30.4	14.5	81	41	4.6	7.6	3.8
48	26-02 Dec.	0.0	0.0	30.7	15.9	75	43	5.3	0.0	3.7
49	03-09 Dec.	26.6	1.0	29.0	12.3	84	35	4.4	8.6	2.7
50	10-16 Dec.	0.0	0.0	28.9	7.5	80	28	3.9	9.7	2.3
51	17-23 Dec.	0.0	0.0	29.5	9.3	71	33	4.2	9.5	2.3
52	24-31 Dec.	0.0	0.0	28.5	11.3	75	39	4.7	8.2	3.4
1	01-07 Jan.	0.0	0.0	29.2	11.5	79	36	4.4	8.7	2.9
2	08-14 Jan.	0.0	0.0	30.0	13.1	79	36	4.3	8.2	3.3
3	15-21 Jan	0.0	0.0	4.4	2.1	10	0	0.6	1.0	0.4
Total		**1033.8**	**55**							

Abstract

DEPARTMENT OF AGRICULTURAL BOTANY

V.N.M.K.V., PARBHANI

Name of student : Patil H.V.
Reg. No. : 11P/2010A

Research Guide : Dr. D.B. Deosarkar
Designation: Head, Department of Agril. Botany

ABSTRACT

The present investigation on 'Studies on heterosis, combining ability and gene action for fibre characters, yield and its components in intra and interspecific hybrids of upland cotton (*Gossypium sp.*)' was carried out at Cotton Research Scheme, Vasantrao Naik Marathwada Krishi Vidyapeeth, Parbhani (MS) during Summer, 2012-13 and *Kharif*, 2013-14 to study the combining ability and heterosis for quality and yield characters. Further, an attempt was made to trace out best parents and crosses for further breeding programmes and also to know the gene action controlling the traits through generation mean analysis for designing appropriate breeding strategy.

In this direction, seven lines and four testers were crosses in L x T design to generate 28 hybrids and evaluated with checks NHH 44 and DCH 32 to know the combining ability of parents and crosses. Since L x T design does not provides comprehensive picture on gene action governing the traits, the generation mean analysis through joint scaling test was done in four crosses for eleven characters.

High PCV and GCV were recorded for micronaire value, seed cotton yield per plot and seed cotton yield quintal per ha. and moderate were observed for seed cotton yield per plant and fiber length. High heritability estimates coupled with high genetic advance were observed for fiber length and seed cotton yield per plant. Estimates of components of variance and their ratio (σ^2 gca / σ^2sca) indicated the preponderance of non-additive gene action for days to 50% flowering, number of monopodia per plant, number of sympodia per plant, plant height, days to maturity, boll weight, number of bolls per plant, ginning percentage, micronaire value, fibre length, uniformity ratio, fibre strength, seed cotton yield per plant' seed cotton yield per plot and seed cotton yield quintal per ha.

Combining ability revealed significant differences for most of the characters within parents and crosses. In lines, significant differences were observed number of monopodia per plant, plant height, number of bolls per plant, micronaire value, seed cotton yield per plant, seed cotton yield per plot and seed cotton yield quintal per ha., where in testers significant differences were recorded days to 50% flowering, days to maturity, boll weight, ginning percentage, fibre length, uniformity ratio, fibre strength, seed cotton yield per plant, seed cotton yield per plot and seed cotton yield quintal per ha. (except for number of monopodia per plant, number of sympodia per plant, plant height, number of bolls per plant and micronaire value). In line x tester significant differences were noted for all the characters (except for number of monopodia per plant and ginning percentage). However, parents vs crosses significant differences were observed for all the traits studied, except for number of monopodia per plant, boll weight, micronaire value, seed cotton yield per plot and seed cotton yield quintal per ha.

Among the lines, PH 1076 and among the testers, PKV Rajat was identified as best general combiner for yield, which was also observed to be good combiners for one or other fibre quality characters. The crosses involving the lines NH 545, PH 1076 and LRA 5166 among the testers were identified as best combiners for earliness. Based on SCA effects, the intraspecific crosses, PH 1076 x PKV Rajat, NH 615 x PKV Rajat and PH 1076 x NH 452 were identified as best specific combiner for yield and fibre traits. For fibre quality traits, both inter and intra specific cross combinations i.e., LRA 5166 x Suvin, NH 635 x PKV Rajat and PH 1076 x Suvin recorded significant negative SCA effect for micronaire value and LRA 5166 x Suvin, PH 1076 x Suvin and PH 1060 x Suvin exhibited for fibre length and NH 635 x NH 625, NH 635 x NH 452, PH 1060 x Suvin and NH 545 x PKV Rajat exhibited positive SCA effects for fibre strength.

Significant heterosis in desired direction was observed in many crosses for various traits under study. The intraspecific hybrid PH 1076 x PKV Rajat exhibited highest significant positive heterosis followed by NH 615 x PKV Rajat and PH 1076 x NH 452 over mid parent, better parent and standard check i.e., NHH 44 and DCH 32.

The significant positive association of number of monopodia per plant, number of sympodia per plant, boll weight, number of bolls per plant, ginning percentage, with seed cotton yield per plant obtained in the present study. Boll weight has significant and positive association with ginning percentage and uniformity ratio. Significant negative association of uniformity ratio and micronaire with fibre strength. Path coefficient analysis revealed that number of monopodia per plant, number of sympodia per plant, number of bolls per plant and ginning percentage were found to have maximum direct positive effect on seed cotton yield per plant and number of bolls per plant exhibited indirect effect on seed cotton yield *viz.,* number of sympodia, fibre length, number of monopodia per plant and plant height.

Generation mean analysis through joint scaling tests deciphered that simple additive dominance model exhibited lack of good fit for all the traits in four crosses studied, indicating the role of non-allelic interactions. Dominance and epistatic interactions played a major role in the inheritance of yield and fibre quality characters in cotton. It can categorically stated that reciprocal recurrent selection or diallel selective mating system are the need of the hour to modify the genetic architecture of cotton for attaining higher yields with desirable fibre properties.

In the present study, it is concluded an intraspecific cross PH 1076 x PKV Rajat and NH 615 x PKV Rajat were identified as promising heterotic hybrids for seed cotton yield and boll number. An interspecific cross LRA 5166 x Suvin was identified as good hybrid for fibre properties along with seed cotton yield. Reciprocal recurrent selection or diallel mating system were suggested as the breeding strategies for the improvement of yield and fibre quality traits in cotton.