DEVELOPMENT AND EXPLOITATION OF HETEROTIC POOLS OF HIRSUTUM AND BARBADENSE FOR DEVELOPING POTENTIAL INTER SPECIFIC HYBRIDS, MOLECULAR MARKER AND GENETIC TRANSFORMATION STUDY IN COTTON

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

Doctor of Philosophy

In

Genetics and Plant Breeding

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CONTENTS

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LIST OF TABLES

Contd....

Table No.	Title
22.	Direct and indirect phenotypic effects of seed cotton yield and different quantitative characters in Line x Tester inter specific crosses (YHB)
23.	Analysis of SSR patterns generated using 40 primers in cotton genotypes
24.	Similarity co-efficients for 32 parents computed from SSR molecular marker data
25.	Genetic distance for 32 parents computed from SSR molecular marker data
26.	Correlation co-efficient of genetic distance (GD) with F_1 performance and heterosis
27.	Number of cotton seedlings co-cultivated, established and transformed in *planta* genetic transformation study
28.	Combining ability status of most potential Line x Tester inter specific crosses (YHB) with respect to yield
29.	Pooled scores of hirsutum testers and barbadense lines based on Simple pooled *gca* score
30.	Pooled scores of hirsutum testers and barbadense lines based on per cent pooled *gca* score
31.	Pooled scores of hirsutum testers and barbadense lines based on weighted per cent pooled *gca* score
32.	Top desirable best HB hybrids with *per se* performance for 5 quantitative characters
33.	Top desirable barbadense lines with *per se* performance for 12 quantitative characters
34.	Range of heterosis over mid parent, standard checks for different quantitative characters recorded in derived F_1 crosses
35.	*Per se* performance and heterosis of top three potential derived F_1 crosses for different quantitative characters
36.	*Per se* performance of top three potential derived F_1 crosses, population mean and commercial checks mean for different quantitative characters
37.	Efficiency of testers against the F_4 barbadense lines in terms of seed cotton yield (kg/ha)
38.	Mean and per cent improvement of derived F_1 crosses involving F_4 lines of cross bench mark crosses for seed cotton yield (transgressive segregation)
39.	Combining ability status of most potential derived F_1 crosses with respect to seed cotton yield (kg/ha)

LIST OF FIGURES

LIST OF PLATES

LIST OF APPENDICES

INTRODUCTION

Cotton, being the king of fibers in preparing human apparel has played a key role in civilization of mankind. Cotton is providing livelihood directly and indirectly to over 60 million people and accounting for about 16 per cent of India's export earnings.

India has a pride place in the global cotton scenario due to several distinct features such as the largest cotton growing area, cultivation of all the four cultivated species, large area under tetraploid cotton, possibly the only country to grow hybrid cotton involving different species of cotton, native home of old world cultivated cotton and wide diversity in agro-climatic conditions under which cotton is grown. There is maximum diversity in the quality of cotton grown in India ranging from 5s counts to 120s counts.

India is the largest cotton growing country with an area of 117.73 lakh/ ha and production of 356.10 lakh bales of cotton lint with 496.39 kg/ha productivity. Karnataka produces around 12.00 lakh bales of cotton lint from an area of 4.85 lakh/ ha with a productivity of 430.35 kg/ha (Anon., 2013). There is a phenomenal impact *Bt* cottons on Indian cotton cultivation. One of the main reasons for increase in area and production of cotton in past decade has been the cultivation of *Bt* cotton.

India was the first country to introduce commercial cultivation of intra hirsutum hybrids in 1960s and then inter specific hybrids in 1970s. The success of inter specific hybrids has led to overcome the acute shortage of ELS (Extra Long Stable) cotton which the country was experiencing during 1970s and the prominent hybrids from University of Agricultural Sciences, Dharwad namely Varalakshmi and DCH 32 were instrumental in saving very critical foreign exchange running to hundreds of crores of rupees. Later in 90s, due to increase of severity of pests and the inherent susceptibility to them which was contributed by barbadense parents, the performance of inter specific hybrids declined. This popularity of inter specific hybrids declined and the intra hirsutum hybrids have occupied major area under hybrids.

During *Bt* era, though hybrids have occupied over 90 per cent area of cotton cultivated in India, there is a very clear decline in diversity of cotton in terms of fiber length classes. There is a steep rise in production of intra hirsutum hybrids, while production of extra long staple and short staple cotton has come down drastically. The situation of ELS inter specific hybrid cultivation has worsened in *Bt* era that even though india boasts of exporting cotton, import of ELS cotton has become inevitable. The main reason for the decline in realized potentiality of inter specific hybrids has been the lack of prioritized research on improving potentiality of barbadense cotton and developing hybrid oriented populations based on them and utilizing them in deriving potential inter specific hybrids. Genetic improvement of barbadense varietal lines for both productivity and fiber quality has been very limited. The standard indian barbadense Suvin, is still regarded as a unique fibre class in international market, but the productivity of barbadense varieties like Suvin has reduced so much, that it is no more remunerative to cultivate. There is an urgent need to develop strong base material to serve the cause of developing new variety of barbadense and this improved barbadense varietal base, is essential for improving performance of inter specific hybrids.

There is a constant need to develop more potential hybrids and adopt noval approaches for improving hybrid performance. In cross pollinated crops like maize, heterotic populations are developed and exploited through population improvement schemes meant for improving combining ability. Such programmes are integral part of hybrid breeding programme and these populations are shared among breeders and used further to obtain more potential hybrids. Studies have shown that even in cotton it is possible to adopt these concepts with suitable modifications in the procedure to suit the mating system of self pollinated crops (Patil and Patil, 2003 and Patil *et al* 2007).

In several studies conducted on improving combining ability in often cross pollinated crops like red gram (Patil, 1997), sorghum (Patil and Pandit, 1991 and Madhusudhana, 1993) and cotton (Patil and Patil, 2003, Mallikarjun, 2005, Somashekar, 2006 and Rama Krishna 2008), attempts were made to exploit the potentiality of the simple traditional method of practicing selection in segregating generations (obtained though hybridization) and utilizing the recombinational variability for improving combining ability as a trait. These studies have clearly indicated that combining ability of lines could be improved by following selection for combining ability (as a trait) in segregating generations.

Mallikarjun (2005), Patil and Patil (2003) and Somashekhar (2006), worked on developing intra hirsutum heterotic population for creating recombinational variability for combining ability. The studies have confirmed that it is possible to develop potential intra hirsutum hybrids through

exploitation of recombinational variability for combining ability. There are no studies to evidence the possibility of exploiting recombinational variability for combining ability in developing potential inter specific hybrids. Realizing the need for developing potential inter specific (H×B) hybrids, a detailed study was initiated at University of Agricultural Sciences, Dharwad during 2007/08 to identify hirsutum and barbadense genotypes capable of giving potential inter specific hybrids.

Based on this study two barbadense and four hirsutum lines giving best hybrid (H×B) combinations between them were selected. To create recombinational variability, the two barbadense genotypes were crossed to get F_1 and it was advanced to F_4 generation. In the present phase of this continuing study, the F_4 lines of this population (barbadense x barbadense) is utilized for assessing recombinational variability for combining ability against selected hirsutum testers. Nature and magnitude of variability for combining ability was assessed against each hirsutum tester included in the heterotic box.

In this study new population of F_4 lines was developed by crossing DB 533 and DB 534. The improvement seen in the barbadense lines was assessed in terms of productivity and fiber quality traits. The variability for combining ability of these F_4 lines was assessed in the study by crossing them with four hirsutum testers. These testers were decided upon based on evaluation of the hybrid involving parental barbadense lines with these hirsutum testers.

Molecular markers have been a valuable tool in cotton breeding investigations. Various marker techniques used in cotton include Restriction Fragment Length Polymorphism (RFLP), Random Amplified Polymorphic DNA (RAPD), Amplified Fragment Length Polymorphism (AFLP), Simple Sequence Repeats (SSR), Inter Simple Sequence Repeats (ISSR) and Sequence Related Amplified Polymorphism (SRAP). They have large number of applications like characterization of gene pool, DNA fingerprinting, phylogenetic analysis, molecular dissection of complex traits, and characterization of genome organization. Several challenges have been overcome in cotton genomic research and now genetic linkage maps of cotton have been developed based on both intra specific (intra hirsutum) and inter specific (*Gossypium hirsutum x Gossypium barbadense*) population and the QTLs responsible for leaf shapes, plant trichomes, photopheriodism, stomatal conductance, disease resistance, yield and fibre quality traits have been mapped.

SSR or microsatellites are short, tandemly repeated DNA sequence motifs that consist of two to six nucleotide core units and were initially described in humans (Litt and Lutty, 1989). They are highly abundant in eukaryotic genome but also occur in prokaryotes at lower frequencies.

These small repetitive DNA sequences provide the basis for PCR-based multi allelic, co-dominant genetic marker system. The high incidence of detectable polymorphism through changes in repeat numbers is caused by an intramolecular mutation mechanism called DNA slippage (Gupta *et al.,* 1996).

Parental genetic divergence has been found to increase the potential of heterosis in crosses among lines. This suggests the use of indirect measures of genetic diversity as possible predictors for heterosis response of hybrids. Experimental data accumulated since the early work of East (1908) and Shull (1909) suggest that heterosis is a function of heterozygosity at a large loci. Enhancing the number of heterozygous loci by crossing less related lines or populations genetically increases the level of heterosis observed in crosses at least over a wide range of genetic diversity.

Recent advances in plant molecular biology techniques have given birth to unprecedented opportunities for the introduction of novel traits into crops. The potential impact of these powerful methodologies on the genetic improvement of crop plants of economic importance has generated considerable interest, enthusiasm and optimism in the scientific community and is in part responsible for the rapid expansion of biotechnology industry. The anticipated role of plant biotechnology in agriculture is attributable to the production of genetically superior plants as well as elegant demonstrations in model experimental systems that new hybrids, mutants and genetically engineered plants can be obtained by these methods. The world wide pre-harvest losses due to insect pests despite the use of insecticides are 15% of total production representing over US$ 100 billion (Krattiger and Anatole, 1997).

Inter specific hybrids are known to be more susceptible to biotic stress. It is hence important to develop *Bt* version for inter specific hybrid. Presently, the *Bt* gene commercialized are owned by private sector. It is necessary to develop public sector's *Bt* event and commercialize them. UAS Dharwad is involved in developing public sector *Bt* cotton genotypes.

Production of transgenic plants is a routine process for many crop species. Transgenes are introduced into plants to confer novel traits such as improved nutritional qualities, tolerance to pollutants, resistance to pathogens and for studies of plant metabolism. Nowadays, it is possible to insert genes from plants evolutionary distant from the host plant, as well as from fungi, viruses, bacteria and even animals. Genetic transformation requires penetration of the transgene through the plant cell wall, facilitated by biological or physical methods (Electroporation, Biolistics, Vacuum infiltration, Ultrasound-mediated transformation, Shock wave-mediated transformation, Silicon carbide whisker-mediated transformation, Microinjection, Macroinjection, Lasermicrobeams and Electrophoresis). There are various methods available to breed genetic resistance against insects and pests, these include conventional breeding and transgenic technology. Exogenous pesticidal transgenes can be introduced into plants by *Agrobacterium* mediated transformation. *Agrobacterium* mediated transformation offers advantages like reducing copy number of the transgene, little co suppression (Konez *et al*., 1994; Hansen *et al*., 1997, Enriquez Obregon *et al*., 1998). However, *Agrobacterium tumefaciens* infects naturally only dicotyledonous plants and also many economically important plants including the cereals are also made to infect with difficulty.

Bacillus thuringiensis is a gram positive, rod shaped spore forming soil bacterium. It produces the crystal insecticidal proteins during sporulation called delta endotoxins. These crystal proteins are toxic to larvae of different insects. e.g, Lepidopterans (Krieg *et al*., 1983; Herrnstadt *et al*., 1986) and dipteran insects, causing eventual death of the larvae (Hoftey and Whiteley 1989; Aslam *et al*., 2000). Many different crystal protein genes called *Cry* genes have been isolated and classified on the basis of amino acid sequence homologies. At least 90 genes encoding protoxin from a wide range of *Bt* isolates have been isolated and sequenced (Maizer *et al*., 1997).

It is now widely accepted that the most suitable explants for transformation are those that require the least amount of time in tissue culture before and after the transformation step. The extensive period of tissue culture often result in genetic mutations that impact negatively on regenerated plants. Preferred explants for transformation include callus derived form meristamatic tissues, immature embryos, proliferated shoot culture, and embryonic axes derived from mature or immature seed for direct meristem transformation in cotton. Transformation method in cotton is limited to specific genotype, only to a single variety, Coker 312. Depending on the application, it may be important to have access to a transformation procedure that is not limited by genotype.

Keeping these aspects in view following objectives were framed for the present study.

1. Development of hirsutum *vs* barbadense heterotic groups.
2. Exploitation of heterotic groups by creation of recombinational variability in *G. barbadense* F_4 population for ability to combine with selected diverse *G. hirsutum* testers.
3. To determine combining ability effects (*gca* and *sca*), variances (GCA and SCA), combining ability patterns of these barbadense and hirsutum lines.
4. Identifying suitable barbadense lines for developing heterotic sub populations against hirsutum testers.
5. Determining correlations, direct and indirect effects of component characters on seed cotton yield.
6. Evaluation of genetic diversity in *G. barbadense* cotton lines and *G. hirsutum* testers based on SSR molecular marker.
7. Determining relationship between molecular diversity and hybrid performance in inter specific hybrids of cotton.
8. Standarizing `in *planta Agrobacterium tumefacience* mediated genetic transformation protocol to develop new events by transforming *G. hirsutum* cotton based on *Cry1Ac-Cry1E*c genes.

REVIEW OF LITERATURE

The available literature pertaining to the present investigation is reviewed under following headings herein:

2.1 Estimation of heterosis

2.2 Combining ability effects and variance

2.3 Development of heterotic groups and their exploitation

2.4 Studies on correlation and path co-efficient analysis

2.5 Molecular marker study in cotton

2.6 *In planta* genetic transformation

2.1 Estimation of heterosis

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

Heterosis produced by the joint effects of all the loci as the sum of their separate contributions can be represented by the formula (Falconer, 1981).

$$HF_1 = \sum dy^2$$

Where,

d = Magnitude of dominance

y = Allelic frequency differences at a locus in the parental populations

The genetic causes involved in the expression of heterosis are dominance and non-allelic interactions (Hayes and Foster, 1976). The magnitude of heterosis can be maximized if the parents are genetically diverse from each other. Parents should differ for maximum number of yield influencing loci so that F_1 exhibits the dominance effect at as many of the yield influencing loci as possible.

A brief review on heterosis in respect to different characters under study is presented here.

2.1.1 Plant height (cm)

Heterosis for plant height was observed by many workers (Khan *et al*., 1986; Bhatade and Rajeshwar, 1994; Rajput *et al*., 1997). Tomar and Singh (1991) observed heterosis for plant height ranging from -6.39 to 22.17 per cent over better parent. Patel (1984) reported heterosis ranging from 17.07 to 36.07 per cent for plant height. Patil (1989) observed mid parental heterosis ranging from -8.2 to 28.4 per cent in *G. hirsutum*. Waldia (1980) and Bhatade *et al.* (1992) observed moderate heterosis, whereas Krishnamurthy and Kothandaraman (1977) observed high positive heterosis.

Many of the earlier studies indicated significant positive heterosis for plant height except White and Richmond (1963) observed non-significant heterosis. Sandhu and Kooner (1979) and Koodalingam *et al.* (1991) who observed significant negative heterosis for plant height.

2.1.2 Number of monopodia per plant

Gill and Singh (1982), Duhoon *et al.* (1983) and Kaushik *et al.* (1984) recorded high and significant heterosis over mid and better parent. Patil (1973) observed non-significant heterosis for monopodia. Krishnadas and Kadambavanasundaram (1997) observed maximum heterosis for monopodia in inter specific hybrids followed by intra hirsutum hybrids.

Patil (1989) reported 38 per cent heterosis with an average heterosis of -6.5 per cent in *G. hirsutum*. Kajjidoni (1982) found heterotic effects for monopodia per plant which were smaller over respective mid parental values but positive in most of the cases.

2.1.3 Number of sympodia per plant

The number of bolls would be the direct outcome of number of sympodia. It is considered as an important component of heterosis for yield.

Patel (1984) observed significant heterosis ranging from 11.41 to 75.51 per cent. Duhoon *et al.* (1983) recorded 91 per cent but Sohu *et al.* (1993) reported heterosis towards unfavourable direction in upland cotton for this trait. Bhat and Rao (1980), Kenchanagoudar (1983), Kaushik *et al.* (1984) and Patil (1989) recorded similar observations, while Krishnadas and Kadambavanasundaram (1997) observed moderate heterosis.

2.1.4 Number of bolls per plant

Patil (1973), Soomre *et al.* (1982); Krishnaswamy and Gunasheelan (1985); Jagtap and Kolhe (1987) and Taware *et al.* (1987) reported significant heterosis over mid parent for number of good bolls in cotton. Iftikhar *et al.* (1985); Gesos and Pulatov (1986) and Khadi *et al.* (1996) noticed positive heterosis over commercial check for this character.

2.1.5 Mean boll weight (g)

For this character significant heterosis was reported by Iftikhar *et al.* (1985); Raut *et al.* (1989); Kadapa and Prajapati (1990) and Carvalho *et al.* (1994). Heterosis over mid parent was reported by Patil (1973) and Bhatade *et al.* (1980). Zhang Jinfa *et al.* (1994) reported both positive and negative heterosis for boll weight.Whereas, significant heterosis over commercial check was reported by Khadi *et al.* (1996).

2.1.6 Seed index (g)

Gupta and Singh (1987) observed -10.29 to 11.19 per cent heterosis for seed index. Pavasia *et al.* (1999) observed significant positive heterobeltiosis for this character. Marani (1963), Channadorai (1973), Gururajarao *et al.* (1977), Singh and Singh (1980) and Nagarajan (1989) reported positive heterosis. While, non-significant heterosis was reported by Gridley (1975), Pathak and Prakashkumar (1976) and Kolte and Thombre (1984).

2.1.7 Ginning outturn (%)

Singh *et al.* (2003) observed heterosis for this trait in the range of 4.3 to 16.9 per cent. Non-significant or low magnitude of heterosis for ginning out turn was recorded by Gridley (1975), Gururajarao *et al.* (1977), Singh (1982), Khan *et al.* (1986) and Kowsalya and Raveendran (1996). Moderate heterosis for this trait was observed by Pavasia *et al.* (1999).

2.1.8 Lint index (g)

Lint index is an important component of lint yield per boll and per plant. Sarsar *et al.* (1986) reported 13.106 per cent and Gupta and Singh (1987) reported -16.80 to 14.41 per cent heterosis for lint index. Singh *et al.* (2003) reported heterosis for this trait in the range of 26.8 to 58.3 per cent.

Marani (1963), Gururajrao *et al.* (1977) and Nagarajan (1989) reported significant and positive heterosis. However, Gridley (1975), Kolte and Thombre (1984) and Katageri and Kadapa (1989) reported non-significant heterosis.

2.1.9 Seed cotton yield (kg/ha)

Significant heterosis for seed cotton yield has been reported by several workers *viz.,* Katarki *et al.* (1970); El-Adl and Millar (1971); Patil (1975); Pathak and Prakashkumar (1976); Sandhu and Kooner (1979); Bhat and Rao (1980); Bhatade *et al.* (1980); Waldia *et al.* (1980); Vijendradas (1982); Thombre *et al.* (1982); Kaushik *et al.* (1984); Kolte and Thombre (1984); Singh and Bhat (1984); Iftikhar *et al.* (1985); Gesos and Pulatov (1986); Mehla *et al.* (1988); Sadykhova and Makhmudov (1986); Shallam *et al.* (1986); Taware *et al.* (1987); Hapase *et al.* (1987); Gunaseelan and Krishnaswamy (1988); Khan *et al.* (1989); Raut *et al.* (1989); Kadapa and Prajapati (1990); Carvalho *et al.* (1994); Xu-Xian *et al.* (1995) and Mallikarjun (2005).

64.3 per cent significant heterosis for seed cotton yield was reported compared to the maximum of 67.3 per cent in intra hirsutum hybrids (Krishnadas and Kadambavanasundaram, 1997). The heterosis over mid parent was revealed in studies by Maksudov and Engalychev (1984); Iftikhar *et al.* (1985); Krishnaswamy and Gunasheelan (1985) and Zhang Jinfa *et al.* (1994). Whereas, Khadi *et al.* (1996) reported the heterosis over commercial checks for seed cotton yield.

2.1.10 Lint yield (g)

In cotton, lint yield is one of the most important economic traits. Several workers *viz.,* Gridley (1975), Gesos and Pulatov (1986), Sadykhova and Mukhmudov (1986), Shallam *et al.* (1986) and Xu-Xian *et al.* (1995) and Mallikarjun (2005) have reported significant heterosis for lint yield.

2.1.11 2.5% span length (mm)

Singh *et al.* (2003) observed a wide range of useful heterosis for halo length ranging from 2.6 to 32.4 per cent. Kalsy and Vithal (1980) observed heterosis in negative direction for this trait. Kolte and Thombre (1984), Jagtap (1986) and Patil (1989) observed heterosis of lower magnitude. Singh *et al.* (1988) observed non-significant heterosis. Lee *et al.* (1967) and Duhoon *et al.* (1983) and Sarsar *et al.* (1986) observed low to medium heterosis for halo length.

2.1.12 Uniformity ratio (%)

Syiam *et al.* (1982) observed non-significant heterosis for maturity co-efficient. However, Krishnadas and Kadambavanasundaram (1997) observed low to very low, heterosis for uniformity ratio and maturity co-efficient in cotton.

2.1.13 Fibre strength (g/tex)

Very few reports are available. No heterosis was observed for fibre strength in intra specific crosses but heterosis was observed for these traits in the inter specific hybrids (Syiam *et al*., 1982, Krishnadas and Kadambavanasundaram, 1997). However, Wang and Pan (1991) reported heterosis in F_1 and F_2 population of *G. hirsutum*.

2.2 Combining ability effects and variance

Cotton is extensively used as a test system for genetic studies on several aspects. At the same time some areas clearly appear to be ignored by cotton workers, particularly the aspects like handling combining ability as a trait and improving it in the manner it is done in cross pollinated crops. There are no studies on creation of variability for combining ability, studying nature of variability for combining ability in segregating generations (F_2, F_3 and F_4 *etc.*). However, such studies are available in cross pollinated crops like maize, where population improvement programmes are regularly followed and new genotypes improved in combining ability are isolated to develop superior hybrids. Innovative breeding procedures involving cycles of crossing, recurrent selection and inter crossing of selected progeny row lines to accumulation additive genes and recombination of desirable parameters for yield and fibre quality components are recommended for adoption.

Estimation of combining ability effects and variance

The concept of combining ability is important in designing plant breeding programmes. It is especially useful in testing procedures, where it is desired to study and compare the performance of lines in hybrid combinations. Combining ability or productivity in crosses is defined as the ability of parents or cultivars to combine amongst each other during the process of hybridization so that favourable genes or characters are transmitted to their progenies.

In a hybrid development programme, the objective is to identify new lines that, when crossed will produce hybrids with superior performance. If resources were unlimited, it would be ideal to test each new inbred or line with every available line in a hybrid combination. However, with increased number of genotypes this is practically impossible to make all possible crosses and evaluate them. Therefore, a breeder must essentially identify a limited number of lines with sufficient genetic potential (combining ability) before their evaluation is done in specific hybrid combinations (Fehr, 1987).

Combining ability of line or inbred is the ultimate factor determining future usefulness of the lines for developing hybrids. Sprague and Tatum (1942) gave the concept of combining ability, and the two expressions of combining ability *i.e.,* general (*gca*) and specific (*sca*) combining ability have had a significant impact on evaluation of genotypes and population improvement. They defined *gca* as the average performance of a line in hybrid combinations with number of genotypes and *sca* as interaction between parents due to which certain hybrid combinations are better or poorer than would be expected on the basis of *gca* of the parental lines included. Breeding value as defined by Falconer (1981), is the twice the deviation of progeny mean from the population mean when the individual in question is crossed to large number of individuals representing a population. In determining *gca* effects of a line in question is crossed to large number of lines and the mean of these crosses

involving the line as a common parent is expressed as deviation from population mean. In this sense, general combining ability can be considered as half of the breeding value. Breeding value is a reliable component of genotypic value and this alone is transmitted to the progeny. Hence, breeding value or *gca* effect will represent the breeding potentiality of the genotype.

The *gca* reflects the breeding value of the parental genotype concerned and selection of genotypes and *gca* effects help in identifying genotypes to be used for developing superior populations. Specific combining ability effect represents the non-reliable component of the genotypic value arising due to contribution from dominance deviation and interaction deviation. Hence, if *sca* effect is the main cause for superiority of a cross, it is inferred that superiority of the cross can't be fixed through selection.

Studies on evaluating combining ability are generally centered around evaluating combining ability variances in Line × Tester analysis, diallel analysis and such other studies *etc.* A wealth of information is generated on components of combining ability variances for yield and other traits in cotton based on such studies. This is presented in the following paragraphs.

Present study revolves around evaluation of variability for combining ability in F_4 populations in cotton. Hence considering paucity of information available in cotton wherever required, basic studies conducted are also quoted and reviewed below.

2.2.1 Plant height (cm)

GCA and SCA variances influence the plant height (White and Richmond, 1963; Sandhu and Kooner, 1979; Patil, 1989). Higher proportion of GCA variance was observed by Chandramathi and Menon (1973), Bhandari (1980), Kolte and Thombre (1984) and Tomar and Singh (1991). However preponderance of *sca* effects was observed by White and Richmond (1963), Waldia (1980), Tuteja *et al.* (1996), Mohiuddin (1996), Ramalingam (1996), Patel *et al.* (1997) and Laxman and Ganesh (2003).

2.2.2 Number of monopodia per plant

Singh and Gupta (1970) and Bhandari (1980) reported both GCA and SCA variances for monopodia per plant. Several workers have reported higher magnitude of GCA variance than SCA variance resulting in preponderance of additive genetic variance Patil (1989). However predominance of non additive gene action was reported by Waldia (1980), Ramalingam (1996), Patel *et al.* (1997) and Laxman and Ganesh (2003).

2.2.3 Number of sympodia per plant

Importance of both GCA and SCA variance for sympodia per plant were reported by few workers (Singh and Gupta, 1970; Kalsy and Garg, 1980; Gunasheelan and Krishnaswamy, 1988). High level of additive genetic variance than SCA variance was observed by Singh and Singh (1980), Duhoon *et al.* (1983) and Patil (1989). Preponderance of *sca* effects was reported by Kolte and Thombre (1984), Kaushik *et al.* (1984) and Deshpande and Baig (2003).

Only non additive gene action was also reported to be important for number of sympodia (Bhatade *et al.*, 1992; Dagaonkar and Malkandale, 1993; Laxman and Ganesh, 2003).

2.2.4 Number of bolls per plant

Predominance of *gca* effects was reported by Pathak and Singh (1970), Duhoon *et al.* (1983), Amalraj and Gawande (1985) and Tomar and Singh (1992). Predominance of non additive variance was reported by Mohiuddin (1996), Ramalingam (1996), Patel *et al.* (1997), Deshpande and Baig (2003) and Laxman and Ganesh (2003).

While Singh and Gupta (1970), Wilson and Wilson (1975), Goudar *et al.* (1996) and Amolik *et al.* (1997) reported significance of both *gca* and *sca* effects for bolls per plant.

2.2.5 Mean boll weight (g)

Importance of both *gca* and *sca* effects for boll weight was observed by Patil (1973), Gupta and Singh (1986), Jagtap *et al.* (1992), Dagaonkar and Malkandale (1993), Murthy and Ranganathacharyulu (1998) and Rao and Reddy (2001).

Sandhu and Kooner (1979), Deshpande and Baig (2003) and Laxman and Ganesh (2003) reported the preponderance of SCA variance.

2.2.6 Seed index (g)

Predominance of *sca* effects was reported by Mohiuddin (1996), Ramalingam (1996) and Ahuja and Tuteja (2000) and Laxman and Ganesh (2003). However only *sca* effects was reported by Bhatade *et al.* (1992), Dagaonkar and Malkandale (1993) and Manickam and Gururajan (2004).While Bhatade *et al.* (1980) and Patil and Chopde (1983) observed both additive and non additive genetic variance.

Additive genetic variance and significant *gca* effect was reported by Singh and Singh (1980), Jagtap and Kolhe (1987) and Patil (1989).

2.2.7 Ginning outturn (%)

Importance of *sca* effects was reported for ginning out turn (Singh and Gupta, 1970; Patil 1989; Bhatade *et al*., 1992; Tuteja *et al*., 1996; Pavasia *et al*., 1998; Deshpande and Baig, 2003; Laxman and Ganesh, 2003), Verma *et al.* (2004) and Manickam and Gururajan (2004).

Duhoon *et al.* (1983) reported the predominance of *sca* effect for ginning out turn while Marani (1963), Nagarajan (1986) and Patil (1989) reported the significant *gca* effects for GOT.

2.2.8 Lint index (g)

Predominance of *sca* effects for lint index was reported by Tuteja *et al.* (1996) and Laxman and Ganesh (2003), whereas predominance of GCA variance was observed by Neelima (2002). Bhatade and Bhale (1983) and Manickam and Gururajan (2004) reported significant *sca* effects. Rao and Reddy (2001) reported the importance of both additive and non additive gene effects for this trait.

2.2.9 Seed cotton yield (kg/ha)

The analysis of combining ability for seed cotton yield indicated the importance of both GCA and SCA variances. (Miller and Marani, 1963; Chahal, 1971; Bhandari, 1978; Gupta and Singh, 1986; Patil, 1989; Jagtap, 1986; Amolik *et al*., 1997).

Preponderance of GCA variances in the presence of SCA variance has been reported by Singh and Singh (1980), Amalraj and Gawande (1985), Mehla *et al.* (1988), Gupta and Singh (1986), Kajjidoni *et al.* (1999) and Tomar and Singh (1991). Significant *sca* effect in the presence of *gca* effect has been reported by Bhandari (1978), Gupta and Singh (1986), Patil (1989), Goudar *et al.* (1996), Tuteja *et al.* (1996), Amolik *et al.* (1997) and Rao and Reddy (2001).

2.2.10 Lint yield (g)

For this character, significance of both GCA and SCA variances were reported by Cano-Rios and Davis (1981), Singh *et al.* (1988), Xu-Xian *et al.* (1995). The preponderance of only GCA variance was revealed by Sadykhova and Makhamudov (1986); Gesos and Torev (1986); Cano-Rios (1987); Singh *et al.* (1988); Tomar and Singh (1992), Dagaonkar and Malkhadale (1993), Xu-Xian *et al.* (1995) and Echekwu and Alabi (1995). In contrast to this, SCA variance was reported by Ansingkar and Bhale (1984), Shallam *et al.* (1986) and Echekwu and Alabi (1995).

2.2.11 2.5% span length (mm)

Preponderance for SCA variance than GCA variance was reported by Hapase *et al.* (1987), Deshpande and Baig (2003) and Laxman and Ganesh (2003). Predominance of GCA variance for this trait was reported by Gupta and Singh (1986) and Nagarajan *et al.* (1994).

Importance of both additive and non additive variance was observed by Bhatade *et al.* (1980), Duhoon *et al.* (1983), Gupta and Singh (1986) and Amalraj (1989). Pavasia *et al.* (1999) observed predominance of *sca* effects of halo length.

2.2.12 Uniformity ratio (%)

Importance of additive type of variance was noticed by Ma *et al.* (1983), Nadarajan and Sree Rangaswamy (1991); and Amudha and Raveendran (1997). While, both additive and dominance variance was reported by Manickam and Gururajan (2004).

2.2.13 Fibre micronaire value (µg/inch)

Tabarah (1970), Nadarajan and Sree Rangaswamy (1991), Subramanyam *et al.* (1991) and Verma *et al.* (2004) reported the importance of GCA variance.

Predominance of both additive and dominance variance was reported by Nadarajn and Sree Rangaswamy (1991), while dominance variance for this trait was observed by Ma *et al.* (1983), Sambamurthy *et al.* (2004) and Manickam and Gururajan (2004).

2.2.14 Fibre strength (g/tex)

Predominance of SCA variance for this trait was observed by Zhang *et al.* (1994), Omara *et al.* (1996) and Manickam and Gururajan (2004). Importance of both additive and non-additive variance was reported by Verma *et al.* (2004).

2.2.15 Fibre strength to length ratio

There were no previous reports made on the combining ability effects and variance for fibre strength to length ratio.

2.2.16 Fibre elongation (%)

Predominance of SCA variance was reported by Manickam and Gururajan (2004).

Abdallah *et al.* (1999) carried out studies to widen the genetic base of Egyptian cotton (*Gossypium barbadense*) and to develop a practical foundation for breeding high lint-yielding and early maturing cultivars. A factorial mating design II was used to study genetic diversity among and between 3 populations, viz. parents, F_1s and F_2s. Five accessions of American Pima cotton (males), seen as sources of improved earliness and productivity, were crossed with 12 lines of Egyptian cotton. The results indicated that additive gene action was greater than dominance gene action for both yield and earliness. The Egyptian genotypes G89, G85; G83 and Dandera and the Pima cultivars PS7 and PS6 were the best general combiners for the characters studied.

El-Adl *et al.* (2001) conducted a study to determine heterosis extent and combining ability estimates in 30 F_1 hybrids. The largest amount of heterosis vs mid-parents was 7.79% for lint yield per plant, while the lowest amount of heterosis was 0.91% for the number of bolls per plant. The mean squares in the F_1 hybrids for general combining ability (*gca*) were highly significant for all traits. The mean squares of *gca* were higher than those of specific combining ability and showed highly significant differences for all traits. Dominance genetic variance was higher than the additive genetic variance and reciprocal variance for all traits, except boll weight. The intrinsic performance of parental cultivar recorded a good index of their *gca* effects in most cases.

Idris (2006) conducted an experiment to evaluate some Egyptian cotton (*Gossypium barbadense*) hybrids with respect to yield, yield attributes and some fibre properties. There was significant variation among the cultivars for yield, harvest index of boll, lint percentage and lint index. The hybrids showed significant differences with respect to yield, boll weight, fibre length and pressly index. There were significant differences between the control and hybrids with respect to yield, boll weight, harvest index of boll, lint percentage and fibre length.

Abdel-Hafez *et al*. (2007) conducted heterosis and combining ability analysis using line x tester design between 5 female parents *viz*, GIZA 45, GIZA 85, GIZA 86, GIZA 89 and GIZA 90, and 4 genetically diverse male parents, Suvin, Pima S6, Karshneseki-2 and TNB-1. The crosses exhibited significant and highly significant positive heterosis relative to mid and better parents for most yield and yield component traits and also showed desirable heterosis for most fiber properties. The parents showed significant positive general combining ability effects for both seed cotton yield and lint yield/plant, lint percentage and seed index. The crosses exhibited highly significant specific combining ability effects for yield and yield components and fiber properties, respectively. The parents were good combiners for most yield and its components for halo length and fiber length at 2.5%. The results of the present study emphasize the importance of including of the imported barbadense cotton germplasm in improvement of local cotton cultivars.

Ahmed (2007) evaluated a half diallel set of crosses involving five cotton parental genotypes, four belonging to *Gossypium barbadense* and one of *Gossypium hirsutum.* The ratio of general to specific combining ability GCA/SCA variances was found to be less than unity for all measured traits except days to the first flower under and boll weight, indicating that the main genetic variation for these traits was due to non-additive gene action. The best drought tolerant parents were Aleppo 40 and Pima s6 and the best drought tolerant hybrids were Pima S6 x Aleppo 40, GR1 x SR3, GR1x Aleppo 40, GR1 x Pima s6 and Giza 85 x Aleppo 40. The hybrids showed considerable heterosis for seed cotton yield per plant and most of the other studied traits. The parental genotype Aleppo 40 was the best general combiner for seed cotton yield per plant and most of the other studied traits.

Basal *et al.* (2009) studied eight barbadense cotton cultivars and fifteen F_1 hybrids obtained by crossing five lines and three testers in the line x tester mating system. The predominance of non-additive gene action was estimated for all the traits except for seeds per boll, which were controlled by additive type of gene action due to high GCA variance.

El- Mansy *et al.* (2010) hybridized nine diverse *G.barbadense* cotton genotypes *i.e.*; Pima S6 as American Egyptian cotton, Karshenky 2 as Russian genotypes, Suvin as Indian genotype and six Egyptian genotypes *i.e.* Monoufi, dandara, Giza 86, Giza87, Giza 89 x Pima S6 and Giza 92, following half diallel crossing system in order to investigate the genetic mechanism controlling variation. Analysis of combining ability revealed significant *gca* and *sca* for most studied characters indicating importance role of additive and non-additive effects in the inheritance these characters. The additive and non-additive gene effects were significant and involved in the inheritance of all studied characters. Estimation of heritability in narrow sense was low for earliness index and lint yield to moderate and high for the rest characters. A moderate to high narrow-sense heritability for fiber characters suggest that there was potential in the plant material for improving these characters through single plant selection.

Mohammad Reza Zangi and Nadali Bbaein Jelodar (2010) determined combining ability and heterosis in crosses of *G.hirsutum* and *G.barbadense* for agro morphological traits and yield. High variation was observed for characteristics among parents and the F_1 combinations. Barbadense 5539 and Termeze14 (*G.barbadense*) had negative *gca* for plant height, bolls per plant and sympodia branches per plant. Barbadense genotypes also showed negative *gca* for monopodia per plant and boll weight. The GCA: SCA ratios for the studied traits were higher than one indicating the presence of additive genetic effects for most of the characteristics studied.

Allard (1960) defined progeny test, to categorize a genotype based on the performance of its offspring produced in some definite system of mating. Davis (1927) suggested the use of top cross procedure in maize, which is a type of progeny test, where the inbreds are crossed to a common tester parent and the difference in the performance of the progeny thus obtained reflects the combining ability of the inbreds.

New dimension for the use of progeny test or top cross test were suggested after Sprague and Tatum (1942) introduced the concept of general combining ability effect and specific combining ability effect. Different recurrent selection procedures were proposed in the context of improvement of general combining ability effect and or specific combining ability effect.

Joshi (1960) has opined that selection from segregating material from artificially hybridized populations can be successfully used for further out crossing and thus for further improvement in combining ability.

2.3 Development of heterotic groups and their exploitation

2.3.1 Development of heterotic groups

The term heterotic group refers to “a group of related or unrelated genotypes from the same or different populations, which display similar combining ability and heterotic response when crossed with genotypes from other genetically distinct germplasm groups” (Melchinger and Gumber, 1998).

In the recent years the concept of developing heterotic populations is put to test in self pollinated crops like cotton, segregating populations based on diverse pairs of genotypes can be the ideal base material required for implementing procedures like reciprocal selection for improving combining ability (Patil and Patil, 2003 and Patil e*t al.,* 2011). In hybrid research study on cotton, a large number of crosses involving varietal lines are used for assessing combining ability status. On constantly observing the most potential crosses attempts are made to infer about the causes of high heterosis.

If more lines are found to be giving superior crosses with a tester then it is possible to initiate multiple crosses among such lines selected for combining ability and this can lead to creation broad gene pool of recombination variability for combining ability as the population developed in this manner based on number of components improved in ability to combine with the tester. This heterotic gene pool can be exploited for developing superior hybrid combinations with the tester concerned.

Several criteria have been suggested to choose promising heterotic groups: (i) high mean performance and large genetic variance in the hybrid population in the target region(s) (ii) high *per se* performance and good adaptation of the parent populations, and (iii) a higher ratio of the variance due

to general (σ2 GCA) versus specific combining ability (σ2 SCA) (Melchinger and Gumber, 1998; Reif *et al*., 2005a).

Fan *et al*. (2001) used a diallel design to study combining abilities among 10 maize lines (five lines from the International Maize and Wheat Improvement Center [CIMMYT] and five major commercial lines from China). According to SCA_PY method, they classified CML171, CML161, CML166 into one heterotic group; Chang 631/o2, Zhongxi 096/o2 into another heterotic group; and Qi 205 into a third heterotic group.

Huang and Li (2001) evaluated 45 maize inbred lines from China, U.S. Corn Belt, and tropical regions by using 44 restriction fragment length polymorphism (RFLP) markers equally distributed across the 10 maize chromosomes. The 45 inbred lines were grouped into six heterotic groups: Mo17 was assigned to group II; Tangsipinttou (TSPT) and Huangzao 4 (HZ4) were assigned to group IV and Dan 340 was assigned to group VI.

Menkir *et al*. (2004) used two testers representing the two heterotic patterns to test 38 tropical maize inbred lines. The two testers successfully classified 23 of the 38 tested inbred lines into two heterotic groups based on the SCA_PY method.

Fischer *et al*. (2010) identified two heterotic groups in triticale by employing principle coordinate analysis and an enumeration algorithm for maximizing F_1 performance, mid parent heterosis, and σ2 GCA/ σ2 SCA ratio for grain yield. Twenty one inbred lines and their 210 diallel crosses were evaluated for grain yield at five agroecologically diverse locations in Germany.

2.3.2 Exploiting heterotic groups through creation of variability for combining ability

Response to selection for any character is dependent on the existence of variability for that character. Quick gains are possible through selection during breeding. Cotton improvement programmes primarily lay emphasis on improvement of hybrids by improving the performance of hybrid parents. Emphasis is not laid on creation of variability and assessing the nature and magnitude of the variability for combining ability. Like other characters, even for combining ability, variability can be created either by inducing mutations or by crossing genotypes and generating recombinational variation. Though such studies are not available in cotton, in sorghum, attempts were made to assess the nature of induced variability for combining ability by crossing the mutant lines with male sterile tester (Shashidhar *et al*., 1989 and Patil *et al*., 1991). These studies clearly indicated that inducing mutations can be used as technique to create variability and exploit the same by practicing selection for combining ability.

The other approach to create variability is by recombination of genotypes and evaluating the recombinants in segregating generations for combining ability. In cross pollinated crops like maize, this principle is involved in breeding procedures like recurrent selection for general and specific combining ability. These procedures as such cannot be reproduced entirely in self and often cross pollinated crops like cotton because of the difficulty of intermating the selected plants. However, the segregants selected for high combining ability can be selfed to fix the high combining ability of lines in segregating generation.

In sorghum , Patil and Pandit (1991) created variability using B $\times$ R crosses and assessed F_2 segregants for combining ability with the help of male sterile testers. Similarly, Madhusudhan (1993) created variability using B $\times$ R crosses and confirmed it by assessing F_3, F_4 and F_5 segregants for combining with male sterile testers. Keshall *et al.* (1985) selected 74 maize lines from random mating population. Out of them, 34 lines showed significant improvement in combining ability. Otte *et al.* (1984) also concluded in similar manner that through selection improvement in combining ability can be achieved. Atkins (1979) followed pedigree method after initial crossing of maintainer and restorer parents. The female lines thus developed revealed good combining ability for grain yield when tested with number of newly developed restorer lines.

Manivasakam and Kamalanathan (1987) revealed that mean and variability are the important factors for selection for *per se* performance. Mean serves as a basis for eliminating undesirable crosses and variability indicates the extent of recombinational variability available for initiating effective selection. They have emphasized the point that selection for the improvement of quantitative characters can be effective only when the segregating generations possess the potential variability.

Large variability was noticed in segregating generation for yield and related traits in cotton by many workers *viz.,* El-Gohary *et al.* (1985), Mahdy *et al.* (1987), Manivasakam and Kamalanathan (1987), Mirakhamedov *et al.* (1987), Mehla *et al.* (1988), Simongulyan and Kim (1990), Munasov *et al.*

(1990), Tagiev (1991), Virk *et al.* (1991), Subramanyam *et al.* (1991), Akhmedov (1991), Dever and Gannaway (1992); Akumuradov and Chapau (1992); Verma *et al.* (2004) and Manickam and Gururajan (2004).

In cotton, there are few studies on creation and exploitation of variability for combining ability. Mallikarjun (2005) observed presence of variability for combining ability in F_4 population of two crosses. However, in many studies creation of variability for *per se* performance with respect to different quantitative characters is demonstrated.

In this approach (Patil and Patil, 2003) in a crop like cotton diverse single cross F_1s can be identified and utilized as sources for initiating reciprocal selection for combining ability in the segregation generations of the two crosses.

The genetically diverse single crosses were identified based on predicted double cross performance. The average performance of non-parental crosses was used to predict distance between the single crosses (Patil *et al.*, 2004). Both *gca* and *sca* effects contributing to superiority of two crosses indicated that procedures such as reciprocal selection for combining ability can be utilized to enhance the heterosis level (Patil *et al.*, 2004).

2.3.3 Selection for combining ability

Generally in cotton, combining ability is assessed in stable lines picked up in later segregating generations in which the lines would be homozygous. Commonly this is done with the help of line × tester and diallel methods (Gaziyants and Zhalilov, 1983; Iftikhar *et al.*, 1985; Gesos and Pulatov, 1986; Hapase *et al.* 1987; Raut and Misalkar, 1988; Amalraj, 1989; Khan *et al.*, 1989; Dagaonkar and Malkhandale, 1993; Nagarajan *et al.* 1994; Panchal *et al.*, 1995; Khadi *et al.*, 1996); Verma *et al.* (2004) and Manickam and Gururajan (2004).

Lot of efforts and time are involved in developing these stable lines before evaluating them for combining ability. If such lines prove to be poor in combining ability, effort made in developing these lines goes waste. The possibility of evaluating early segregating lines for combining ability has been studied in different crops. It has been demonstrated in these crops that, combining ability assessed in early generations remains stable, which indicates that it is possible to screen the lines for combining ability in these generations.

One of the important tasks of the breeder is to identify the stage of selfing or inbreeding at which tests for combining ability can be made most efficiently. An early evaluation of combining ability is always desirable for the purpose of eliminating those lines not likely to be of value in the breeding programme. Testing of inbreds at an early stage would however additionally reduce the amount of time, land, labour *etc.* consumed in the programme (Falconer, 1981).

Richey and Mayer (1925) suggested that, in any crop lines resulting from the products of five and more generations of selfing have no appreciable within line differences in their combining ability status. Jenkins (1935) has presented data in maize, suggesting that inbred lines acquired individuality as aspect of top crosses vary early in the inbreeding process and remained relatively stable for combining ability there after.

Several workers have agreed with early generation testing of maize inbreds for combining ability (Vahtin, 1958; Fawzi, 1962 and Gerasenkov and Goncharova, 1972). Further, they have reported that evaluation for combining ability is possible in early generations of inbreeding.

In cotton, the studies on ideal generation for initiating selection for combining ability are not available. However, studies aimed at evaluating variability for *per se* performance have clearly indicated that the performance of line by F_4 is stabilized and selection can be initiated on line basis in F_4 generation. However, there are no studies suggesting that combining ability status of a line is stable and reliable by F_4 generation or not.

In general, Manickam and Gururajan (2004) observed that *per se* values of parents were not related to their corresponding *gca* effects or that of crosses to their corresponding *sca* effects. The deviation of crosses based on *sca* effects were expected. Since, they are only the estimates derived from the average *gca* effects of the corresponding parents. Hence, larger *sca* effect need not necessarily result in exceptional performance of a cross.

Ramakrishna (2008) extended reciprocal selection for improving combining ability to cotton by altering its procedure to suit mating system of cotton. With the help of diallel study involving seven single crosses, best double cross combination, RAHH-198 x ZCH-21405 was identified. These

opposite F_1s were used as base populations and they were advanced to F_4. Twenty four F_4 lines from each of these opposite populations were crossed reciprocally to the opposite F_1s. Additionally these two sets of F_4 lines were crossed to four diverse testers (Two Line x Tester sets of 24 x 5 crosses).

Patil *et al*. (2011) gave results of reciprocal selection for combining ability followed in cotton. In self pollinated crops, firstly opposite groups of genetically diverse groups of genotypes have to be identified in first phase of the present study, seven single crosses from private and public sector were involved in development of 21 double crosses and their evaluation. Based on this evaluation best double cross ZCH-21405 X RAHH-198 was identified and the two single crosses involved in it were selected as opposite base material and were advanced to F_4 generation for initiating reciprocal selection for combining ability. These opposite population in a segregating generation can act as base population for initiating reciprocal selection for combining ability. Random 23 F_4 lines of cross 1 (ZCH-21405) were crossed with the cross 2 (RAHH-198) as tester and vice-versa. Evaluation of these 46 derived F_1's was done by comparing them with commercial check hybrids and with bench mark double cross.

2.3.4 Choice of tester(s) to assess combining ability

In maize and other crops top crosses may be employed either to evaluate combining ability of inbred lines involved in a hybrid breeding programme or to evaluate breeding values of genotypes in segregating generations (F_4 lines). In such situations the choice of proper tester(s) that provide best discrimination among the lines (genotypes) is essential. The importance of choice of tester in assessing combining ability has been extensively studied in maize (Russell and Eberhart, 1975; Comstock, 1979 and Zambezi *et al*., 1986).

Contrasting results have been reported and both broad and narrow genetic base testers have been used for estimating the combining ability of inbred lines. However, Hallauer and Miranda (1981) concluded that narrow genetic base testers were effective for evaluation of inbreds, when it is intended to isolate a complementary genotype by using one of the parent of a hybrid as tester, in fact, here selection is done for a genotype whose genetic constitution nicks well with that of tester, it may be difficult to know how far selection was effective in improving *gca* or *sca* or both *gca* and *sca*. Hence, in such studies or such situation the broad term "evaluation of combining ability" itself may be appropriate.

In maize, the use of inbred lines as testers resulted in significant improvement not only of combining ability with specific testers, but also general combining ability as measured by crosses with unrelated broad base population (Horner *et al*., 1973 and Walejko and Russell, 1977). According to Hull (1945), the most efficient tester would be one that is homozygous recessive at all loci and as far as possible testers with homozygosity for dominant alleles at any locus should be avoided.

Allison and Curnow (1966) defined the best tester as one that maximizes the expected mean yield of the population produced from mating of selected genotypes.

Authors like Rawlings and Thompson (1962), Comstock (1964) and Allison and Curnow (1966) all arrived at similar conclusion with respect to the choice of the better tester *i.e.,* either an inbred line homozygous recessive or a population with low favourable gene frequency at important loci is the most effective tester both for discriminating among inbred lines in a hybrid breeding programme and for population improvement in a recurrent selection scheme.

Cress (1966) emphasized that the choice of a tester to maximize gain from selection for a heterogeneous population depends on the average performance of the test cross *i.e.,* the tester with highest average cross performance is choosen.

Green (1948) compared the relative value of two testers and observed striking difference in their genetic structure between two testers, based on the average performance of top cross with both testers rather than top cross of either tester alone.

Rawlings and Thompson (1962) added the significant contribution to the study of testers. The authors pointed out that most efficient tester is the one which increases the mean or average and variances in the inbreds.

Lopez-Perez (1979) made the study on comparison of five different testers, says that S_1 line test cross made with an unrelated high yielding tester had the greatest genetic variance. Use of an unrelated high yielding inbred line as tester for selecting lines having good general and specific combining ability was recommended.

Kappel and Tsiger (1984) studied divergence of interchanged testers for successful hybrid breeding programme and they classified the tester based on the highest mean values among the testers. Nawar and El-Hosary (1984) evaluated the eleven testers of different genetic resources at different locations and ranked the three testers *i.e.,* DC 17, VC sidic 7421 and composite 108 as the most efficient testers.

Md Liakat Ali and Tepora (1986) reported that the inbred line ph 109-1 had highest genetic variance and mean in the test cross progeny and proved to be the most effective testers based on comparative performance study of four type of testers in evaluating the maize.

Abel and Pollak (1991) ranked the unadapted maize by testers based on the high mean and heterotic group among testers. The effective tester is the one which detects the favourable alleles, possesses high pollen producing capacity and good agronomic characters. Further, it should give consistent results from environment to environment for yield.

Arceo and Molina (1991) studied maize lines as testers for general combining ability by crossing two high and two low yielding testers to eight high and eight low general combining ability inbreds, concluded that low yielding varieties are better *gca* testers than high yielding varieties.

Rissi and Hallauer (1991) made the study on evaluation of relative merits of four testers (two broad based and two narrow based testers) for evaluating the inbred lines in hybrid development programme. They were the opinion that good tester is the one which increases the variance components of F_1s obtained from inbred lines. Further, they reported that line $\times$ tester interactions were greater with broad based than narrow based testers. On the contrary, again they suggested that genetically narrow based testers such as inbred lines and single crosses can be effectively used to identify lines having good general combining ability. There was evidence that unrelated testers and inbred line testers with poor general combining ability and good *per se* performance were better testers for discriminating among S_2 lines. El-Sheikh (1993) made the study on comparison of efficiency of high and low yielding testers in evaluating S_1 lines in maize.

2.4 Studies on correlation and path co-efficient analysis

2.4.1 Correlation co-efficient analysis

Different characters of a plant are often correlated with each other. This may either be due to pleiotropy, *i.e.*, manifold effects of a gene or genes on different parts of the plant, or due to genetic linkage (Harland, 1939).

Seed cotton yield was reported to be negatively correlated with the length of stem internode, area of the largest leaf, number of vegetative branches and lint length, but it was positively correlated with ginning percentage and yield of lint Griffee *et al*. (1929).

Gururajan (2000) reported correlation co-efficient between yield and boll number, which was positive significant, but between yield and boll weight was negative relationship.

Girase and Mehetre (2002) reported significant positive association of boll number, boll weight, plant height, sympodia number, seed index, lint index and total dry matter with seed cotton yield.

Neelam and Potdukhe (2002) observed that number of bolls per plant, seed index and lint index had positive correlation with seed cotton yield per plant and appeared to be interrelated with each other.

Altaher and Singh (2003) studied the correlation co-efficient analysis among 40 different cotton varieties from all the three cotton growing zones of india. The character association studies revealed that significant positive association between yield per plant with bolls per plant, plant height, boll weight, number of monopodia, first fruiting node and fibre fineness.

Muthuswamy and Vivekanandan (2004) worked out correlation involving 48 crosses of 12 lines tester combination and reported that seed cotton yield was significant and positively correlated with GOT. Boll weight had positive significant association with lint index and GOT. Seed index had positive significant association with lint index.

The plant height showed positive correlation with seed cotton yield in E_2, while negative correlation was recorded in E_3. Length of sympodia was positively correlated with seed cotton yield in E_3, while non-significant correlation was observed in E_1 and E_2 (Ashok *et al*., 2004).

Muhammad Iqbal (2006) reported positive significant correlation of node of first fruiting branch, monopodial branches/ plant, boll number and boll weight with yield.

Sun-Junling *et al*. (2006) reported in correlation analysis that the correlation co-efficients of phenotypic characters and quality characters, including lint percentage boll weight, plant height, fibre length fibre strength and micronaire, between M_4 and M_5 were highly significant, suggesting that the genetic variation in the irradiated progenies was heritable.

Verma *et al.* (2006) reported that seed cotton yield per plant had positive and highly significant correlation with number of bolls per plant, number of sympodia and ginning outturn.

The association of yield with monopodia was negative (Griffee *et al*., 1929 and Patil, 1974). Contrary to this, Venkataraman and Santhanam (1962) reported positive association of monopodia with yield but Singh *et al*. (1968) noticed non significant positive correlation with yield. Significant positive correlations between number of monopodia per plant and seed cotton yield per plant were observed by Vijendradas (1981).

The sympodia per plant was represented to be significantly and positively correlated with seed cotton yield by many workers (Miller *et al*., 1958; Singh *et al*., 1968a; Gill and Singh 1981; Singh and Singh 1981; Musande *et al*., 1981; Bhatade, 1982; Shaikh and Upadhyay, 1982; Gawand *et al*., 1984; Basu and Bhat, 1987; Choudhary *et al*., 1988; Arshad *et al*., 1993 and Killi, 1995).

Annapurve *et al.* (2007) studied the phenotypic and genotypic correlation in American cotton and reported that both phenotypic and genotypic correlation were significant for most of the characters like number of bolls per plant, boll weight, boll bursting and yield per plant.

Neelima and Chenga Reddy (2008) conducted the correlation co-efficient studies involving 4 lines, 10 testers and their 40 F_1 crosses in *G. hirsutum* and revealed that number of sympodia per plant, number of bolls per plant, boll weight, seed index and micronaire value showed significant positive association with seed cotton yield both at genotypic and phenotypic level indicating that these characters can be simultaneously improved.

2.4.2 Path co-efficient analysis

The method of path co-efficient analysis provides an effective means of finding out direct and indirect causes of association of various component characters. The method was developed by Wright (1921) and was first applied to plant breeding by Dewey and Lu (1959).

Balakotaiah (1973) in a study of yield components, on the basis of both the phenotype and genotype effect found that monopodia, sympodia and seed index had considerable direct and positive effects. He concluded that selection for higher sympodia per plant and seed index could improve lint yield. Bhatade (1982) reported high positive direct effect of number of sympodia per plant on seed cotton yield. High indirect effect of the trait on yield was observed by Gill and Singh (1981) and Choudhary *et al*. (1988).

Boll number per plant was found to have positive and high direct effect on yield per plant (Shaikh and Upadhyaya, 1982; Gawand *et al*. 1984, Dhanda *et al.* 1987; Shandhu *et al*. 1986; Singh *et al* 1987; Bodar *et al* 1988; Alam and Islam 1991; Sambamoorthy *et al.* 1994 and Killi. 1995). However, Butany *et al*. (1968) reported negative direct effect of number of bolls per plant on seed cotton yield per plant, while Tomar and Singh (1992) reported positive indirect effect of this trait on yield per plant.

Positive and high direct effect of ginning percentage on yield of seed cotton was observed by Singh *et al*. (1987) and Choudhary *et al*. (1988). However, Govilla and Sharma (1981) reported no direct influence of ginning percentage on yield of seed cotton.

Singh *et al*. (1987) and Bodar *et al*. (1988) from their studies reported very high positive direct and indirect effects of seed index on seed cotton yield per plant. However, Govilla and Sharma (1981) reported that seed index does not have any direct influence on seed cotton yield. Lint index also contributed to yield per plant indirectly (Tomar and Singh, 1992). Positive direct effect of monopodia per plant on seed cotton yield per plant was revealed by Gill and Singh (1981) and Vijendradas (1981), Gawand *et al*. (1984) and Alam and Islam (1991) noticed a high positive direct effect of plant height on seed cotton yield, whereas Gill and Singh (1981) reported high positive indirect effect of plant height on seed cotton yield.

Muthu *et al.* (2004) conducted the path co-efficient analysis of parents and F_1s of line x tester crosses (9x6) in upland cotton. They reported that, days to first flowering, monopodia per plant, bolls per plant, boll weight, ginning out turn, 2.5 per cent span length fibre, fineness and elongation per cent exhibited direct positive contribution towards seed cotton yield. However, Altaher and Singh (2003) in a similar study of 40 cotton genotype revealed that the lint index, bolls per plant and boll weight had highest direct positive effect on the seed cotton yield.

Verma *et al.* (2006) in a path co-efficient analysis study involving 51 genotypes having different cytoplasm sources developed through successive back crossing and reported that selection for high seed cotton yield seemed to be positive through number of bolls per plant, number of sympodia, ginning out turn as these exerted positive direct effects and exhibited positive significant association with seed cotton yield.

Gururaj (2006) revealed that compact genotypes showed differences for per cent deviation from the population mean. However, the mean per cent deviations were positive for plant height (6.37%), number of monopodia per plant (72.38 %), inter boll distance (1.54%), number of bolls per plant (24.46%), boll weight (8.12%), seed index (8.31%) and GOT (6.1%). Negative per cent deviations were recorded by number of sympodia per plant, sympodia length at fifty per cent height (-6.40%), diameter of plant (-0.57%) and halo length (-4.11%). However, potential genotype had the some difference in their path of productivity as obtained in the genotypes RAH-216 (number of sympodia per plant), RAH-205-91 (for diameter of plant and inter boll distance) and 433 0503AYC (for halo length).

Neelima and Chenga Reddy (2008) studied the path co-efficient analysis in 4 lines, 10 testers and their 40 F_2s of *G. hirsutum* indicated that bolls per plant through boll weight, lint index and boll weight through lint index exerted high positive indirect effects on seed cotton yield.

Hanamaraddi (2010) revealed that top performing genotypes have positive value for seed cotton yield (40.53%), number of bolls (40.21%), boll weight (11.11%), plant height (7.09%), halo length (7.21%), number of nodes (6.55%), seed index (4.85%), lint index (4.04%), ginning out turn (2.48%) number of seed per boll (2.38%) and number of seed (1.92%). And also show negative per cent deviations for monopodia (-1.96%) and inter boll distance (-2.25%). These negative deviations for number of monopodia and inter boll distance are highly desirable.

2.4.3 Bio- physical characters

The photosynthetic rates of cotton leaves under a given environmental conditions is a function of the various biophysical and biochemical processes involved during the diffusion of CO_2 from atmosphere to chloroplast and the subsequent enzymatic reactions. The important parameters associated with biophysical processes of carbon exchange rates in cotton is reviewed below.

Ackerson and Humbert (1981) reported that plants adopted to water deficit conditions maintained photosynthesis to a much lower leaf water potential than control plants.

Hutmacher and Kreig (1983) noticed that photosynthetic rate of leaves had a curvilinear relationship with leaf conductance of upper leaves. Increase in leaf conductance of CO_2 above 0.3-0.4 mole/m_2/sec did not resulted in significant increase in net photosynthetic rate per unit leaf conductance. Further, development of water stress caused greater reduction in photosynthesis than leaf conductance, indicating non-stomatal limitation of photosynthesis. Thus, it was concluded that non-stomatal factors were major photosynthetic rate determinants in cotton.

Bhardwaj *et al.* (1988) reported that the cotton (*G.hirsutum L.*) with small thicker leaves exhibited greater potential for enhanced conductance with varying carbon exchange rates.

Bhardwaj *et al.* (1988b) reported negative association of boll weight with cumulative temperature as well as photosynthetically active radiation (PAR), while boll period was positively associated with cumulative temperature and PAR in cotton *(G.hirsutum L.).*

Bowman (1989) studied the relationship between leaf water status, gas exchange and spectral reflectance in cotton leaves and found that photosynthetic rate and stomatal conductance decreased curvilinearly as leaf water potential decreased as approached zero at -1.2 mpa.

Puech-suanzes *et al.* (1989) found no significant differences among cultivars of cotton (*G.hirsutum* L.) in net leaf photosynthesis per unit area as related to leaf conductance and photosynthetic photon flux density under water stress conditions.

The leaf transpiration and stomatal resistance are directly related to number of stomatal present per unit leaf area (Van de Roovart and Fuller, 1935). It has been suggested that a reduced stomatal frequency would be expected to reduce stomatal conductance (Penman and Schofield, 1951) which in turn reduce rate of water loss and increase the ratio of photosynthesis to transpiration in wheat (Jones, 1977). Similary Austin (1977) reported that low stomatal frequency increased stomatal resistance and decreased the transpiration in barley which inturn increased the yield due to increased water use efficiency under rainfed conditions.

Shimshi and Ephrat (1975) were of the opinion that wheat cultivars with a wide stomatal aperture produce higher yields without consuming more water. However, they also stated that permeability was significantly correlated with short term transpiration, short term photosynthesis and yield.

Wong *et al.* (1979) reported that stomatal conductance was correlated with photosynthetic rate and stomatal aperture is determined by the capacity of mesophyll to fix carbon. Further, Hutmacher and Kreig (1983) noticed that photosynthetic rate of leaves had a curvilinear relationship with leaf conductance.

Gopinath and Madalageri (1985) reported heterosis for stomatal frequency and leaf area over mid parent values in F_1 hybrids of egg plant. In a similar observation Hazra *et al*. (1989) noticed marked heterosis for length, breadth and number of stomata on upper and lower surface in F_1s from ten genotypes of *vigna unguiculata.*

Dhopte *et al.* (1988) reported that boll number and transpiration rate had direct positive effect on yield, while stomatal conductance had a direct negative effect.

Kuroda and kumura (1990) observed significant correlation between stomatal conductance and carbon exchange rate and further stated that increased carbon exchange rate was attributed to increased mesophyll activity which changed in parallel with stomatal conductance.

Lowered conductance should improve the stability of yield, because it reduces the water loss. However, it will reduce yield potential because of trade off between CO_2 and H_2O exchange, thus affecting the production (Ludlow and Muchow, 1990).

Buttery *et al.* (1992) reported high positive association of yield in soybean with stomatal frequency, stomatal conductance and transpiration rate.

2.5 Molecular marker study in cotton

Plant breeders desire their new varieties to be distinct, uniform and stable. In the past the ability to discriminate between varieties was heavily dependent on morphological traits. Lately, DNA markers have been employed as a promising method of finger printing. High resolution of molecular markers compared with other markers makes them a valuable tool for varietal and parental identification for protection of cotton breeders rights. DNA markers further add to repertoire of tools for determination of evolutionary relationship between *Gossypium* species and families.

Molecular markers also allow an understanding of the relationship between chromosomes of related *Gossypium* sp. Similar to other crops, an understanding of the evolutionary and genomic relationships of cotton species and cultivars is critical for further utilization of extant genetic diversity in the development of superior cultivars (El-zik and Thaxton, 1989). Apart from this, molecular markers are employed for genetic diversity estimation in place of morphological markers as number of morphological descriptors in various crops is in vogue for characterization purpose. High polymorphism independent of the effects related to environmental conditions and physiological stage of plant makes molecular markers a reliable tool for diversity studies. Parental genetic divergence has been found to increase the potential of heterosis in crosses among lines. This suggests the use of indirect measures of genetic diversity as possible predictors for heterosis response of hybrids.

Initially isozymes were applied to *Gossypium* as a taxonomical tool to distinguish differences at species level. Cherry *et al*. (1972) observed minor differences in isozyme banding pattern of A and B genome species whereas greater band variation between the more distantly related species in the C, D and E genome. Isozymes have been used to investigate the genetic diversity in *G. hirsutum* (Wendel *et al*., 1992). This study assayed 50 enzyme systems within wild *G. hirsutum* accession and upland cultivars. Thirty isozymes were found to be polymorphic with *G. hirsutum* but of these only 14 were polymorphic between upland cultivars and allelic diversity was minimal, which indicated a low level of diversity in upland cultivars.

Wendel *et al.* (1994) used allozyme analysis to assess levels and patterns of genetic diversity in *Gossypium mustelinum* and its relationship to other tetraploid species. They inferred low level of genetic variation compared to other tetraploid species. Isozyme assays resolved little or no variability within species of real use and numbers are limited and their expression is often restricted to a specific developmental stage of tissues. DNA markers have been employed for this purpose. Brubaker and Wendel (1994) examined genetic diversity in upland cultivars using RFLP markers. Their study found that despite surveying 205 loci from 23 upland cultivars, only 6 had unique, multi locus genotypes again suggesting limited diversity.

SSR are short tandemly repeated DNA sequence motifs that consist of two to six nucleotide core units and represent a new class of genetic markers which accelerated cotton genome mapping work. Liu *et al.* (2000) used 65 SSR primer pairs to amplify 70 marker loci localized to a specific cotton genome. The SSR markers identified in this study provide a framework that can be used with further conventional linkage mapping to other DNA markers to expand the genome-wide coverage of the cotton genetic map.

Liu *et al*. (2000) indicated that Simple Sequence Repeats (SSR) provide an accurate way of determining genetic diversity in cotton. Forty two SSR loci were assigned to cotton chromosomes. The aneuploid stocks provide to be powerful tools for localizing SSR markers to individual cotton chromosomes. Multiplex PCR bins of the SSR primers and semi automated detection of the amplified products were optimized in the experiment.

Cantrell *et al*. (2000) studied molecular variation in the converted race stock collection by using Simple Sequence Repeats (SSR). DNA markers and determined the genetic distance of each race stock from a typical *G. hirsutum* cultigens', TM_1. Fifty six fluorescently labeled SSR primers pairs arranged in multiplex bins were used to genotype 97 day-neutral BC_4F_4 race stock accessories. The majority of the accessions had genetic distances <0.25 from the *G. hirsutum* standard TM_1.

Ravi *et al*. (2003) assessed the genetic diversity among 40 cultivated varieties and five wild relatives of rice involving Simple Sequence Repeats (SSR) and Randomly Amplified Polymorphic DNA (RAPD) markers. They were evaluated for polymorphisms after amplification with 36 decamer primers and 38 SSR primer pairs. A total of 499 RAPD markers were produced among the 40 cultivated varieties and five wild relatives with a polymorphism percentage of 90.0. Out of 38 SSR primer pairs used, only locus *viz*., RM115 was monomorphic. SSR analysis resulted in a more definitive separation of clusters of genotypes indicating a higher level of efficiency of SSR markers for the accurate determination of relationships between accessions that are too close to be accurately differentiated by RAPD markers.

Saha *et al*. (2003) revealed the importance of SSR markers for the comparative mapping of transcribed genes. Thirty one SSR primer pairs of 220 tested led to PCR amplification of discrete fragments of cotton cDNA clones amplified with different SSR primer pairs contained repeat motifs. They further showed that sequences from the SSR containing cDNAs were conserved across *G. barbadense* and *G. hirsutum*.

Candida *et al*. (2005) indicated that genetic diversity and the relationship between varieties are of great importance for cotton breeding, thier work was designed to estimate the informativeness of the cotton (*Gossypium hirsutum L*.) simple sequence repeat (SSR) microsatellite locus and to estimate the genetic distance between 53 cotton cultivars as well as to select a set of SSR primers which are able to differentiate the 53 cotton cultivars studied. After extracting DNA from the 53 cultivars and characterized it using 31 pairs of SSR primers, they obtained a total of 66 alleles with an average of 2.13 alleles per SSR locus and values of polymorphism information content (PIC) varying from 0.18 to 0.62, the dissimilarity co-efficient varying from 0 to 0.41. Statistical analysis using the unweighted pair-group method using arithmetic average (UPGMA) revealed seven subgroups which were consistent with the genealogical information available for some of the cultivars. The SSR genetic profile obtained for each of the cultivars made it possible to discriminate 52 of the 53 cultivars.This study of the genetic diversity of cotton cultivars with SSR markers support the need to introduce new alleles into the gene pool of the breeding cultivars.

Rungis *et al*. (2005) utilized SSR markers for quantifying the level of polymorphism between *G. hirsutum* and *G. barbadense* within the species. Their investigation showed that though inter specific polymorphism was high, the level of polymorphism within *G. hirsutum* cultivars was low (~ 5%). SSR markers were employed to estimate genetic distance among selected genotypes (*G. hirsutum*) and its relationship with F_2 performance (Gutierrez *et al*., 2002). The results on genetic distance revealed a lack of genetic diversity among all the genotypes and it was a poor predictor of

overall F_2 performance. However, when genotypes with maximum range of genetic diversity were present, it was a better predictor for some traits.

RAPD, the oldest PCR-based technique (Williams *et al.,* 1990) relies on use of short, random PCR primers to amplify random portions of the genome. It has many advantages such as non-radioactive detection, no prior sequence information for a genome is required, universal primers work in genome, very small amount of genomic DNA is needed, experimental simplicity and no need for expensive equipments beyond a thermocycler and a transilluminator (Rafalski, 1997). Multani and Lyon (1995) generated RAPD markers with 30 random primers and found that *G. barbadense* accessions can be easily distinguished from *G. hirsutum* varieties by 104 markers. Cultivar specific markers were found to be consistent and have the potentiality to be used as genetic finger prints for varietal identification.

Genetic diversity of 31 available *Gossypium* species, three sub-species and one inter specific hybrid was studied by Khan *et al.* (2000). They screened these genotypes with 45 RAPD primers to distinguish the genotypes. The result indicated inter specific genetic relationship of several species as related to their centre of origin. The study further revealed a broader genetic base of most of species besides indicating the genetic relationship of *G. hirsutum* to standard cultivated *G. barbadense, G. herbaceum* and *G. arboretum*. They concluded that for constructing genetic linkage maps, RAPD markers are more efficient than morphological markers, isozymes and RFLP as RAPD detected the variation in closely related genotypes too.

Kumar *et al*. (2003) studied genetic diversity of 30 elite cotton germplasm lines including 20 *G. hirsutum*, seven *G. arboreum*, one each of *G. herbaceum, G. thurberi* and *Gossypium klotzschianum* using RAPD markers and morphological characters. They reported one 1100 bp *G. arboreum* specific band. *G. klotzchianum* was reported to exhibit the least similarity co-efficient of 0.5 with all other species studied. Clustering using morphological characters was found to be more or less similar to the clustering obtained through RAPD analysis. Results of study indicated narrow genetic base within *G. hirsutum* and *G. arboreum* genotypes.

Tabar *et al*. (2004) used RAPD analysis to evaluate genetic diversity among commercial Indian cotton varieties belonging to *G. hirsutum* and *G. arboreum* and revealed that the intervarietal genetic relationships were related to their pedigree and tetraploids show much narrow genetic base than diploids.

Vafaie-tabar *et al*. (2003) evaluated genetic diversity among 7 diploid (*G. arboreum*) and 15 tetraploid *(G. hirsutum*) cotton cultivars using random amplified polymorphic DNA (RAPD) and morphological markers. RAPD markers were efficient and detected 88% polymorphism. The diploid tetraploid cultivars could be divided into separate clusters at 30% similarity with RAPD and 20% similarity with morphometric markers. Classification of the cultivars based on the two markers showed a high degree of agreement with a correlation of (+) 0.90. Both markers revealed higher diversity among diploids than among tetraploids.

Sinha *et al*. (2008) reported that the knowledge of genetic divergence in cotton is essential to enhance the crop improvement programme for abiotic, biotic and other agricultural important traits. Drought tolerance is one of the major limiting factors in cotton production. RAPD and ISSR markers were used to evaluate the genetic diversity among drought tolerant tetraploid and diploid genotypes. The RAPD primers amplified a total number of 795 bands out of which 35 per cent were polymorphic. The ISSR primer (GATA) showed 78% similarity and the primer (GC) has shown 80% similarity. The diploid and tetraploid genotypes were grouped into separate clusters and tetraploid has shown less genetic diversity than diploids.

A number of efforts have been made in various crop plants to investigate the relationship between DNA marker - based genotype variation of the parents to be used in a hybrid breeding programme and heterosis with varying results.

For example, Diers *et al.* (1996) reported that marker- based genetic distance was not consistently correlated with heterosis for inbred diallels and for cultivar diallels in rape seed. Sheng *et al*. (2002) reported significant correlation between genetic distance and seed yield but the determinative co-efficient was very low (0.1024). However, Riaz *et al*. (2001) found that the genetic distance of sequence – related amplified polymorphism (SRAP) in American *B. napus* inbred lines was significantly correlated with hybrid yield performance and heterosis.

Meredith and Brown (1998) studied the relationship between genetic distance estimated by restriction fragment length polymorphic (RFLP) markers among 15 cultivars and one strain from the

USA and yield heterosis of 120 F_2 hybrids produced by a half –diallel genetic design and found that the correlation were very low (r=0.08). Wu *et al.* (2002) studied the correlation between genetic distance measured by random amplified polymorphic DNAs (RAPD), inter simple sequence repeat (ISSR) and simple sequence repeat (SSR) markers among six domestic and two exotic cultivars and inter specific F_1 and F_2 hybrids, and found the correlation between these was low.

Gutierrez *et al*. (2002) used five US, four Australian cultivars and two day- neutral converted lines of *G.hirsutum* to analysis the association between genetic distance based on SSR markers and performance of agronomic and fibre traits of F_2 bulk populations and deduced that significant correlations ranged from negative to positive depending on the traits, genetic background and environment.

Zhang *et al.* (2007) studied the relationship between parental molecular marker diversity and hybrid performance in both intra and inter specific hybrids of cotton to evaluate the feasibility of predicting hybrid performance using molecular markers. Three cytoplasmic male sterile (CMS) lines were crossed with 10 restorer lines to produce 22 F, hybrids during 2003. Of 22 F_1 crosses, 14 hybrids were intra specific (*G. hirsutum* x *G. hirsutum*) and eight inter specific (*G. hirsutum* x *G. barbadense*). These 22 F_1, hybrids and their parents were evaluated for yield and fibre quality traits at Zhejiang University, Hangzhou, China during 2004 and 2005. Genetic distances (GD) among the parents were calculated from 56 random-amplified polymorphic DNAs (RAPD) and 66 simple sequence repeat (SSR) marker data, and their correlation with hybrid performance and heterosis were analysed.

Mohammadi *et al.* (2008) investigated the correlation between the potential of molecular markers and hybrids performance in Maize. Significant correlation was found between GD value of parental lines and hybrid performance for the test cross and diallel data. In diallel analysis significant correlation was observed between total grain yield per ear (TGW) and genetic distance based on SM co-efficient, whereas the correlation of GD and specific combining ability of hybrids for this trait was not. Through the stepwise multiple regression analysis a total of 19 informative SSR markers distributed over all chromosomes, except chromosomes 7 and 8, were detected. GD values based on informative markers in general were grater compared to that of based on all markers and significant improvement was observed in the correlations between GD estimates based on informative markers and TGW as well as SCA.

2.6 *In planta* genetic transformation

Technology for gene delivery plays an important role in the process of plant genetic engineering. Foreign genes are introduced into genome of recipient species either by physical, chemical or biological means. Since the first transgenic plant appeared in 1983, studies on plant transformation techniques have achieved a great progress.

Plant transformation mediated by the soil plant pathogen *Agrobacterium tumefaciens* is simple method for plant transformation. There are two tumorgenic species *i.e. Agrobacterium tumefaciens* and *Agrobacterium rhizogene. Agrobacterium tumefaciens* is a gram negative soil bacterium, causes crown gall tumors (neoplastic disease) on many dicotyledonous and some monocotyledonous plants (Broer *et al*., 1995). During plant infection *A. tumefaciens,* transformed plants by transferring a part of its DNA called transferred DNA (T-DNA) from its tumour inducing (Ti) plasmid to the plant genome. The virulence (Vir) region of the Ti plasmid codes for the function required for processing and transfer of T-DNA (Lyer *et al*., 1982; Stachel and Nester, 1986). The discoveries that T-DNA codes for oncogene which is only transferred to plant cell genome (Bevan *et al*., 1983a) and non virulent or disarmed strains *i.e.* containing T-DNA from which oncogenes have been removed and replaced by any other gene of interest, behave in the same way as virulent strain do, that opened a new avenue in transformation of interested gene to higher plants (Fig. 1).

2.6.1 *Agobacterium* mediated transformation

Zhou *et al.* (1983) reported cotton transformation through injection of DNA directly into embryos in immature cotton bolls. Since the injected DNA was obtained from Sea Island cotton (*G. barbadense L.*) plants with different morphological characteristic in the recipientupland cotton (*G. hirsutum L.*) plants were obtained. The putative transformed plants were identified by phenotypes such as boll size and fibre length. The absence of any discrete foreign gene precluded analysis by DNA hybridization to genomic southern blots.

Horsch *et al*. (1985) described a protocol of co-cultivating *Agrobacterium* with leaf discs instead of protoplasts to overcome problems of regeneration of plants through protoplasts.

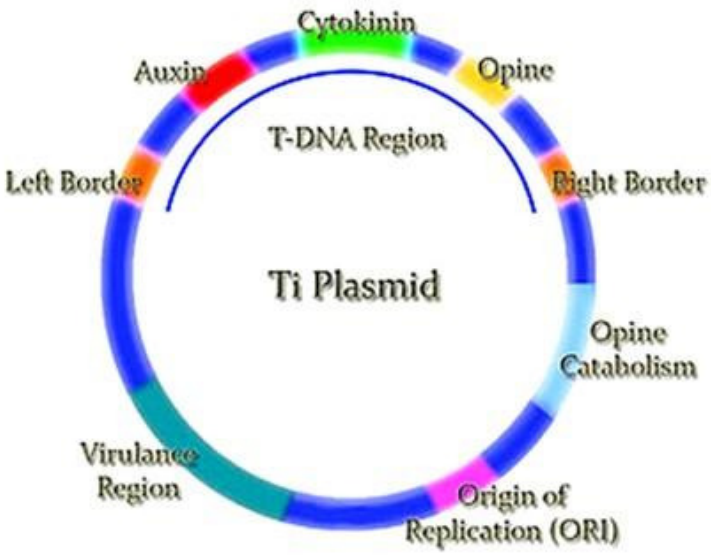


Fig. 1. Ti Plasmid Construction in *Agrobacterium tumefaciens*

Gynheung (1985) reported that tobacco calli were transformed at levels up to 50 per cent by co-cultivation of tobacco cultured cells with *Agrobacterium tumefaciens* harbouring the binary transfer DNA vector, PGA-472, containing a Kanamycin resistance marker. Transformation frequency was dependent on the physiological state of the tobacco cells, the nature of *Agrobacterium* strain and, less so on the expression of vir genes of the tumour inducing plasmid. Maximum transformation frequency was obtained with exponentially growing plant cells, suggesting that rapid growth of plant cells is an essential factor for efficient transformation of higher plants.

Firoozabady *et al.* (1987) found that cotton cotyledon tissues are efficiently transformed and regenerated. Cotyledon pieces from 12 day old aseptically germinated seedling were inoculated with *Agrobacterium tumefaciens* strains containing avirulent Ti plasmids with a chimeric gene encoding kanamycin resistance. After three days co-cultivation, the cotyledon pieces were placed on a callus initiation medium containing kanamycin for selection. High frequencies of transformed kanamycin resistant calli were produced 80 % of which were induced to form somatic embryos. Somatic embryos were germinated and plants were regenerated and transferred to soil. This process for producing transgenic cotton plants facilitates transfer of genes of economic importance to cotton.

Umbeck *et al.* (1987) reported preliminary results on cotton (*G. hirsutum L.*) transformation *via Agrobacterium* using hypocotyls as explants. Selection and regeneration were not thoroughly characterized.

Chee *et al.* (1989) have confirmed that about 0.01 per cent of the total seeds infected with *Agrobacterium tumefaciens* harbouring *npt*-II gene have shown transformation in case of germinating seeds of *Glycine max*.

Fredrick *et al*. (1990) reported the expression of insecticidal proteins HD-73 *Cry1Ac* and *Cry1Ab* in cotton. Coker 312 was transformed by *Agrobacterium* mediated transformation. Total protection from insect damage of leaf tissue for these plants was observed in laboratory assays when tested with Lepidopteran insects. Potrykus (1990) reported that shoot apical meristem of plant generates the whole plant at higher frequency. Gene transformation to meristem cells could therefore, overcome many of the regeneration problems of tissue culture systems in many important crop species.

Schrammeijer *et al*. (1990) reported transformation of sunflower (*Helianthus annuus* L. cv. Zebulon), shoot apical meristems were dissected from seeds and co-cultivated with a disarmed *Agrobacterium tumefaciens* strain harboring a binary vector carrying genes encoding *GUS* and *npt*-II activity. The influence of the media conditions, the time of co-cultivation and the stage of the developing seed on shoot development and meristem transformation was analysed. Transformants were selected by their ability to grow on kanamycin. Transformation was confirmed by assays for *GUS* and *npt*-II. *GUS* positive shoots were rooted on rockwool and transferred to soil. Transformation of

shoot meristem cells occurred at low frequencies. Chimaeric expression of the two genes was observed in transformed plants.

Srivastav *et al*. (1991) used disarmed *Agrobacterium tumefaciens* vector to transform *G. hirsutum.* Three days old inoculated hypocotyls were selected on kanamycin medium. Different phytohormones were used for the induction of calli. The calli obtained were selected for continuous proliferation on kanamycin medium. They observed that calli were resistant to the antibiotic and expressed the *npt*-II enzyme.

Gould *et al*. (1991a) reported method of regenerating cotton plants from the shoot apical meristem of seedling for use with particle gun and *Agrobacterium* mediated transformation. This method was developed to circumvent the problems of genotype restriction and chromosomal damage frequently encountered in cotton regeneration in tissue culture through somatic embryogenesis. The normal and fertile plants *G. barbadense* Pima S-6 and S-19 cultivar of *G. hirsutum* were regenerated using *Agrobacterium* mediated transformation method. Shoot regeneration from these tissues was direct and rapid.

Cousins *et al*. (1992) have succeeded in producing transgenic plants from Australian cultivar Siokra 1-3 through *Agrobacterium* mediated transformation system. Transgenic plants expressed novel genes *i.e. npt-II* (Neomycin Phospotransferase) or the *GUS* (glucoronidase) gene. The critical factors in transformation were the use of a super virulent disarmed Ti plasmid with binary transformation vector and a highly regenerable Australian genotype of cotton.

Medford (1992) reported that meristem is often confused with the complete shoot apex, which also contains the leaf primordia and the young leaves. Further more, the meristem as a tissue may represent a complicated pattern of cells. Each of these cells may differ physiologically due to its unique position in the meristem.

Sautter *et al*. (1995) reported that shoot apical meristems provide a tissue, which regenerates *in situ* a fertile plant for most of the given genotypes. Transformation of meristem cells may lead to transgenic sectors in chimeras. These sectors may contribute to the gametes and, thus, to transgenic offspring, which then should be homohistonts and not sectorial chimeras like their parents.

Agarwal *et al*. (1997) reported induction of multiple shoots in cotton with cotyledonary nodes devoid of cotyledons and apical meristems. Explants from 35 day old seedlings yielded the maximum number of shoots (4.7 shoots/explant) using Murashige and Skoog (MS) basal medium supplemented with 6-benzylaminopurine and kinetin (2.5 mg/1each). Explants from 35 day old seedlings raised in glass bottles produced a higher number of multiple shoots (8.3 shoots/ explant) than those grown in glass tubes and cultured on the same shoot induction medium. Elongation of multiple shoots was obtained on liquid or agar MS basal medium without phytohormones. *In vitro* shoots were rooted on half-strength agar-solidified MS basal medium or with 0.05 or 0.1 mg/1 naphthaleneacetic acid. Hardening and survival of tissue culture plantlets was 95% under greenhouse conditions.

Pannetier *et al.* (1997) reported that regeneration of somatic embryos is relatively low and not fully mastered. The expression level of native *Bacillus thuringiensis* genes in plants is very low. It will protect the cotton from *S. littoralis* and development of insect resistance varieties.

Dillen *et al*. (1997) indicated that temperature plays an important role in transformation with *A. tumefaciens.* In their results, the best transformation efficiency was obtained at 22 ^{o}C in both *Phaseolus acutifolius* callus and tobacco leaves, irrespective of the type of helper plasmids. Although *in vitro* co-cultivation is normally done at 25 ^{0}C, they showed that a lower temperature (19-22 ^{0}C) was more optimal because *in planta* tumour formation occurred more frequently at 22 ^{0}C.

Saeed *et al*. (1997) reported that in order to develop transgenic plants *via* the biolistic gun method regenerable embryogenic tissues are required. Meristem shoot tips of 19 cultivars of cotton were cultured on several media formulations and assessed for shoot and root development. The best shoot development was observed on media containing 0.46 mM kinetin while rooting was observed on media containing 2.68 mM NAA and 0.46 mM kinetin. No intervarietal variability was observed. A complete protocol was developed from meristem tip culture to field transfer. This methodology was simple and replaces the prevailing existing protocols for meristem tip culture of cotton so far.

Mahalaxmi and Khurana (1997) have studied the age and physiological status of the plant and reported that the meristematic tissues, explants from the young plants and cells undergoing dedifferentiation are the choicest material for *Agrobacterium* mediated transformation. The age and physiological status of the plant plays an important role during plant microbial interactions. Usually, 3-

4 days old seedlings were used for agro-infection in maize, wheat and other cereals than dry dissected seeds with exposed apical meristems. Immature embryos of maize were differentially susceptible to *Agrobacterium;* the best stage corresponded to 12-22 days after pollination when the two leaf initials were formed, indicating a specific window of competence in the host plant. It was also observed that leaves were more competent than roots, scutellum or seed remnants in maize, rice and in wheat and barley.

Cervera *et al.* (1998) have suggested that low efficiency of transformation was due to an insufficient length of co-cultivation, however they have also reported that it was more difficult to eliminate *Agrobacterium* after longer periods of co-cultivation. Further they have also reported that the 5 day culture period resulted in over growth of *Agrobacterium* and a subsequent decrease in the regeneration frequency of transformed shoots, although 5 day co-cultivation was the most effective for increasing the frequency of transient *GUS* expression in citrange explants. Therefore, the period of co-cultivation should be optimized.

Gould and Maria Magallenes Cedeno (1998) presented a protocol for rapid genotype independent transformation and regeneration of cotton (*Gossypium spp*.) from shoots isolated from germinating seedling. They inoculated the isolated shoots with a super virulent strain of *Agrobacterium tumefaciens,* subjected them to a mid antibiotic selection, and directly regenerated as shoots *in vitro*. By this method, the shoots did not dedifferentiate and mutation rates were low. Rooted shoots could be obtained within 6-10 weeks of isolation and inoculation depending on the cotton cultivar.

Wang *et al*. (1998) have successfully done transformation of four upland cotton cultivars *via Agrobacterium* mediated transformation. Hypocotyl segments from asceptic seedling were screened and somatic embryos and regenerated plants were obtained on various media. Transgenic cotton plants were confirmed by ELISA, PCR and southern analysis, and bioassays demonstrated that the transgenic plants had significant resistant to larva of cotton bollworm.

Hemphill *et al.* (1998) reported a clonal propagation system to regenerate mature cotton (*G. hirsutum* L.) plants from *in vitro* grown tissues. Shoot apices, lateral nodes and cotyledonary nodes were co-cultivated with *Agrobacterium tumefaciens* and grew to a two leaf stage by this *in vitro* culture system. They further reported that this procedure resulted in 121 kanamycin selected shoots and 40 mature viable plants, which produced viable T_1 seeds. Mature T_1 plants expressed *GUS* activity in pollen grains that suggested that the transgene was inherited by progeny.

Moralejo *et al.* (1998) have described a procedure for genetic transformation of *Eucalyptus globulus* (Labill) and they have studied the influence of explant pre-cultivation and reported that when seedlings were pre-cultivated for 4-6 days, the level of *GUS* transient expression was significantly greater than that of control (*i.e.* without pre-culture) and that the seedlings pre-cultured for 6 days seemed to be more suitable for stable integration of transgenes. They further reported that the improvement of DNA uptake could be due to stimulation of cell division by the hormones in the pre-cultivation medium, since mitotic cells would be more susceptible to *Agrobacterium* or would have a higher level of transcription.

However, they also opine that the physiological status optimal for DNA uptake (transient expression) is not necessarily optimal for integration of foreign DNA in the host genome. Infact, division of cells would not be sufficient for transformation, and integration may primarily depend on the availability of DNA repair enzymes. These proteins, although not yet identified are thought to play a key role in the last steps of T-DNA integration (Tinland 1996).

Jorge *et al*. (1998) reported that cytokinins are involved in shoot development of plants. Events of multiple bud formation and shoot development in apical embryonic axes of cotton treated for 2 or 20 days with the cytokinin benzyladenine (BA) were compared with the development of untreated control axes. Meristematic regions (supernumerary vegetative buds) were observed in axes treated for 20 days with BA. An average of 3.4 shoots per embryonary axis was obtained when explants were cultured on medium supplemented with 3 mg l-1 BA. Higher and lower concentrations of the growth regulator yielded fewer shoots per explant. Result shows that BA is directly responsible for re-programming the embryonic apical meristem axes of cotton toward the production of multiple buds and subsequent shoot development.

Zapata *et al.* (1999) reported that transgenic cotton (*G. hirsutum*) plants of Texas cultivar were obtained using *Agrobacterium* mediated transformation coupled with the use of shoots apex explants. Regeneration of primary plants was carried out in a medium containing 100 mg/1 of kanamycin and

the progeny obtained by selfing T_0 plants were subjected to kanamycin screening. Surviving plants showed more than one copy of T-DNA. The use of shoots apex circumvents the problem of genotype dependent regeneration of cotton.

Donaldson and Simmonds (2000) have reported the overall rate of *in vitro* transformation for co-cultural explants placed on selection media ranged from 27-92 per cent depending on the cultivar. However transformation was predominantly confined to nonregenerable hypocotyl callus or other non-regenerable tissue, in regeneration, competent tissue of the cotyledonary node or in differentiated tissue was rare.

Sunilkumar Rathore (2001) reported green fluorescent protein (GFP) proved to be a valuable tool in elucidating the timing and localization of transient gene expression and in visualizing conversion of transient events to stable transformation events. Strain LBA4404 proved to be significantly better than EHA105. Acetosyringone significantly increased the stable transformation efficiency in cotton at 21 ^{0}C compared to 25 ^{0}C.

Maqbool *et al*. (2002) reported that three oat (*Avena sativa* L.) cultivars have been successfully transformed using an efficient and reproducible *in vitro* culture system for differentiation of multiple shoots from shoot apical meristems. The transformation was performed using microprojectile bombardment with two plasmids (pBY520 and pAct1-D) containing linked (*hva1-bar*) and non-linked (*gus*) genes. The *hva1* and *bar* genes cointegrated with a frequency of 100% as expected and 61.6% of the transgenic plants carried all three genes. Molecular and biochemical analyses in R_0, R_1 and R_2 progenies confirmed stable integration and expression of all transgenes. Localization of the GUS protein in R_0 and R_1 plants revealed that high expression of *GUS* occurred in vascular tissues and in the pollen grains of mature flowers.

Satyavathi *et al.* (2002) have given a protocol for consistent production of transgenic cotton plants in three indian varieties established utilizing *Agrobacterium* mediated transformation. Shoot tip explants were transformed by co-cultivation with *Agrobacterium tumefaciens* strain LBA-4404. The strain harbors a binary vector pBAL2 carrying the reporter gene b-glucuronidase intron (*GUS-INT*) and the marker gene-neomycin phosphotransferase (*npt*-II). Regeneration potential of explants or different hormones was studied in detail. Among the different combinations of BAP and NAA tested, 0.1 mg per ml of BAP and NAA in the medium influenced efficient regeneration of shoots by organogenesis. Shoot bud proliferation and elongation was achieved in 3-4 weeks time on medium supplemented with GA_3. The putatively transformed shoots were harvested and placed for rooting on medium containing IBA and 75 mg/l kanamycin. Transgenic plants were recovered in 12-16 weeks from the time of gene transfer to establishment in pots. Molecular analysis of the field established plantlets was carried to confirm the transgenic nature. The presence of *gus* and *npt*-II genes in the transgenic plants was verified by histochemical *GUS* assay and polymerase chain reaction (PCR) analysis, respectively. Integration of T-DNA into the genome of putative transgenics was further confirmed by southern blot analysis. A total of 70-75 transgenic plants were raised in pots. Progeny analysis of these plants showed a classical mendelian pattern of inheritance.

Veluthambi *et al.* (2003) reported that the naturally evolved unique ability of *Agrobacterium tumefaciens,* to precisely transfer defined DNA sequences to plant cells, has been very effectively utilized in the design of a range of Ti plasmid-based vectors. *Agrobacterium* chromosomal virulence genes (*chv*), T-DNA delimited by a right border and a left border and Ti plasmid virulence genes (*vir*) constitute the T-DNA transfer machinery. The inability of *Agrobacterium* to transfer DNA to monocotyledonous plants was considered its major limitation. *Agrobacterium* T-DNA transfer is now viewed as 'universal' based on successful transformation of yeast, *Aspergillus* and human cells.

Chinchane *et al*. (2004) carried out a transformation work on diploid cotton (*G. arboreum*) cultivar PA 255 (Parbhani Turab) using *Agrobacterium tumefaciens* strain LBA4404 containing *npt*-II gene and *Cry 1A*(c) gene. The combination of MS medium containing BAP (2mg/lit.) and kinetin (1mg/lit.) concentration was found to be the best for induction of multiple shoots and later shoots were tested for gene expression by ELISA and southern blot hybridization. Some of the shoots tested positive.

Ouma *et al.* (2004) reported in two cultivars of cotton, Delta pine 50 (DP_{50}) and Stoneville 474 (STV474) the effects of thidiazuron (TDZ), naphthalene acetic acid and silver nitrate ($AgNO_3$) on shoot regeneration from hypocotyl explants which was cultured *in vitro* excised from 14 day-old seedlings. The best treatment for formation of adventitious shoots in DP50 was the treatment containing 0.175 mg/l TDZ, 0.01 mg/l NAA and 5.1 mg/l $AgNO_3$, while treatment containing 0.08 mg/l 8 TDZ, 0.01 NAA mg/l and mg/l 10.2 $AgNO_3$ was optimum for the formation of adventitious shoots for STV474.

Saeed *et al.* (2004) reported that cotyledonary nodes obtained from aseptically raised seedling were cultured on modified Murashige and Skoog medium (MS) supplemented with different doses of Kinetin. Cotyledonary nodes produced the maximum number of shoots (3.43 shoots/ explant) when cultured on MS medium supplemented with 0.25 mg/l Kinetin. The highest percentage (93.3 %) of root development and root length (5.85 cm) was obtained when shoots were cultured on MS medium supplemented with 0.5 mg/l napthalene acetic acid (NAA) and 0.1 mg/l Kinetin.

Ikram-ul-haq (2004) successfully transfered gene through *Agrobacterium* mediated gene delivery system *via* vacuum infiltration for 2 month old embryogenic calli of cotton cv. Cocker –312 and with optimized selective transformed callus growth and somatic embryogenesis by the use of kanamycin antibiotic.

Leelavati *et al*. (2004) presented a protocol for efficient transformation and regeneration of cotton. Embryogenic calli co-cultivated with *Agrobacterium* carrying *Cry* IIa5 gene were cultivated under dehydration stress and antibiotic selection for 3-6 weeks to generate several transgenic embryos. Seventy five globular embryo clusters were observed on selection plates and these embryo clusters were cultured on multiplication medium followed by development of cotyledonary embryos on embryo maturation medium to obtain an average of 12 plants per petri plate of co-cultivated callus. Eighty three per cent of these plants have been confirmed to be transgenic by southern blot analysis and ten kanamycin resistant plants per plate was obtained.

Wu *et al.* (2005) reported high frequency of transformation *via Agrobacterium* mediation, coupled with the use of embryogenic calli as explants. *Agrobacterium tumefaciens* strain LBA4404 harbouring binary vector pBin 438 carrying a synthetic *Bacillus thuringiensis* active *Cry1 Ac* and *API-B* chimeric gene. The transgenic plants were highly resistant to cotton bollworm (*Heliothis armigera*) larvae, with mortality ranging from 95.8 to 100 per cent.

Shuangxia *et al.* (2005) reported transforming embryogenic callus mediated by *Agrobacterium tumefaciens* in cotton. *Agrobacterium* concentration and physiological status of embryogenic callus on transformation efficiency were superior strain LBA-4404 and proved significantly better than $C_{58}C_3$. Relatively low co-cultivation temperature (19 ^{0}C) and short co-cultivation duration (48h) were optimal for developing a highly efficient method of transforming embryogenic callus. Concentration of Acetosyringone at 50 mg/1 during cocultivation significantly increased transformation efficiency. Embryogenic callus growing 15 days after subculture was the best physiological status for transformation.

Guo *et al*. (2007) transferred three constructed harbouring novel *Bacillus thuringiensis* genes *Cry1C, Cry2A, Cry9C* and *bar* gene into four upland cotton cultivars via *Agrobacterium* mediated transformation. As high as 84.8 per cent resistant calli were confirmed positive by PCR tests and total 50 transgenic plants were regenerated. Bioassay showed 80 % of the transgenic plantlets showed resistance to both insect and herbicide. This result showed that *bar* gene can replace antibiotic marker genes.

Katageri *et al.* (2007) reported development of transgenic cotton using shoot apical meristems, which was isolated from seedlings as explant. Synthetic gene encoding *Cry*1*Ac* endotoxin of *Bacillus thuringiensis* was used for transformation. Regeneration of shoots was carried out in selection medium containing kanamycin (100 mg/l) after co-cultivation of the explants with *Agrobacterium tumefaciens.* Progeny obtained by selfing T_0 plants was grown in the greenhouse and screened for the presence of neomycin phosphotransferase (*npt*II) and *Cry1Ac* genes by polymerase chain reaction (PCR) and Southern hybridization. Expression of *Cry1Ac* in the leaves of the transgenic plants was detected by strips and quantified by Quan-T ELISA kits. Insect bioassays were performed with the larvae of cotton bollworm (*Helicoverpa armigera*). Results of the field tests showed considerable potential of the transgenic cotton for resistance against cotton bollworm.

2.6.2 Elimination of *Agrobacterium tumefaciens*

One of the major problem occurs during plant tissue transformation with *A. tumefaciens*, is the effective elimination of the *Agrobacterium* after transfer of genetic information has taken place. If *A. tumefaciens* is not eliminated, it will overgrow the tissue and affect the further growth of explants. Antibiotics are used for this purpose, but the levels of antibiotics needed to kill the organism may have deleterious effects on the regeneration. Therefore, the level of antibiotic requirement is to be standardized for individual crops.

Pollock *et al*. (1983) have reported that through many antibiotics have been described for the effective elimination of *Agrobacterium,* Cefotaxime have minimal toxicity on most of the tissues and efficiently eliminate *Agrobacterium* cells. Carbenicillin or Cefotaxime antibiotics showed plant hormone like activity on plant tissues, especially when the plant tissues were grown in a medium containing low concentration.

2.6.3 Improvement of efficiency of *Agrobacterium* transformation

The frequency of *Agrobacterium* mediated transformation is very low. Recently it has been demonstrated that the efficiency of transformation can be enhanced by supplementing with other methods such as preculture of the explants. Pre-culturing of the explants on the regenerating medium prior to inoculation of *Agrobacterium* increased the frequency of transformants in pigeonpea to 62 per cent from cotyledonary node and 27 per cent from shoot tip (Geetha *et al.,* 1999) 28.8 per cent from callus and 1.2 per cent from shoots regenerated (Lawrence and Koundal, 2001), cowpea (Muthukumar *et al.,* 1996), chickpea (Kar *et al.,* 1996). Likewise, there are different techniques to enhance the efficiency of *Agrobacterium* mediated transformation, one can adopt appropriate technique, which is simple, economically feasible, less laborious, time saving and beneficial for a given crop species.

2.6.4 *Cry* genes

Major crops such as rice, cotton and pigeon pea are damaged by lepidopteron pests on regular basis, which necessitates use of large amounts of pesticides to manage the pests. An effective and safe strategy for insect pest management is to deploy insecticidal protein genes in transgenic crops. Since the first *Cry*1*Ac Bt* cotton variety was commercialized, there have been numerous advancements for insect control with transgenic technology. Since the insects are developing resistance against the commercially available transgenic cotton with *Cry*1*Ac* gene, it necessitates the development of new transgenics with other genes encoding *Bt*-toxins to delay the development of resistance. Armes *et al*. (1996) have reported the resistance to insecticides in Indian cotton ecosystem. Further, there are expectations that change in the pest complex due to single toxin protein.

Adamczyk and Gore (2004) have investigated the efficacy of transgenic cotton genotypes containing *Cry*1*AC*, *Cry*1*F* and *Cry*1*Ac* stacked with *Cry*1*F* against beet armyworms, fall army worm in the laboratory bioassays and small experimental field plots, and observed that cotton containing *Cry* 1*F* was more toxic than cotton containing only *Cry*1*Ac*.

Dongre *et al.* (2004) have developed insect resistant cotton with *Cry1Aa*$_3$ gene and their insect bioassay studies have revealed encouraging results with reference to gene expression studies using ELISA.

2.6.5 Polymerase chain reaction

Kary Mullis invented the polymerase chain reaction (PCR) in 1985 (Mullis K.B., 1990). One of the major applications of this outstanding invention is to know the presence of a transgene. The polymerase chain reaction results in the selective amplification of a transgene, if an appropriate primer is provided. Any region of transgene can be chosen, so long as the sequences at the borders of the region are known. The border sequences must be known because in order to carry out a PCR, two short oligonucleotides, must hybridize to the DNA molecule, one to each strand of the double helix. These oligonucleotides, which act as primers for the DNA synthesis reactions, delimit the region that will be amplified. Amplification is usually carried out by the DNA polymerase-I enzyme from *Thermus aquaticus*, which lives in hot springs, and many of its enzymes, including Taq polymerase, are thermostable, meaning that they are resistant to denaturation by heat treatment. Thermostability of Taq polymerase is an essential requirement in PCR methodology along with dNTPs, $MgCl_2$, reaction buffer, specific primers and sterile water. To begin PCR amplification, the enzyme is added to the primed template DNA and incubated so that it synthesis new complimentary strands. The reaction mixture is then heated to 94 ^{0}C so that the newly synthesized strands detach from the template, and then cooled, enabling more primers to hybridize at their respective positions, including positions on the newly synthesized strands. Taq polymerase, which unlike most types of DNA polymerase is not inactivated by the heat treatment, now carries out a second round of DNA synthesis. The cycle of denaturation, hybridization and synthesis is repeated, usually 25-30 times, resulting in eventual synthesis of several hundred million copies of the amplified DNA fragment. At the end of a PCR, a sample of the reaction mixture is usually analysed by agarose gel electrophoresis, sufficient DNA

having been produced for the amplified fragment to be visible as a discrete band after staining with ethidium bromide. This may by itself provide useful information about the presence of transgene that has been amplified.

Gould *et al.* (1998) have subjected Maize DNA from six F_1 of C56 and from one F_2 of C1 to PCR amplification of 250 bp fragment within the *GUS* coding region. In a separate amplification, primers for a 1000 bp fragment within the NOS/NPT II gene were used. Amplification of the expected fragments were achieved from the DNA of four C56 F_1 as well as from the DNA of an F_2 of the C1 family. These results indicated the presence of both *GUS* and *npt*-II in the progeny of two original transformants.

Manoharan *et al.* (1998) have used the technique to demonstrate the presence of TDNA in the transgenic plants. Two specific primers derived from *npt*-II gene sequences were used to detect a 0.7 kb fragment. The amplified DNA samples were electrophoresed on 0.8 per cent agarose gel. Fragment (0.7 kb) co-running with the amplified product from PBI-121 could be detected from the transgenic plants but not from non transformed plant.

Zhang *et al.* (1998) have reported that the resistance to the bollworm was observed in the R_2-progeny derived by selfing the five R_1 plants, which was evident from the high mortality rate of bollworm. On the basis of resistance analysis some resistant plants were sampled for the presence of the *Bt* transgene with PCR. The amplified band on the *Bt* transgene appeared in the samples of R_1 plants S 545 and S 591. The PCR products were subjected to southern blot analysis with the labelled transgene as probe. All the amplified bands could hybridize with the probe, proved that the PCR bands were not amplified from contaminating DNA, but from the *Bt* transgene, thus establishing that transgene was heritable through selfing.

Geetha *et al.* (1999) subjected the putatively transformed plantlets to PCR analysis to detect the presence of *uid* A and *npt*-II genes. In the transformants with *GUS* activity, an expected fragment of 500 nucleotide uid A was amplified. An additional confirmation was also done using *npt*-II primers and PCR analysis revealed amplification of a 700 base pair fragment. No amplification was found in non transgenic plants of pigeonpea.

Krishnamurthy *et al.* (2000) have reported the detection of the *npt*-II coding sequence in the progeny when genomic DNA was subjected to PCR using the following primers and conditions: forward 5^1TCATCTCACTTGCTCCTG-3^1 and reverse 5^1AGC CAACGCTATGTCCTG-3^1 primers at a concentration of 50 pM to amplify a 363 bp region (position 1860-2222 of Tn_5) of the *npt*-II gene (pHP 23 served as a positive control) with 0.5 g genomic DNA of each sample, 2 mM $MgCl_2$, and 2 units of a (native) Taq Polymerase (and the recommended buffer) from Gibco in a 50 µl assay. Cycling conditions were denaturation, 1 min at 94 ^oC; annealing, 1 min at 50 ^oC, elongation 2 min at 72 ^oC; annealing, 1 min at 50 ^oC, elongation 2 min at 72 ^oC (30 cycles) and a final elongation step of 10 min. For detection of 363 bp fragment DNA was separated on 1 per cent agarose gels. All the 4 plants indeed showed the presence of the expected 363 bp fragment, which is part of the coding region of the *npt*-II gene. In one of the putatively transformed lines, an additional fragment of approximately 2.5 kbp was amplified, probably due to re-arrangement of two or more incomplete copies.

Prasad *et al.* (2000) have carried out PCR analysis of the *npt*-II gene for initial screening of putative transformants of *Brassica juncea* for the presence of *npt*-II gene. About 85 per cent of the putative transformants gave the 0.7 kb full length *npt*-II gene. These results clearly indicated the successful integration of the gene cassette in these putative transformed lines of *Brassica juncea.*

Weir *et al.* (2001) have performed PCR in 10 µ1 of reaction solution using 25-40 ng of wheat genomic DNA, 100 µ M each dNTP, 10 pmol of each primer and 1 unit of Taq DNA polymerase. The cycling program was 1 cycle of 95 ^oC for 5 min, 35 cycles of 95 ^oC for 30s, 56 ^oC for 30s and 72 ^oC for 2 min. Primers to amplify the *npt* gene were 5^1-AAAAGCCTGAACTCACCG-3^1 and 5^1-TCGTCCATCACAGTTTGCC-3^1. The PCR products were visualized by running the completed reaction in a one per cent agarose gel containing ethidium bromide and then photographed. PCR analysis of lines transformed with PBGxI and selected with hygromycin B showed that *npt* gene was present in callus lines showing different intensities of GFP expression, with the production of a well defined product of 250 bp.

Satyavathi *et al.* (2002) have carried out PCR amplification of the *npt*-II gene using specific primers to check the presence of transgene in the plant genome. Plant DNA was isolated from immature leaves and DNA concentration was estimated spectrophotometrically. The *npt*-II specific primer sequences (51-31) GAG GCT ATT CGG CTA TGA CTG and ATC GGG AGG GGC GAT ACC

GTA were used. Each PCR reaction was performed in 25 µ 1 (total volume) of reaction mixture consisting of 10 x reaction buffer, 150 ng DNA, 200 mM dNTPs, 25 mM $MgCl_2$, 100 ng of each primer DNA and 1 U of Taq DNA polymerase. The PCR reaction buffer consisted of 10 mM Tris HCl (pH 8.3), 25 mM KCl and 0.01 per cent gelatin. PCR was carried out in a thermal cycler under the following conditions, 94 ^{o}C for 3 min as preheating, then 35 cycles of 94 ^{o}C denaturing for 30 S, 55 ^{o}C annealing for 45 S, 72 ^{o}C synthesis for 1 min and 7 min at 72 ^{o}C as final extension. Amplified DNA fragments were electrophoresed on 1.0 per cent agarose gel and detected by ethidium bromide staining and photographed under ultraviolet light.

2.6.6 *In planta* genetic transformation

In most of cases, transgenic plants are produced by methods which include the transformation of individual plant cells followed by regeneration of whole plants from such cells (Christou, 1995; Fraley *et al.,* 1983; Potrykus, 1991). Although these approaches work well for some species, in others it has proven difficult to regenerate whole plants from tissues susceptible to transformation. So the efforts were made to develop protocols for *in planta* transformation where there is no need of *in vitro* regeneration. There are only a few species for which transformation systems without tissue culture based regeneration steps are available (Anthony *et al.,* 2000).

MATERIAL AND METHODS

3.1 Development of heterotic groups

Utilization of heterosis depends on genetic diversity existing between the parents, magnitude of dominance at the yield influencing loci and the genetic distance between the chosen parental genotypes. It is possible to maximize heterosis by enhancing genetic distance between two chosen parental populations. Many population improvement schemes are followed in cross pollinated crops to increase genetic diversity, to create heterotic groups and exploit them. These schemes can be extended to self pollinated crops by introducing slight modifications in the procedures to suit the crossing system of self pollinated crops. In present study heterotic box was developed by involving barbadense and hirsutum varieties and it was exploited by creating recombinational variability for combining ability.

If two lines A and B are found to give potential crosses with testers T_1 and T_2, it is possible to increase the genetic distance between these opposite pairs A, B *vs*, T_1 and T_2 by following population improvement scheme for improving combining ability defined in cross pollinated crops by introducing suitable changes to match the crossing system seen in self pollinated crops. The recombinational variability realized in a segregating generation like F_3/F_4 can be evaluated by crossing these lines with opposite testers representing opposite heterotic group.

To increase productivity ELS (Extra Long Stable) cotton emphasis is necessary to implement this programme in inter specific hybrids. Realizing the need for developing potential inter specific (*G. hirsutum x G. barbadense*) hybrids, a detailed study was initiated at UAS Dharwad to identify hirsutum and barbadense genotypes capable of giving potential inter specific hybrids. Based on this study done during earlier years in 2009-2010 two barbadense DB 533 and DB 534 and four hirsutum DH 98-27 (T_1), ZCH 8 (T_2), 178-24 (T_3) and DH 18-31 (T_4) lines giving best hybrids (H x B) combinations between them were selected. After identifying this heterotic box, these barbadense lines DB 533 and DB 534 were crossed in 2007-2008 and the material was advanced during succeeding years. To confirm the potentiality of heterotic group, the detailed evaluation of inter specific hybrids involving these lines along with other crosses was taken up during 2010-2011 (Fig. 2).

3.1.1 Line x Tester for confirmation of inter specific heterotic groups (YHB)

The main objective of this line x tester study was to determine the combining ability status of the barbadense and hirsutum lines included in the heterotic box. These lines were compared with other barbadense and hirsutum lines. For the pattern of combining ability and the potentiality of the inter specific hybrids developed based on them.

In this experiment, 92 (YHB trial) inter specific crosses (*G.hirsutum x G.barbadense*) along with three checks (MRC 6918 *Bt* check, RAHB 87 and DCH 32 non *Bt* checks) were subjected to line x tester analysis (23 hirsutum testers and 4 barbadense lines). This experiment was laid out in Randomized Block Design (RBD) with two replications (Fig. 3) & (Plate 1). Each entry was sown in 2 row plots spaced at 90 cm x 60 cm with recommended dose of fertilizer and seeds were sown on 28-6-2010, 2-3 seeds were dibbled per spot in each row and thinning was attended to retain one healthy plant per hill at 25 days after sowing. All the recommended package of practices were followed to raise healthy crop.

3.1.2 Comparison of hybrids based on heterotic box with checks (Best HB)

The efforts on creating recombinational variability have begun with two barbadense lines. However, to compare the potentiality of these 8 hybrids with other potential hybrids developed over years at Dharwad centre and best commercial hybrids (*Bt* and non *Bt*), a separate evaluation of these hybrids was taken up. The general procedure of conducting the trial remained same as above.

For mean performance of 49 (best HB trial) hybrids, the hybrids along with three checks (MRC 6918 *Bt* check, RAHB 87 and DCH 32 non *Bt* checks) was laid out in one replication. Each hybrid was sown in 4 rows plots with spacing of 90 cm x 60 cm with recommended dose of fertilizer and the trial was sown on 27/6/2010 (Fig. 3 and Plate 2).

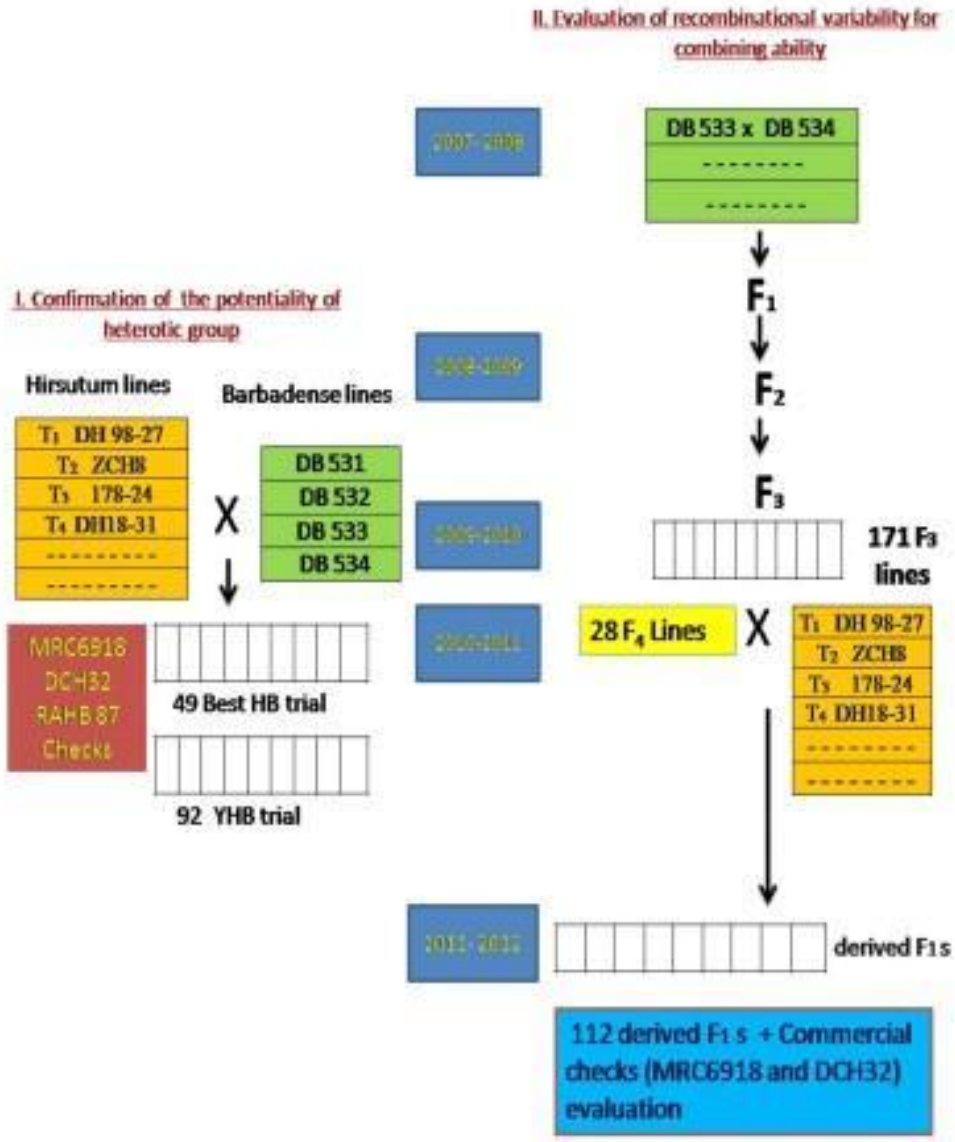


Fig 2. Schematic presentation of the procedure following in the study to improve combining ability

Main Central Path	B8	Bendi	YHB 10-11 (287-312 X 2= 52 ROWS)	Bendi	YHB 10-11 (261-286 X 2= 52 ROWS)
	B7		YHB 10-11 (235-260 X 2= 52 ROWS)		YHB 10-11 (209-234 X 2= 52 ROWS)
	B6		YHB 10-11 (183-208X 2= 52 ROWS)		YHB 10-11 (157-182X 2= 52 ROWS)
	B5		YHB 10-11 (131-156 X 2= 52 ROWS)		YHB 10-11 (105-130X 2= 52 ROWS)
	B4		YHB 10-11 (79-104 X 2= 52 ROWS)		YHB 0-11 (53-78 X 2=52 ROWAS)
	B3		YHB 10-11 (27-52 X 2= 52 ROWS)		YHB 10-11(1-26 X 2= 52 ROWS)
	B2		BEST HB 10-11 (41-52 X 4=52 ROWS)		BEST HB 10-11 (27-40 X 4=52 ROWS)
	B1		BEST HB 10-11(13- 26 X 4=52 ROWS)		BEST HB 10-11 (1-13 X 4=52 ROWS)
PATH					

Fig. 3. Field plan for development of heterotic groups

Plate 1 : General view of Line x Tester inter specific crosses (YHB trial) at UAS, Dharwad

Plate 2: General view of the best HB hybrids at UAS, Dharwad

3.2 Evaluation of recombinational variability for combining ability

3.2.1 Choice of the material

To create recombinational variability for combining ability (Fig. 2), the elite barbadense lines DB 533 and DB 534 were crossed during 2007-2008. During two seasons 2008-2009 and 2009-2010 these barbadense crosses were advanced to F_2 and F_3 generations, respectively. The F_3 lines were evaluated for productivity and fibre quality parameters realizing the emphasis laid on developing ELS (Extra Long Stable) cotton hybrids out of 171 F_3 lines, only those F_3 lines with acceptable fibre strength were utilized in the study on recombinational variability of combining ability (Table 1).

During 2010 -2011 those twenty eight F_4 lines of barbadense cross DB 533 × DB 534 depending on the higher value of fiber tenacity, were crossed with the selected four hirsutum testers *viz.,* DH 98-27 (T_1), ZCH 8 (T_2), 178-24 (T_3) and DH 18-31 (T_4) selected based on earlier study. Each barbadense F_4 line involved in a set of crosses (112 crosses refer to as derived F_1 crosses) was subjected to line x tester analysis.

3.2.2 Crossing Programme

The crossing programme was taken up during 2010. The F_4 lines and four common testers were sown on staggered dates. To obtain derived F_1 crosses seeds, the flower buds of the proper size from testers (used as female) were hand emasculated in the evening between 3.00 to 6.00 pm. The emasculated flowers were covered by butter paper packets for avoiding out crossing as well as ensuring their easy identification at the time of crossing. The emasculated flowers were pollinated during the next day morning between 9.30 am and 11.30 am by brushing the pollen from one of the F_4 lines (used as male) on the stigmatic surface. The pedicel of each pollinated flower was tied with price label bearing date and lines number for identification of crossed bolls. In this manner derived F_1 crosses seeds were obtained. Simultaneously, the barbadense population of F_4 lines was selfed and material was advanced to F_5 generation during the same year.

3.2.3 Evaluation of derived F_1 crosses and F_5 barbadense lines

There was a need for improving performance of inter specific hybrids. This was possible through genetic improvement of barbadense varietal lines. So that both productivity and fiber quality of barbadense were improved. An improved barbadense varietal base is essential for improving performance of inter specific hybrids.

The entire experimental material was planted on a medium black soil at College of Agriculture, Dharwad under irrigated condition. All the 53 F_5 (included Suvin variety as check) lines, four hirsutum testers and derived F_1 crosses along with the straight crosses (Bench Mark Crosses (BMC)) and ruling commercial checks (MRC 6918 *Bt* check and DCH 32 non *Bt* check) were sown during *kharif* 2011 in a Randomized Block Design with two replications and a spacing of 90 cm between rows and 60 cm between the plants within a row (Plate 3). Recommended fertilizer doses were applied and other cultural practices were carried out at regular interval. Plant protection measures were taken at appropriate time to control pests and diseases.

To facilitate line × tester analysis, the crosses obtained were randomized and were sown in one block along with checks, bench mark crosses and parents were sown in adjoining block.

3.2.4 Collection of data and recording of observations

Three plants in each entry were selected randomly and tagged. These tagged plants were used for recording observations on the following characters.

Morphological characters

3.2.4.1 Plant height (cm)

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

3.2.4.2 Number of monopodia per plant

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

Table 1. Performance of selected F_3 barbadense lines involved in the study of recombinational variability

Sl. No.	Cotton / Entry	Abbreviation	2.5% SL (mm)	UR %	Micronaire value (µg/inch)	Maturity Ratio (%)	Tenacity (g/t)	Elongation %
1	DB 533 x DB 534 F3 IPS 62	L_2	33.53	44.80	3.11	0.62	30.03	6.03
2	DB 533 x DB 534 F3 IPS 49	L_8	33.50	45.00	3.10	0.62	30.00	6.00
3	DB 533 x DB 534 F3 IPS 23	L_9	35.70	47.00	3.20	0.63	29.80	5.60
4	DB 533 x DB 534 F3 IPS 36	L_{10}	35.80	48.00	3.50	0.67	29.40	5.60
5	DB 533 x DB 534 F3 IPS 15	L_{11}	36.70	47.00	3.00	0.59	29.30	5.50
6	DB 533 x DB 534 F3 IPS 1	L_{12}	37.70	46.00	3.00	0.59	28.50	5.80
7	DB 533 x DB 534 F3 IPS 33	L_{13}	37.40	47.00	3.20	0.63	28.40	5.40
8	DB 533 x DB 534 F3 IPS 24	L_{14}	36.80	46.00	3.20	0.62	28.30	5.60
9	DB 533 x DB 534 F3 IPS 16	L_{15}	35.40	48.00	3.30	0.63	28.30	5.60
10	DB 533 x DB 534 F3 IPS 52	L_{16}	33.20	47.00	3.90	0.69	28.30	6.10
11	DB 533 x DB 534 F3 IPS 12	L_{17}	37.10	46.00	3.20	0.63	28.30	5.30
12	DB 534 x DB 533 F3 IPS 22	L_{18}	32.20	47.00	3.20	0.65	28.20	6.00
13	DB 533 x DB 534 F3 IPS 14	L_{19}	36.90	48.00	3.40	0.65	28.20	5.40
14	DB 533 x DB 534 F3 IPS 34	L_{20}	38.20	46.00	3.20	0.62	28.20	5.50
15	DB 533 x DB 534 F3 IPS 55	L_{21}	35.70	46.00	3.50	0.65	28.00	5.40
16	DB 533 x DB 534 F3 IPS 17	L_{22}	32.10	46.00	3.00	0.64	27.80	6.10
17	DB 533 x DB 534 F3 IPS 32	L_{23}	38.40	45.00	3.10	0.62	27.80	5.40
18	DB 533 x DB 534 F3 IPS 38	L_{24}	38.40	47.00	3.00	0.61	27.80	5.40
19	DB 533 x DB 534 F3 IPS 13	L_{26}	32.60	47.00	3.30	0.66	27.70	5.90
20	DB 533 x DB 534 F3 IPS 48	L_{25}	31.40	45.00	3.70	0.69	27.70	6.00
21	DB 533 x DB 534 F3 IPS 6	L_{27}	33.00	46.00	3.70	0.67	27.60	5.80
22	DB 533 x DB 534 F3 IPS 8	L_{28}	37.10	43.00	3.10	0.61	27.60	5.60
23	DB 533 x DB 534 F3 IPS 44	L_1	32.37	48.40	3.99	0.70	27.40	6.07
24	DB 533 x DB 534 F3 IPS 71	L_5	39.37	47.70	3.25	0.64	25.97	5.93
25	DB 533 x DB 534 F3 IPS 105	L_3	34.60	45.83	3.80	0.69	25.67	6.00
26	DB 533 x DB 534 F3 IPS 26	L_4	36.97	46.40	3.55	0.67	25.53	6.00
27	DB 533 x DB 534 F3 IPS 30	L_6	37.77	47.87	3.32	0.63	25.50	5.87
28	DB 533 x DB 534 F3 IPS 25	L_7	31.77	47.20	3.61	0.66	25.13	6.13

Plate 3. General view of the derived F_1 crosses at UAS, Dharwad

3.2.4.3 Number of sympodia per plant

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

3.2.4.4 Number of bolls per plant

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

3.2.4.5 Mean boll weight (g)

Seed cotton obtained from a random sample of 20 bolls per plant was used to determine boll weight in grams.

3.2.4.6 Reproductive points on sympodia

The total numbers of reproductive points on the sympodial branches were counted.

3.2.4.7 Sympodial length at 50 per cent plant height (cm)

Sympodial branch length at 50 per cent plant height was chosen for measurement and expressed in centimeter.

3.2.4.8 Inter branch distance (cm)

The distance between two branches at 50 per cent plant height was taken and expressed in centimeters.

Yield parameters

3.2.4.9 Seed index (g)

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

3.2.4.10 Ginning outturn (%)

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

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

3.2.4.11 Lint index (g)

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

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

3.2.4.12 Seed cotton yield (kg ha^{-1})

It is the mean seed cotton yield harvested till final picking from the net plot area and expressed in kg ha^{-1}.

Physiological parameters

The physiological observations (Plate 4) have taken by using portable photosynthesis system of Infra Red Gas Analyzer (IRGA), which measures gas exchange parameters apart from environmental parameters. There are several methods of measuring CO_2 fixation or exchange in plants but, the modern techniques of determining CO_2 fixation using infra red gas analysis (IRGA) of CO_2 is most widely employed owing to the precision of detecting very small changes in CO_2 concentrations. This method is very sensitive for CO_2 uptake by small leaves or even segments of leaves. The IRGA records the change in CO_2 concentration in the system and the rate of change with time gives an estimate of the CO_2 or water exchange rate. The main advantage of this method is that it can be used at a wide range of CO_2 concentrations, light, relative humidity and temperature and for studying the effects of these environmental factors that parameters influencing photosynthesis or gas exchange parameters.

Plate 4 : Recording the physiological parameters by using IRGA instrument

3.2.4.13 Photosynthetic rate ($\mu molCO_2m^{-2}s^{-1}$)

Photosynthesis, the conversion of light energy to chemical energy and the utilization of the chemical energy. The rate of photosynthesis is affected by a number of factors including light levels, temperature, availability of water, and availability of nutrients. If the conditions that the plant needs are improved the rate of photosynthesis increases.

3.2.4.14 Stomatal conductance ($\mu molm^{-2}s^{-1}$)

Stomatal conductance, measured in $\mu mol\ m^{-2}\ s^{-1}$ is the measure of the rate of passage of carbon dioxide CO_2 entering, or water vapor exiting through the stomata of a leaf. Stomata are small pores on the top and bottom of a leaf that are responsible for taking in and expelling CO_2 and moisture from and to the outside air. The rate of stomatal conductance, or its inverse, stomatal resistance, is directly related to the boundary layer resistance of the leaf and the absolute concentration gradient of water vapor from the leaf to the atmosphere.

3.2.4.15 Transpiration rate ($mmol\ H_2Om^{-2}s^{-1}$)

Loss of water in the form of water vapour from the internal living tissue of the leaf through the aerial parts such as leaf, green stem, etc., under the influence of sunlight is called as transpiration. The excess amount is transpired through the aerial parts of the plants. Thus, only 5 per cent of the absorbed water is retained in the plants and remaining 95 per cent is lost through aerial parts the leaves are most important for transpiration.

Fiber properties

The seed cotton sample of 150 g was collected from each treatment in each replication. The samples were ginned, 50 g lint represented a fiber sample. Fiber measurements were made on Premier Automatic Rapid Tester (premier ART) instrument at Agricultural Research Station, Dharwad. The premier ART incorporates the latest technology of high volume instrumental testing and provides the accurate and precise measurement of all the important cotton fiber properties.

3.2.4.16 2.5% span length (mm)

Fiber length at 2.5 per cent span was estimated by using premier ART instrument.

3.2.4.17 Fiber uniformity ratio (%)

Uniformity ratio was found out by using premier ART instrument expressed in percentage and computed as below.

$$\text{Uniformity ratio (\%)} = \frac{\text{50\% span length}}{\text{2.5\% span length}} \times 100$$

3.2.4.18 Fiber micronaire value (μg/inch)

This character was measured by micronaire module of the premier ART instrument. When the chamber lid is closed, a piston at the chamber bottom compresses the fiber to a fixed and known volume. A regulated stream of air is then forced through the sample and the pressure drop across the sample is measured as the fineness value.

3.2.4.19 Fiber maturity ratio (%)

It is an index of the extent of fiber development. The maturity depends mainly on the degree of secondary thickening of a fiber. Fiber maturity is measured by caustic soda method. The fibers are swollen in 18 per cent caustic soda and then are examined under microscope. The fibers are classified on the basis of ratio of cell wall and the lumen. The ratio of lumen and cell wall (L:W) is less than one in case of mature fibers; more than one but less than two for half mature fibers, and more than two for immature fibers.

3.2.4.20 Fiber strength (g/tex)

Fiber strength was determined by using premier ART instrument, expressed in g per tex and computed as below.

$$\text{Fiber strength (g/tex)} = \frac{\text{Breaking strength (kg)}}{\text{Weight of tuff (mg)}} \times \text{Length of sample (mm)}$$

3.2.4.21 Fiber elongation (%)

Fiber elongation at break was assessed by premier ART instrument. The fiber stretching ability to absorb energy to resist impact damage due to breaking load was recorded by the instrument and expressed as percentage of the original gauge length of the specimen. It was computed as below.

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

3.2.5 Statistical analysis

The mean value of three random plants in derived F_1 crosses, straight crosses and parental lines were employed in statistical analysis separately. The data on parents and crosses involved in line × teste was analysed first by partitioning the variability into parents, crosses and parents Vs crosses (Panse and Sukhatme, 1961). This analysis was used for comparing all the derived F_1s obtained in the study, their parental lines, checks *etc.* A simple RBD analysis was carried out to assess the differences in the entire set of derived F_1 crosses (112 hybrids which have taken depend on the seed weight, which were more than 10g and less than 40g) and other genotypes included in the study.

3.2.5.1 Combining ability analysis

Analysis of variance

Analysis of variance was done separately for each character for all the treatments. The model of the analysis of variance is given below.

Source	d.f.	SS	MS	F-ratio
Replications	r-1	SS_r	M_r	M_r/M_e
Treatments	t-1	SST	MT	MT/M_e
Error	(r-1) (t-1)	SS_e	M_e	

Where,

r = Number of replications

t = Number of treatments

Significance of treatment mean squares and replications mean squares were tested by comparing with error mean squares and referring to 'F' table at 5 and 1 per cent level probabilities of significance.

3.2.5.2 Line × Tester analysis

Evaluation of hybrids and parents involved in line × tester analysis was taken up separately by conducting a relevant RBD analysis first, and partitioning the variation among crosses later through combining ability analysis.

ANOVA table for parents and hybrids

Source of variation	d.f.	MSS
Replication	(r-1)	-
Treatments	(e-1)	-
Parents	(p-1)	-
Parents vs crosses	1	-
Crosses	(1t-1)	-
Lines	(1-1)	M_1
Testers	(t-1)	M_2
Lines × testers	1	-
Error	(e-1) (r-1)	EMS
Total	(1tr-1)	-

Where,

r = Number of replications

e = Number of treatments

l = Number of lines

t = Number of testers

3.2.5.3 Estimation of heterosis

Heterosis of F_1 over mid parent (MP) and commercial check (MRC 6918 and DCH 32) were calculated by methods of Turner (1953) and Hayes *et al*. (1955) as given below.

Per cent heterosis in F_1 over mid parent (MP) = $\frac{\overline{F_1} - \overline{MP}}{MP} \times 100$

Where, Mid parent (MP) = $\frac{P_1 + P_2}{2}$

Per cent heterosis in F_1 over commercial check (CC) = $\frac{\overline{F_1} - \overline{CC}}{CC} \times 100$

Where,

MP = Mid parent

CC = Commercial check

3.2.5.4 Test of significant for heterosis

Mean sum of squares due to error from RBD analysis was considered to compute standard error (S.E.) of estimated heterosis as follows.

S.E. for heterosis over mid parent

S.E. (Hmp) = $\sqrt{\frac{3/2 \times EMS}{r}}$

S.E. for heterosis over commercial check

S.E. (Hcc) = $\sqrt{\frac{2\ EMS}{r}}$

Where,

EMS = Error mean sum of squares

The critical difference values in each case were worked out by multiplying their corresponding S.E. values with table 't' value at error degree of freedom at 5 and 1 per cent levels of significance.

3.2.5.5 Efficiency of tester

The efficiency of testers in distinguishing the F_4 lines for their combining ability was assessed mainly by using mean variance, range and co-efficient of variance (%) *etc.* parameters. The twenty eight F_4 lines were crossed to four testers and the mean of 28 derived F_1 crosses corresponding to each tester was worked out. Secondly, the variability among the derived F_1 crosses corresponding to a tester was assessed by variability parameters (Co-efficient of variance) as described in the chapter Materials and Meathods (section 3.2.5.14).

3.2.5.6 Combining ability analysis

The variation among the hybrids was further partitioned into genetic components attributable to general combining ability (*gca*) and specific combining ability (*sca*) following the method suggested by Kempthorne (1957).

The analysis was based on the following mathematical model.

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

Where,

Y_{ijk}= Any character measured of the cross (i x j) in the k^{th} replication

μ = Population mean

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

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

S_{ij} = *sca* effect of $(i \times j)^{th}$ cross

e_{ijk} = Random error effect associated with $(ijk)^{th}$ observation in k^{th} replication

ANOVA for combining ability analysis

Source of variation	d.f.	MSS	Expectations
Replication	(r-1)	-	-
Hybrids	(lt-1)	-	-
Lines	(l-1)	M_1	$\sigma^2e + r [Cov(FS) - 2Cov(HS) + rt [Cov(HS)]$
Testers	(t-1)	M_2	$\sigma^2e + r [Cov(FS) - 2Cov(HS) + rl [Cov(HS)]$
Line $\times$ tester	(l-1) (t-1)	M_3	$\sigma^2e + r [Cov(FS) - 2Cov(HS)]$
Error	(r-1) (lt-1)	M_4	σ^2e

The experimental material used in this study consisted of random F_4 lines derived from a cross. The random lines were crossed to genetically diverse testers. A random sample of 28 F_4 lines and their parental lines were used in line $\times$ tester study, makes the situation ideally suited for estimating components of variance *i.e.,* GCA variance and SCA variance and estimating genetic components of variance their off (additive variance and dominance variance).

3.2.5.7 Estimates of variances

The GCA and SCA variance were expressed in terms of co-variances of full sibs (FS) and half-sibs (HS) as indicated below.

$$\text{COV (HS)} = \text{GCA variance} = \frac{M_1 + M_2 - 2M_3}{r(1+t)}$$

$$\text{COV (HS) lines} = \frac{M_1 - M_3}{rt}$$

$$\text{COV (HS) testers} = \frac{M_2 - M_3}{rl}$$

$$\text{SCA variance} = \text{COV (FS)} - 2\,\text{COV (HS)} = \frac{M_3 - M_4}{r} = \sigma^2 lt$$

3.2.5.8 Estimate of combining ability effects

The following effects were calculated from two way table of lines vs testers in which each figure was a total of the two replications.

$$\mu = \frac{X\ldots}{Ltr}$$

$$\hat{g}_i = \frac{X_i\ldots}{tr} - \frac{X\ldots}{ltr}$$

$$\hat{g}_j = \frac{X_{.j.}}{lr} - \frac{X\ldots}{ltr}$$

$$\hat{S}_{ij} = \frac{X_{ij.}}{r} - \frac{X_i\ldots}{tr} - \frac{X_{.j.}}{lr} + \frac{X\ldots}{ltr}$$

Where,

$X\ldots$ = Total of all hybrids

$X_i\ldots$ = Total of i^{th} line over all testers and replications

$X_{.j.}$ = Total of j^{th} tester over all lines and replications

$X_{ij.}$ = Total of ij^{th} cross over all the replications

3.2.5.9 Pooled score for *gca* effects

Procedure for estimation of pooled scores is described in the chapter discussion (section 5.2.2).

3.2.5.10 Standard errors of the effects

The variances of the estimates were calculated following the formula given below. The standard errors of the estimates are the square roots of their variances.

i. S.E. (*gca* for line) = $\left(\frac{M_4}{rt}\right)^{1/2}$

ii. S.E. (*gca* for testers) = $\left(\frac{M_4}{rl}\right)^{1/2}$

iii. S.E. (*sca* effect) = $\left(\frac{M_4}{r}\right)^{1/2}$

The critical differences were calculated by multiplying the standard errors with table 't' value at 5 and 1 per cent levels of probability for error degrees of freedom.

3.2.5.11 Characterization of combining ability pattern (status) of F_4 lines

Characterization of combining ability status of a line was done based on relative performance of the 28 F_4 lines against a tester(s). Based on the performance of these crosses (seed cotton yield), four classes were made in the decreasing order of superiority. These crosses were given a ranking of 1 (>mean + SD), 2 (mean to mean + SD) 3 (mean to mean – SD) and 4 (<mean – SD) as suggested by Patil (1995). Thus, for a tester T_1/A, four classes of combining ability status were defined namely A_1, A_2, A_3 and A_4, respectively. Similarly, B_1, B_2, B_3 and B_4 classes were defined representing the decreasing order to superiority of the crosses with tester T_2. Same procedure was followed in making classes for C and D, respectively.

Each line was characterized with respect to its combining ability status (pattern) considering the four testers. With the help of this information, the nature and magnitude of variability for combining ability was assessed.

3.2.5.12 Test of significance for genotypic differences

The significance of difference between group mean of derived F_1 crosses was compared by using student't' test in the following manner.

$$\text{Calculated 't' value} = \frac{\bar{X}_1 - \bar{X}_2}{SED}$$

$$SED = +$$

Where,

$$\sqrt{\frac{V_1}{n_1} \quad \frac{V_2}{n_2}}$$

$\bar{X}_1$ = Mean of sample 1

$\bar{X}_2$ = Mean of sample 2

V_1 and V_2 are variances of sample 1 and sample 2, and n_1 and n_2 are sample size in each case. The calculated't' value was compared with Table't' value at pooled degrees of freedom.

3.2.5.13 Variance

The formula given for unclassified data was used to calculate variance as below.

$$\sigma^2 = \frac{\Sigma x_i^2 - n(\bar{x})^2}{n-1}$$

Where,

σ^2 = Variance

x_i = Value of variable

$\bar{x}$ = Mean

n = Number of observations

3.2.5.14 Co-efficient of variance (CV)

This was calculated for all the variances using the formula.

$$CV\ (\%) = \frac{\bar{\sigma}}{\bar{x}} \times 100$$

Where,

σ = Standard deviation

$\bar{x}$ = Mean

3.3 Correlation co-efficient analysis

Analysis of co-variance was computed in a fashion similar to that of analysis of variance formula and these statistics were made use of in calculating, phenotypic and genotypic correlation co-efficients.

3.3.1 Phenotypic correlation co-efficient (r_p)

The degree of phenotypic association amongst characters was computed as per the formula given by Weber and Moorthy (1952)

$$r_p = \frac{Cov_{p1.2}}{\sqrt{\sigma^2_{p1} \cdot \sigma^2_{p2}}}$$

Where,

r_p = Phenotypic correlation co-efficient

$Cov_{P1.2}$ = Phenotypic co-variance between two traits (1 and 2)

σ_{P1} = Phenotypic standard deviation of first trait (1)

σ_{P2} = Phenotypic standard deviation of second trait (2)

3.3.2 Intergeneration (F_3-F_5) correlation

Correlation co-efficient of each character (fiber quality characters) between F_3 and F_5 generation was found out by calculating the phenotypic correlation co-efficient exactly as described under 3.3.1 taking the same character in both the generations.

Intergeneration correlation co-efficient analysis was done for entire populations of selected F_3 and F_5 progenies for all the fiber quality characters.

3.3.3 Regression analysis and narrow sense heritability estimates

Narrow sense heritability estimates were made based on the regression of F_5 on F_3 using the following (Cahaner and Hillet, 1980).

$$b\ (F_5F_3) = \frac{\text{Co-variance of } F_3 F_5 \text{ for the character}}{\text{Variance of } F_3}$$

Regression of each character between F_5 and F_3 was found out by calculating the regression co-efficient taking the same character in both the generations. Regression co-efficient between F_5 and F_3 generations was estimated as heritability value using multiplicative factor of 2/3 or 0.67. Heritability estimates were computed for entire population of selected progenies for all the characters. Based on inbreeding co-efficients of the generations involved in regression analysis.

The heritability estimates were categorized according to Robinson *et al.* (1949) and given below.

0-30 % - Low

30-60 % - Moderate

60 % and above – High

3.4 Path co-efficient analysis

Path co-efficient analysis was carried out using phenotypic correlation values of yield components one seed cotton yield as suggested by Wright (1921) and illustrated by Dewey and Lu (1959). Standard path co-efficients which are the standardized partial regression co-efficients were obtained using statistical software package called WINDOWSTAT. These values were obtained by solving the following set of 'P' simultaneous equations by using the above package.

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

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

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

Where P_{01}, P_{02}, ----------P_{0P} are the direct effects of variables 1,2, ----------p on the dependent variable 0 and r_{12}, r_{13} ,-------r_{1P}------ $r_{P(P-1)}$ are the possible correlation co-efficients between various independent variables and r_{01}, r_{02}, r_{03} ------- r_{0P} are the correlations between dependent and independent variables.

The indirect effect of the i^{th} variable *via* j^{th} variable is attained as (P_{oj} x r_{ij}). The contribution of remaining unknown factor is measured as the residual factor, which is calculated as given below.

$P^2ox = 1- [P^2_{01} + 2P_{01} P_{02} r_{12} + 2 P_{01} P_{03} r_{13} +----------+ P^2_{02} + 2P_{02} P_{03} r_{13} +…….+P^2_{0P}]$

Residual factor = $(P^2_{ox})^{½}$

3.5 Molecular marker study in cotton

The 28 of F_4 barbadense lines along with four hirsutum testers (DH 98-27, ZCH8, 178-24 and DH 18-31) were subjected to diversity analysis using SSR marker system.

3.5.1 Methodology

3.5.1.1 DNA extraction (CTAB method)

The DNA was extracted from the parental lines by following CTAB extraction method (Saghai-Maroof *et al*., 1984) with required modifications.

1. One to two grams of fresh weight of young leaves from shoot apex of two to three leaf seedlings was taken in eppendorf tube and labeled.
2. 500 µl of extraction buffer (Appendix 8) was added to eppendorf tubes containing the sample.
3. The tissue was crushed until it became fine.
4. 80 µl of PVP %.
5. The samples were incubated at 65 ^{0}C for 20 minutes and kept at room temperature.
6. 600 µl of lysis buffer was added and 60 µl (5%) of sarcosine buffer (Appendix 8), vortexed gently for 30-40 seconds.
7. The samples were incubated at 65 ^{0}C for 20 minutes (mix thoroughly in between) and wait till it came to room temperature.
8. The supernatant was spined at 13,000 rpm for 12 minutes.
9. Supernatant was transferred to another eppendorf tube.
10. Equal volume of chloroform:Isomyl Alcohol were added and mixed thoroughly.
11. The supernatant was added to the tube and centrifuged at 13,000 rpm for 12 minutes at room temperature.
12. The supernatant was collected around 450 µl to the fresh tube (1.5 ml) and added double volume with pre-chilled (Isopropanol) and left for 30 minutes and mixed thoroughly.
13. The supernatant was spined at 13,000 rpm for 10 minutes at room temperature.
14. The supernatant was discarded, 70% alcohol wash (90 µl) was gave and centrifuged for 3 minutes.
15. The pellet of DNA was dried completely and kept it for overnight.
16. The DNA was dissolved in 30 µl T_{10} E_1 buffer and kept it in room temperature for 20 minutes.
17. The DNA was treated with 3 µl of RNAase and kept at 37 ^{0}C for 20 minutes and later at 65 ^{0}C for 30 minutes.

3.5.1.2 DNA quantity and quality estimation

The concentration of DNA was assessed spectrophotometrically and also by gel electrophoresis using 0.8 per cent agarose gel with known concentrations of uncut DNA.

To test the quality of DNA, samples were run on 0.8 per cent agarose gel with 1X TAE buffer and stained with ethidium bromide and checked for contamination by RNA (which usually runs ahead) (RNA is to be removed by RNAase) and the DNA was evaluated by comparing it with a standard undigested DNA sample. Serial dilutions were carried out to get desired quantity (30 mg) of DNA for PCR.

3.5.1.3 Optimization of polymerase chain reaction

3.5.1.3.1 Template DNA

The purified genomic DNA extracts (30 ng) of parental lines were used as template DNA per reaction (20 µl).

3.5.1.3.2 SSR primers

Primers designed and information obtained from cotton marker data base used in the present study (Table 2).

3.5.1.3.3 dNTPs

The four individual dNTPs such dATP, dGTP, dCTP and dTTP were obtained from M/s. Bangalore Genei Pvt. Ltd., Bangalore.

3.5.1.3.4 Thermocycler

Eppendorf, Master cycler gradient supplied by Eppendorf, 2231, Hamburg Germany was used for cyclic amplification of DNA.

3.5.1.3.5 Amplification reaction mixture

One primer at a time was used to study the polymorphism between genotypes by PCR assay. Master mix required was prepared afresh together to avoid handling errors. The master mix was distributed uniformly (13 µl/tube) and 2 µl of template DNA from respective genotypes was added to make the total reaction volume to 20 µl.

Sl. No.	Components	Quantity
1.	10X assay buffer	2.0 µl
2.	dNTP mix (2.5 mM each)	2.0 µl
3.	Primer (5 pM/µl)	
	a. Forward (5 pM/µl)	0.5 µl
	b. Reverse (5 pM/µl)	0.5 µl
4.	Taq DNA polymerase (3U/µl)	0.5 µl
5.	Template DNA (15 ng/µl)	2.0 µl
6.	Sterile double distill water	7.5 µl

3.5.1.3.6 PCR amplification

PCR amplification for SSR's analysis was performed according to Williams *et al.* (1990) with certain modifications. The amplification conditions were as follows.

Sl. No	Steps	Temperature (^{0}C)	Duration (min)	No. of cycles
1.	Denaturation (initial) of genomic DNA	94	5	1
2.	Denaturation of DNA	94	1	
3.	Annealing of primers	48 $\pm$ 5	1	25
4.	Extension of primers	72	1	
5.	Final extension of primers	72	5	1
6.	Hold (storage)	4	∞	-

Table 2. List of 40 SSR primers involved in the study of molecular marker with sequences

Sl. No.	Oligo Name	Oligo Sequence (5' to 3')
1	BNL3627 (F)	TATGGGCCTGTCCACCTAAG
	BNL3627 (R)	CAAAGCAACATGCACACACA
2	BNL3147 (F)	ATGGCTCTCTCTGAGCGTGT
	BNL3147 (R)	CGGTTCAGAGGCTTTGTTGT
3	BNL2921 (F)	CGAGAGATTTTAAAGGGAAACA
	BNL2921 (R)	GGGAGTGGTCTGATGGAAAA
4	BNL4082 (F)	GTAAAATGAAATAAAATAAAAGGAGAGA
	BNL4082 (R)	TTCAACACCGCCAAACATAA
5	BNL3871 (F)	TTGCAATTCGCTTTGACTTG
	BNL3871 (R)	CATGCGCCATTTCTCTCTTA
6	BNL1034 (F)	TTGCTTTCAATGGAAAACCC
	BNL1034 (R)	CGTCGCAAAGTTGAGAATCA
7	BNL1227 (F)	CATCAAGATCTATCTCTCTCTATACCG
	BNL1227 (R)	TTTACCCTCCGATCTCAACG
8	BNL341 (F)	ACCTGGGGTACTTGTCCACA
	BNL341 (R)	CCATCCCATTTGTGATACCC
9	BNL1231 (F)	TAATAAAAGGGAAAGGAAAGAGTT
	BNL1231 (R)	TATGGCTCTAGAATATTCCCTCG
10	BNL1878 (F)	TGCTTCAACTGCTCTTGCAT
	BNL1878 R)	TCGATATCTGGAACACCCAC
11	BNL3867 (F)	TAATTGAGTTGTTTTCTTACTTGCC
	BNL3867 (R)	TGCCAATTTAGCAATCACCA
12	BNL116 (F)	GCGGCATGCTTTCTTCATCATATA
	BNL116 (R)	ATAACCTGTGACATCTTTTTTTGC
13	BNL3511 (F)	TAGAACATAGGGAGGCGTGG
	BNL3511 (R)	AATGGAGAGACAATGATTTTTCG
14	BNL3031 (F)	AGGCTGACCCTTTAAGGAGC
	BNL3031 (R)	AACCAACTTTTCCAACACCG
15	BNL3085 (F)	TGGACATCCTTCTGGAAACC
	BNL3085 (R)	TGTGGAGTCATCAATATGTTGC
16	BNL3569 (F)	GCCAATCACCGAGAACAATT
	BNL3569 (R)	CGCTTATTGCCTTGATTGGT
17	BNL1421 (F)	TGAAGATTTGGAGGCAATTG
	BNL1421 (R)	GAAATCAAGCCTCAATTCGG
18	BNL1495 (F)	TGAAGATTTGGAGGCAATTG
	BNL1495 (R)	ATAAATGGCATCAGCCCAAA
19	BNL1521 (F)	TGAAGAAAGAAAAAGAGAAAGGG
	BNL1521 (R)	CTCACCACGTGGCACTTATG
20	BNL2655 (F)	TTGCATAAGTTTTGGGAGGC
	BNL2655 (R)	GGTTAGACTCTTTATTTTAAACACACG

Contd....

Sl. No.	Oligo Name	Oligo Sequence (5' to 3')
21	BNL3145 (F)	AACGAGGGAAAACGGAGAGT
	BNL3145 (R)	CAAAACGACGCCATTTAGGT
22	BNL580 (F)	CTATGTTTGGCCTTGGCATT
	BNL580 (R)	TAGTGACAGATATCCCCGGC
23	BNL542 (F)	TCGATCACATTTATAAGAACTATTGG
	BNL542 (R)	TTCATTTTGAACATTCGCCA
24	BNL686 (F)	ATTTTTCCCTTGGTGGTCCT
	BNL686 (R)	ACATGATAGAAATATAAACCAAACACG
25	BNL3383 (F)	GTGTTGTCATCGGCACTGAC
	BNL3383 (R)	TGCAATGGTTCAGTGGTGAT
26	BNL1611 (F)	CAATGAACAAAAAATGTAAGGG
	BNL1611 (R)	TGGGCATTTAGCCATTTACC
27	BNL1531 (F)	CTGCAACAAGAGCCTGTGTC
	BNL1531 (R)	ATGGAGATTGGCTGAGATGG
28	BNL2920 (F)	TTCTTGCATTGAATAATACTGGC
	BNL2920 (R)	CTTAATTCTAAAAATCAATAAATTTAGCC
29	BNL2882 (F)	CAACCTTTGGTAATCTTCTTTCG
	BNL2882 (R)	CGCTAACGCATTTGACATCT
30	BNL1059 (F)	CCTTCTCTGACACTCTGCCC
	BNL1059 (R)	TGTATTCTCTTCTTTTCCTTATACTTTT
31	BNL3418 (F)	GATGCCAGTGAGATCCCAAT
	BNL3418 (R)	TCAGTGGAGATGGTCATATGC
32	BNL3259 (F)	TTTTGAAATTCCAGCGAAGG
	BNL3259 (R)	GTCAATACCTGCTTCTCCACG
33	BNL1440 (F)	CCGAAATATACTTGTCATCTAAACG
	BNL1440 (R)	CCCCCGGACTAATTTTTCAA
34	BNL3171 (F)	GAAAAATTGAGGAAGGACATACG
	BNL3171 (R)	GGCCACAACCGAATTTACTG
35	BNL3408 (F)	ATCCAAACCATTGCACCACT
	BNL3408 (R)	GTGTACGTTGAGAAGTCATCTGC
36	BNL3994 (F)	TTGAGGGCATCCAAATCCAT
	BNL3994 (R)	CCTCCACCATACACGTGCTA
37	CIR246 (F)	TTAGGGTTTAGTTGAATGG
	CIR246 (R)	ATGAACACACGCACG
38	CIR381 (F)	TTTCCATCCTTTTGTGA
	CIR381 (R)	AAGGAGAAGAACAAGCAA
39	CIR070 (F)	AACCACCAACCATTCA
	CIR070 (R)	TGGGACTCGGTCATC
40	CIR100 (F)	GAGAGGCGATGCTAAA
	CIR100 (R)	GGGATACAAATGGAGAAA

3.5.1.3.7 Electrophoresis

PCR products were confirmed for amplification on 1.2 % agarose gel before loading them in the sequencing gel. For separation of amplified DNA fragments, non-denaturing polyacrylamide gel electrophoresis (PAGE) and capillary electrophoresis (ABI 3700) were employed (Plate 5).

3.5.1.3.8 Non-Denaturing gel electrophoresis (PAGE)

Steps for gel preparation and electrophoresis

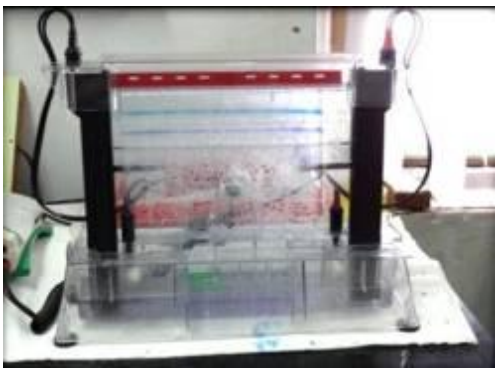
1. The glass plates were washed with 70 % alcohol or surgical spirit. (Ensure the plates to be clean and dry. Leave for 10-15 minutes).
2. The all accessories were washed with distilled water and then with spirit.
3. Bindiscilin solution (20 µl bind silane +980 µl silane stock) was applied to glass plate.
4. Repulscilin solution (250 µl of repulscilin + 750 µl of solution A) was applied to core plate.
5. The plates were set and the comb inserted in the reverse orientation.
6. The instrument was placed on the table such that glass plate should incline at 40^0 angle. (Ensure the comb portion to be at the elevation side).
7. 52.5 ml of distilled sterile water was taken in a beaker and added 15 ml of 30 % acrylamide solution, 7.5 ml 10X TBE buffer, 450 µl 10% APS(Ammonium presulphate) (Appendix 9) and 100 µl TEMED and were mixed. Immediately the solution was injected in between the glass plates (solidification is fast) and left side for 40 minutes to facilitate solidification.
8. 200 ml of 5X TBE was taken and diluted it by adding 1800 ml of distilled water (0.5 X TBE).
9. The bottom support was removed and placed the instrument in tank vertically. The top of the apparatus filled with 0.5 X TBE and the ½ of the tank with 0.5 X TBE.
10. The comb on the glass plate was washed with tissue paper to remove the axcess gel on it then the plate was washed with syringe tube to change the comb spacer to facilitate early movement of sample.
11. The comb was placed in inverted order such that the edges of teeth just touch the gel.
12. The cables and temperature sensor were fixed and connected it to the power pack and the electrophoresis was started with the following settings (Temperature 45^0C – 50^0C, power 75-80 V, Time 45-60 minute or until the temperature reached to 45^0C) *PRE RUN STEP.*

    Note: High temperature might damage the glass plates so care should be taken.
13. During the pre run time 9 µl STR/20 µl sample was added and denaturation was proceeded. (The samples were placed in boiling water for exactly 4 minutes and immediately transfered to ice).
14. The pre run was stopped when the temperature of apparatus reached to 45 ^{0}C and the samples were loaded.
15. The electrophoresis was started with the same pre run conditions and stopped after the die reached up to 1/3 of the gel. (approx 30-45 minutes).
16. Later the plates were removed from the tank and carefully separated the glass plate from the core plate. (Very important step, maximum care should be taken).

Steps for staining

1. The glass plate was placed in stop solution condition (Appendix 9).
2. The glass plate was washed twice with distilled water with interval of 2 minutes each shaking condition.
3. Later the glass plate was placed in staining solution (Appendix 9) for 20 minutes shaking condition. (Meanwhile prepare the developing solution and place it for cooling at 4-5 ^{0}C).
4. Quick wash (30 seconds-1 minute) in water.



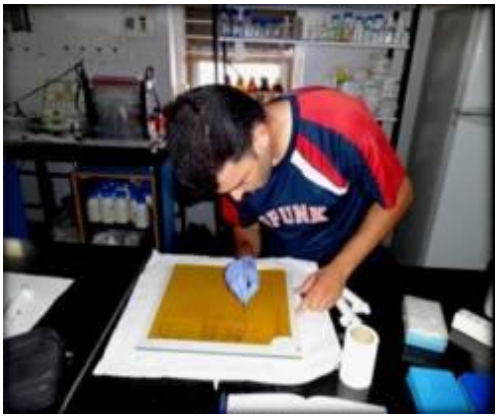


Plate 5 : Non-Denaturing Gel Electrophoresis (PAGE) procedure

5. The developer solution (Appendix 9) was added after removing the staining solution and shaked (manually) until the bands appeared.
6. The stop solution was added after removing developer solution and kept it for 5 minutes.
7. The glass plate was removed and water wash was given for 5 minutes and the plate was allowed to dry and later the results were observed.

3.5.2 Scoring the amplified fragments

The amplification of DNA profiles for all the primers were compared with each other and the bands of DNA at each amplification level of every primer were scored as present (1) or absent (0) thus generating the 0, 1 matrix.

$$\text{Per cent polymorphism (\%)} = \frac{\text{Total No. of polymorphic bands}}{\text{Total No. of bands generated by 40 primers}} \times 100$$

3.5.3 Analysis of SSR profiles

Pair similarity co-efficients were calculated for all pairwise combinations of the parental lines according to the method developed by Nei and Li (1979): *Sij= 2Nij / (Ni+ Nj),* where *Sij* is the similarity between parents *i* and *j; Nij* is the number of bands present in both parents; *Ni* is the number of bands present only in parent I; Nj is the number of bands present only in parent j. GD (genetic distance) was calculated as GD= 1- *Sij*. The similarity matrix from SSR markers, which were computed using NTSYS-PC version 2.1 (Rohlf 2001) were used to construct dendrograms based on UPGMA (the unweighted pair group method with arithmetic means). Using the same NTSYS software, a cophenetic value matrix was calculated to test the goodness of fit for the cluster analysis to the original distance matrix.

For studying the relationship between SSR molecular makers and hybrids performance and heterosis, the mid parent heterosis (MP) and heterosis over *Bt* check MRC 6918 and non *Bt* check DCH 32 were calculated.

3.6 *In Planta* genetic transformation

In this study, genotype independent *in planta* transformation of cotton (*G. hirsutum*) variety RCR4, using injection method and cut method has been reported. *Agrobacterium tumefaciens* strain carrying the *npt*II and *Cry1Ac-Cry1Ec* genes was used for plant transformation. The integration of the genes was confirmed by using PCR (T_0 generation).

The present investigations were carried out at Agricultural Research Station, Dharwad farm, University of Agricultural Sciences, Dharwad during 2012.

3.6.1 Materials

3.6.1.1 Genotype

One variety, RCR4 (*Gossypium hirsutum, L*.) was used in the present investigation.

- This line is productive line with high Relative Growth Rate (RGR).
- Developed by Dr. S.S.Patil, Senior cotton breeder, Agricultural Research Station, Dharwad farm, University of Agricultural Sciences.
- It is known to be productive in rainfed situation.
- The parentage of this line RAH 100 X RAH 101.

3.6.1.2 *Cry* genes

The genes used for transformation was obtained from NBRI Luknow and it was spared by Dr. P.K.Singh under NMITLI project funded by Counsil of Scientific and Industrial Research New Delhi, India.

3.6.2 Methodology

3.6.2.1 Preparation of explants

- Delint the genotype seeds by using sulfuric acid (H_2SO_4) were dipped for 10 minutes with constant stirring followed by the repeated washes with water. Keep the seeds under the sunshine to dry completely.
- Delinted and surface sterilized seeds soaked in sterile water over night were used to establish the plants for transformation.

3.6.2.2 Sowing and establishment of plants

The seeds were sown on 1-1-2012 in 200 plastic packets containing sterilized black soil mixed with Bavistin (5 g/1L), 2 seeds were dibbled per packet and thinning was attended to retain one healthy plant per plastic packet at 25 days after sowing. All the recommended package of practices were followed to rise healthy crop.

3.6.2.3 *Agrobacterium* strain and binary vectors

The disarmed *Agrobacterium* strain LBA 4402 harbouring binary vector pCAMBIA, carrying *Cry1Ac-Cry1Ec* genes linked to the CaMV35S promoter, the *nos* transcription terminator (amplified from Pb 101.1 with *MfeI* and *EcoRI* restriction sites at the ends) and *npt*-II gene under the control of nopaline synthase (nos) promoter and terminator was used in transformation studies. Hygromycin resistance as selection marker and *Cry1Ac-Cry1Ec* genes are used to control *Helicoverpa armigera* and *Spodoptera litura*.

3.6.2.4 Maintenance of *Agrobacterium*

The *Agrobacterium* LBA 4402 containing above mentioned genes was maintained on solid Yeast Extract Mannitol Agar (YEM) medium (Appendix 10) containing kanamycin at 50 mg/ml and 25 mg/ml rifampicin. It was subcultured once in every 30-40 days on fresh medium and incubated at 28 ^{0}C temperature for 48 hours followed by 4-6 ^{0}C for rest of the period.

3.6.2.5 Preparation of *Agrobacterium* culture for co-cultivation

3.6.2.5.1 Liquid culture

A colony of bacteria grown for 48 hours was taken from petridish and was inoculated in 150 ml of liquid YEM medium containing 50 mg/l of Kanamycin and 25 mg/l rifampicin and incubated for 45-48 hours at 22 ^{0}C under orbital shaker with 150 rpm.When bacterium growth reached to OD (600 nm) of 0.6 g pellet of bacterium obtained after centrifuge at 8000 rpm for 5 minute. It was resuspended in 150 ml of MS medium and 150 µM of acetosyringone was added to the *Agrobacterium* culture before 30 minute of its use.

3.6.2.5.2 Solid culture

A load of bacteria from a stock plate was taken from petridish to streak on a fresh petridish having solid YEMA medium with 50mg/l of Kanamycin and 25 mg/l refampicin. The dish was incubated at 22 ^{0}C for 48 hours in dark. The bacteria were carefully collected after 48 hours into a 2 ml new autoclaved eppendorf tube and 100 µM Acetosyringone was mixed before 30 minute of its use by vortexing for few seconds.

3.6.2.6 Transfer the genes to the plant tissue and establishment in the greenhouse

1. The seedling shoot is embedded in the stem between the cotyledons, break off one cotyledons to expose shoot apex and cut the tissue in the shoot apex to make wound (Fig. 4).
2. The disarmed *Agrobacterium* strain LBA 4402 harbouring binary vector pCAMBIA, carrying *Cry1Ac-Cry1Ec* genes linked to the CaMV35S promoter, *nos* terminator and *npt* II gene transfer to the injuried tissue on 01/2/2012 by using micropeppite (Plate 6).
3. Seedlings covered with plastic bags to maintain high humidity (Plate 6).
4. They were watered twice a week. Seedlings were then transferred to earthen pots on 5/3/2012 containing soil and vermicompost in equal proposition and pots were placed in transgenic green house for flowering.

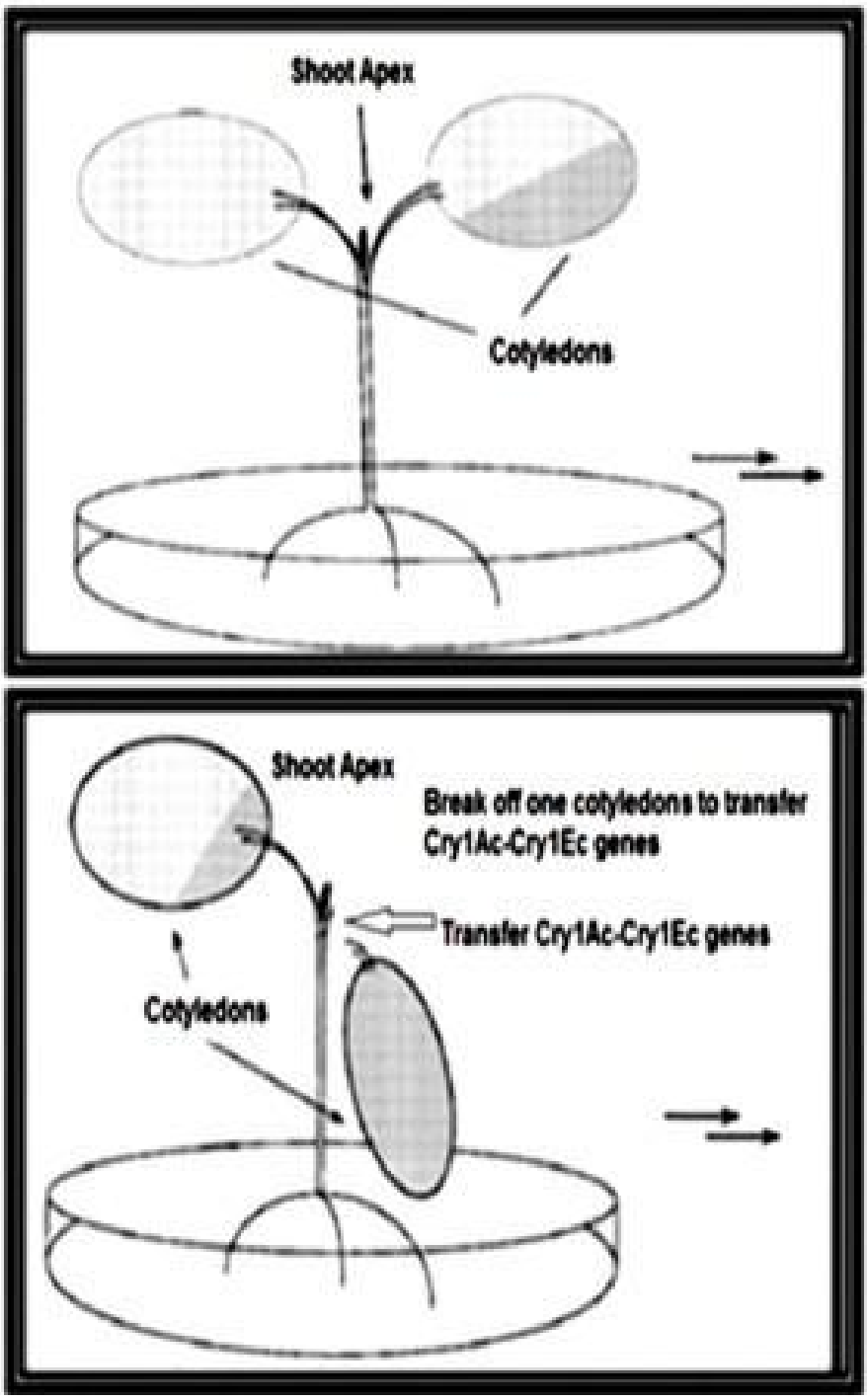


Fig 4: Transfer the genes (*Cry1Ac- Cry1Ec*) to the plant tissue and establishment in the greenhouse

A

B

C

D

Plate 6 : Transfer the genes (*Cry1Ac-Cry1Ec*) to the plant tissue and establishment in the greenhouse

3.6.2.7 Screening through PCR

The putative transformants generated through *in vivo* genetic transformation were subjected to PCR analysis.

3.6.2.7.1 DNA extraction

DNA extraction was done with CTAB method with few modifications.

1. One gram of fresh 2nd or 3rd top most leaf was taken for DNA extraction, leaf was harvested and kept in the 1.50 ml eppendorf tube.
2. By using extraction buffer leaf samples were crushed and kept in water bath for 45 minute at 65 ^{0}C (extraction buffer – Appendix 8).
3. After 45 min, samples were taken out from water bath. The solution was centrifuged at 8,000 rpm for 10 minutes and supernatant was transferred to fresh eppendorf tube.
4. Supernatant was mixed with 500 µl of phenol: chloroform solution and centrifuged at 8,000 rpm for 10 min.
5. By using micropipette, supernatant was collected and transferred to new eppendorf tube. To that eppendorf tube, 500 µl chloroform solution was added and centrifuged at 8,000 rpm for 10 min.
6. Once again supernatant was collected to new eppendorf tube and 800 µl isopropanol was added and kept at 20 ^{0}C for precipitation for 1-2 hours.
7. After 2 hours, tubes were removed from the deep freezer and kept out side to attain room temperature. After that, centrifuged at 5,000 rpm for 5 min.
8. Supernatant was decanted without disturbing the pellet. To that, 70% alcohol was added and centrifuged for 5,000 rpm for 5 min. After centrifuge alcohol was decanted without disturbing the pellet.
9. Pellet was dried and suspended in 100 µl of 1 X $T_{10}E_1$ buffer.
10. 100 µl RNase was added (1 mg/ml) to the DNA and incubated at 37 ^{0}C in water bath for half an hour.
11. DNA was precipitated using 1/10th volume of 3 M sodium acetate and ethanol and incubated over night at 4 ^{0}C.
12. The solution was centrifuged at 13,000 rpm for 2 min and pellet was dried again.
13. Pellet was suspended in 50 µl 1X $T_{10}E_1$ buffer.

3.6.2.7.2 Estimation of quality and quantity of DNA

The concentration and quality of DNA was assessed spectrophotometrically. It was also assessed with 0.8 % agarose gel.

In spectrophotometric analysis, 5 µl of DNA sample diluted with TE buffer and volume made upto 3000 µl was subjected to spectrophotometer reading at absorbance of 230 nm, 260 nm and 280 nm. A good DNA preparation generally exhibits the following spectral property: A260/A280 > 1.80 DNA concentration was calculated using following formula. Concentration of DNA (µg/ml) = O.D. at 260 x 50. To test the quality and quantity of DNA, samples were run on 0.80 per cent agarose in 1x TAE (Tris Acetic acid EDTA) buffer and stained with ethidium bromide and checked for contamination by RNA and the DNA was evaluated by comparing it with a standard undigested DNA sample.

3.6.2.7.3 Plasmid isolation procedure

1. Inoculate 10 ml media with suitable antibiotic and inculate with shaking at 3 ^{0}C overnight.
2. Take 1.5 ml of culture in fresh tube and pellet at 13,000 rpm for 1 minute.
3. Discard the supernatant and take again 1.5ml of culture in fresh tube and pellet at 13,000 rpm for 1 minute.
4. Resuspend the pellet in 150 µl of ice cold solution I (Appendix 11) by vortexing.

5. Add 250 µl of freshly prepared solution II (Appendix 11) and mix by inventing for 5 times and keep in ice for 5 minutes (don't vortex).
6. Add 200 µl of solution III (Appendix 11), mix by vortexing and keep in ice for 4-5 minutes.
7. Spin at max speed (13,000 rpm) for 10 minutes at 4 ^{0}C.
8. Transfer supernatant to fresh tube and equal volume of chloroform: Isomyl Alcohol (24:1) and mix by vortexing.
9. Centrifuge at max speed at 4 ^{0}C for 10 minutes.
10. Transfer aqueous phase to fresh tube.
11. Add 2 volume of pre chilled absolute isopropanol and mix by inverting and incubate at room temperature for 5 minutes.
12. Pellet the DNA at 13,000 rpm for 10 minutes.
13. Wash the pellet with 70% ethanol (90 µl) at 13,000 rpm for 3 minutes.
14. Dry the pellet and dissolve in 20-25 µl of $T_{10}E_1$ or sterile water.
15. Add Rnase at 20 mg/ µl.

3.6.2.7.4 PCR amplification

DNA extracted from leaves of transformants was used as template DNA, Taq DNA polymerase (Bangalore Genei), Taq Buffer (Bangalore Genei), dNTPs (Bangalore Genei), $Mgcl_2$ (Bangalore Genei) and Primers were used for cyclic amplification of DNA. Following *Cry1Ac-Cry1Ec* specific primers were used for confirming transgenic.

Sequence of *Cry1Ac-Cry1Ec* primers:

Forward 5^{I} CCAGAGAACGAGATC TTGGAC 3^{1}

Reverse 3^{1}AGTATTGTACCATCTAACAGCGTA 5^{I}

Sequence of *npt*-II primers:

Forward 5^{I} GAG GCD ATT CGG CTA TGA CTG 3^{I}

Reverse 3^{I} ATC GGG AGG GGC GAT ACC GAT 5^{I}

The PCR mix was made fresh in bulk depending on the number of samples each time. Each 20 µl mix contained:

Taq polymerase	: 0.33 µl
Taq Buffer	: 2.5 µl
dNTPs	:1 µl
$MgCl_2$	: 0.5 µl
Forward primer	: 1 µl
Reverse primer	: 1 µl
Template	: 1 µl
SDDW	: 12.67 µl
Total	: 20 µl

The PCR amplification steps were as follows

Stage	Step	Temperature (C^0)	Duration (min)	No. of cycle
I	1. Initial Denaturation	94	5	1
II	1. Denaturation	94	1	
	2. Annealing	70	1	39
	3. Extension	72	1	
III	1. Final Extension	72	10	1
	2. Hold	4	-	-

After the completion of required cycles of amplification, the samples were stored at 4 ^{0}C in a refrigerator until further use. Here, for amplification of plasmid we standardized the protocol by using 6 temperatures (60.6 ^{0}C, 62.3 ^{0}C, 57.2 ^{0}C, 56.5 ^{0}C, 55.0 ^{0}C and 54.1 ^{0}C) to find out which temperature is suitable for amplification.

3.6.2.7.5 Agarose gel electrophoresis of DNA

1. Sufficient 1x electrophoresis buffer was prepared from 50 x stock.
2. Agarose powder was added (1%) to TAE buffer (1x) and was dissolved by melting at 100 ^{0}C. The solution was cooled to 50 ^{0}C and ethidium bromide was added (0.5 µg/ml) and the comb was positioned at 0.5-1.0 mm above the plate. Then agarose solution was poured into the gel frame and was allowed to polymerize. The gel tank was filled with TAE buffer (1x) just enough to cover the surface of the gel to a depth of 1 mm.
3. The DNA sample was mixed with gel loading buffer and it was slowly loaded into the wells of the submerged gel using a disposable microtips. DNA /Eco RI + Hind II double digest were used as molecular weight marker.
4. The system was connected to the power supply and electrophoresis was carried out at 100 volts for 30-45 min.
5. It was examined by gel documentation system.

EXPERIMENTAL RESULTS

The experimental results obtained in the present study are presented under the following heads.

4.1 Development of heterotic groups (hirsutum vs barbadense*)* based on combining ability and hybrid performance

4.2 Evaluation of recombinational variability for combining ability

4.3 Correlation co-efficient analysis

4.4 Path co-efficient analysis

4.5 Molecular marker study in cotton

4.6 *In planta* genetic transformation

4.1 Development of heterotic groups (hirsutum vs barbadense*)* based on combining ability and hybrid performance

Barbadense lines were crossed to hirsutum testers in line x tester fashion to determine whether the heterotic groups (2 barbadense and 4 hirsutum lines) formed is potential. This line x tester study is denoted as YHB trial fast to distinguish it from other studies. Results of this study are presented below (4.1.1).

After determining potential of the heterotic box, these 8 inter specific crosses were compared with commercial checks and many other potential inter specific crosses developed by the centre. This study distinguished as best HB trial and the results are presented in 4.1.2.

The barbadense lines developed in this study have practical importance based on their *per se* performance. This was evaluated by comparing them with commercial varietal check Suvin. These results are presented in 4.1.3.

4.1.1 Line x Tester analysis for confirmation of inter specific heterotic groups (YHB)

4.1.1.1 Analysis of variance (RBD)

The preliminary RBD analysis was carried out for eight characters under study for 92 crosses and three commercial checks (RAHB 87, MRC 6918 and DCH 32). Mean sum of squares for eight characters are presented in Table 3. 'F' test indicated highly significant variation among the crosses for all the eight characters except plant height and number of sympodia per plant.

4.1.1.2 Mean *per se* performance of Line x Tester inter specific crosses

The mean *per se* performance of 92 hybrids and three commercial checks (*Bt* check MRC 6918 and non *Bt* checks RAHB 87 and DCH 32) are briefly presented in Appendix 1.

4.1.1.2.1 Seed cotton yield (kg ha^{-1})

Among 95 hybrids, seed cotton yield values of all YHB hybrids ranged from 3128.72 [DH 18-31 x DB 533] to 1204.95 [DH 29-1 x DB 531]. Eight hybrids showed higher seed cotton yield than RAHB 87 (2632.14) and twelve hybrids exhibited higher seed cotton yield than MRC 6918 (2358.05) . Fourty two hybrids had high performance with respect to seed cotton yield as compared to DCH 32 (1898.53).

4.1.1.2.2 Plant height (cm)

Plant height values ranged from 304.33 [DH 18-31 x DB 532] to 186.00 [DH 18-31 x DB 531]. The results showed that fourty five hybrids recorded higher plant height than MRC 6918 (247.83), twenty hybrids recorded higher plant height than RAHB 87 (239.17) and twenty three hybrids had higher plant height than DCH 32 (212.67).

4.1.1.2.3 Number of monopodia per plant

Among 95 hybrids evaluated, number of monopodia per plant values ranged from 3.50 [ZCH 8 x DB 531] to 1.17 [DH 35-17 x DB 532 and DH 75- 23 x DB 534]. The results exhibited that twenty four hybrids recorded higher number of monopodia per plant than DCH 32 (2.33) and fifteen hybrids recorded equal performance of monopodia per plant (2.17) to the checks RAHB 87 and MRC 6918.

Table 3. Analysis of variance for different quantitative characters (RBD) in line X tester inter specific crosses (YHB) in cotton

Source	d.f.	Mean sum of squares							
		Seed cotton yield (kg/ha)	Plant height (cm)	No. of sympodia	No. of bolls	Mean boll weight (g)	Seed index (g)	Ginning outturn (%)	Lint index (g)
		1	2	3	4	5	6	7	8
Replications	1	1464781.85**	1722.35	198.14**	94.58**	2.29**	37.90**	12.28	1.85*
Crosses	91	365118.66**	722.32	13.58	43.03**	0.23**	2.56**	13.51**	0.95**
Error	91	47434.74	831.52	12.26	1.94	0.04	0.74	3.45	0.36
S.E (d)	-	159.37	20.26	2.45	1.93	0.45	0.62	1.30	0.42
CD at 5%	-	447.51	57.10	6.93	5.42	0.89	1.74	3.65	1.18
CD at 1%	-	592.58	75.84	9.21	7.18	1.18	2.31	4.83	1.57

* Significant at P = 0.05 ** Significant at P = 0.01

4.1.1.2.4 Number of sympodia per plant

Number of sympodia per plant values ranged from 34.33 [DH 91-1 x DB 534] to 21.67 [DH 18-31 x DB 531]. The results showed that twelve hybrids recorded higher number of sympodia per plant than RAHB 87 (31.50), seventeen hybrids recorded higher number of sympodia per plant than MRC 6918 (29.17) and twelve hybrids had higher number of sympodia per plant than DCH 32 (28.00).

4.1.1.2.5 Number of bolls per plant

Number of bolls per plant values ranged from 46.09 [DH 35-17 x DB 531] to 21.59 [DH 23-4 x DB 533]. The results showed that one hybrid DH 35-17 x DB 531 exhibited high performance with respect to number of bolls per plant as compared to RAHB 87 (45.84), eight hybrids recorded higher number of bolls per plant than DCH 32 (38.84) and fourty eight hybrids had high performance with respect to number of bolls per plant as compared to MRC 6918 (30.84).

4.1.1.2.6 Mean boll weight (g)

Mean boll weight values of 95 YHB hybrids ranged from 4.60 [DH 18-31x DB 533] to 2.88 [DH 35-17 x DB 531].The results showed that two hybrids recorded higher mean boll weight than DCH 32 (4.40), twenty seven hybrids showed equal performance of mean boll weight (3.90) to the checks MRC 6918 and RAHB 87.

4.1.1.2.7 Reproductive points on sympodia

Reproductive points on sympodia values ranged from 8.67 [DH 23-1 x DB 533] to 4.59 [DH 18-31 x DB 531]. The results recorded that fifteen hybrids had higher reproductive points on sympodia than DCH 32 (7.00), thirty eight hybrids showed high performance with respect to reproductive points on sympodia as compared to MRC 6918 (5.84) and two hybrids exhibited equal performance of reproductive points on sympodia to the check RAHB 87 (5.75).

4.1.1.2.8 Sympodial length at 50 per cent plant height (cm)

Among 95 hybrids evaluated, sympodial length at 50 per cent plant height values ranged from 81.92 [DH 18-31 x DB 532] to 52.09 [DH 13-7 x DB 531]. Fifty two hybrids recorded higher sympodial length at 50 per cent plant height than DCH 32 (63.59), fifteen hybrids recorded high performance with respect to sympodial length at 50 per cent plant height as compared to MRC 6918 (60.67) and eight hybrids had higher sympodial length at 50 per cent plant height than RAHB 87 (59.09).

4.1.1.2.9 Inter branch distance (cm)

Among all hybrids, inter branch distance values ranged from 36.00 [DH 37-4 x DB 533] to 26.84 [DH 8-7 x DB 532]. The results showed that fifty seven hybrids recorded high performance with respect to inter branch distance as compared to MRC 6918 (30.34), ninteen hybrids recorded higher inter branch distance than RAHB 87 (29.00) and five hybrids showed higher inter branch distance than DCH 32 (28.34).

4.1.1.2.10 Seed index (g)

Seed index values of 95 YHB hybrids ranged from 15.55 [DH 13-7 x DB 532] to 10.01 [ZCH 8 x DB 533]. Eleven hybrids had higher seed index than DCH 32 (13.78), one hybrid exhibited equal performance of seed index to the check RAHB 87 (13.72) and three hybrids showed higher seed index values than MRC 6918 (13.33).

4.1.1.2.11 Ginning outturn (%)

Ginning outturn values of all YHB hybrids ranged from 34.80 [RAHB 87] to 20.11 [DH 29-1 x DB 532]. Sixteen hybrids exhibited high performance with respect to ginning outturn as compared to MRC 6918 (30.06) and thirty nine hybrids had higher ginning outturn than DCH32 (27.20).

4.1.1.2.12 Lint index (g)

Among all YHB hybrids, lint index values ranged from 7.32 [RAHB 87] to 3.17 [DH 29-1 x DB 532]. Seven hybrids exhibited higher lint index than MRC 6918 (5.72) and twenty one hybrids had high performance with respect to lint index than DCH 32 (5.15).

To estimate fibre quality parameters, one sample was taken from pool of kapas derived from all the replications. Hence, these characters were not subjected to RBD analysis.

4.1.1.2.13 2.5% span length (mm)

2.5 per cent span length values of all YHB hybrids ranged from 40.53 [DH46-1 x DB 534] to 31.90 [DH 13-7 x DB 533]. The results recorded that fifty three hybrids showed higher 2.5% span length than MRC 6918 (36.10), five hybrids exhibited high performance with respect to 2.5% span length as compared to DCH 32 (35.80) and twenty six hybrids had higher value of 2.5% span length than RAHB 87 (34.10).

4.1.1.2.14 Fiber uniformity ratio (%)

Fiber uniformity ratio values ranged from 47.87 [DH 35-17 x DB 531] to 39.27 [DH 49-1 x DB 532]. Ten hybrids showed higher fiber uniformity ratio than two checks MRC 6918 (46.00) and RAHB 87 (46.00) and sixty nine hybrids exhibited higher fiber uniformity ratio than DCH 32 (42.00).

4.1.1.2.15 Fiber micronaire value (μg/inch)

Fiber Micronaire values ranged from 3.86 [DH 75- 23 x DB 531] to 2.39 [DH 11-8 x DB 533]. Four hybrids showed higher micronaire value than RAHB 87 (3.70) and sixty six hybrids exhibited high performance with respect to fiber micronaire value as compared to MRC 6918 (2.90) and DCH 32 (2.90).

4.1.1.2.16 Fiber maturity ratio (%)

Fiber maturity ratio values ranged from 0.69 [DH 46-1 x DB 532] to 0.56 [DH 23-4 x DB 532 and DH 23-21 x DB 532]. The results recorded that four hybrids showed higher fiber maturity ratio values than RAHB 87 (0.66) and fifty three hybrids exhibited high performance with respect to fiber maturity ratio than MRC 6918 (0.60) and DCH 32 (0.60).

4.1.1.2.17 Fiber strength (Tenacity) (g/tex)

Among 95 hybrids, tenacity values ranged from 28.92 [DH 29-1 x DB 533] to 22.12 [DH 13-7 x DB 531], the results recorded that one hybrid DH 29-1 x DB 533 showed higher tenacity value than MRC 6918 (28.60), three hybrids exhibited higher tenacity than RAHB 87 (26.40) and seventy hybrids had high performance with respect to tenacity than DCH 32 (23.30).

4.1.1.2.18 Fiber elongation (%)

Fiber elongation values ranged from 7.20 [RAHB 87] to 6.10 [DH46-1 x DB 534], fourty five hybrids exhibited high performance with respect to fiber elongation as compared to MRC 6918 (6.60) and thirty sexen hybrids showed higher fiber elongation than DCH 32 (6.30).

4.1.1.3 Line x Tester analysis

4.1.1.3.1 Analysis of variance for combining ability

Analysis of variance for combining ability done with respect to hybrids are summarized in Table 4 for eight characters.

Among the lines (males), the mean sum of squares (MSS) were not significant for all characters except mean boll weight and seed cotton yield which showed significant. Testers (females) exhibited significant difference for four characters seed index, ginning outturn, lint index and seed cotton yield which showed highly significant. Whereas, line x tester interactions were highly significant for all characters except plant height and number of sympodia per plant which recorded non significant differences.

The estimates of variance due to general combining ability (GCA), variance due to specific combining ability (SCA), the magnitude of SCA variance were greater than GCA variance for all 8 characters and the variance ratio was less than half in these traits (Table 5).

4.1.1.3.2 Combining ability effects

The estimates of general combining ability effects of females and males are presented in Table 6 and their specific combining ability effects are presented in Table 7 for all the characters.

4.1.1.3.2.1 Seed cotton yield (kg/ha)

The estimates of *gca* effects of tester parents (Fig. 5) in the population based crosses were found to be significantly different for sixteen testers, of which ten testers recorded positive significant *gca* effects and the tester DH 98-27 showed maximum value of *gca* effect for seed cotton yield trait (333.42). Three barbadense lines recorded significant *gca* effects (Fig. 5), of which two lines exhibited

Table 4. Analysis of variance for combining ability of line x tester inter specific crosses (YHB) for different quantitative characters

Source	d.f.		Mean sum of squares						
		Seed cotton yield (kg/ha)	Plant height (cm)	No. of sympodia	No. of bolls	Mean boll weight (g)	Seed index (g)	Ginning outturn (%)	Lint index (g)
		1	2	3	4	5	6	7	8
Replications	1	1464781.85**	1722.35	198.14**	94.58**	2.29**	37.90**	12.28	1.85*
Crosses	91	365118.66**	722.32	13.58	43.03**	0.23**	2.56**	13.51**	0.95**
Line Effect	3	1344213.43**	705.20	0.99	56.37	0.61*	1.94	7.76	0.63
Tester Effect	22	903079.19**	541.25	11.19	45.34	0.28	3.86*	20.30*	1.46*
Line x Tester Effect	66	141294.17**	783.46	14.95	41.65**	0.20**	2.16**	11.51**	0.80**
Error	91	47434.74	831.52	12.26	1.94	0.04	0.74	3.45	0.36

* Significant at P = 0.05 ** Significant at P = 0.01

Table 5. Variance due to general and specific combining ability for different quantitative characters in line x tester inter specific crosses (YHB)

Sl. No.	Characters	Variance Due to GCA	Variance Due to SCA	GCA/SCA
1.	Plant height (cm)	11.49800	6463.54050	0.00275
2	Number of sympodia	0.01625	123.35975	0.00000
3	Number of bolls	0.91925	343.62825	0.00275
4	Mean boll Weight (g)	0.01025	1.65775	0.00675
5	Seed index (g)	0.03150	17.79225	0.00175
6	Ginning outturn (%)	0.12650	94.93500	0.00100
7	Lint index (g)	0.01050	6.56300	0.00150
8	Seed cotton yield (kg/ha)	21916.52625	1165676.92500	0.01700

positive significant *gca* effects recorded by the line DB 533 (242.92) and DB 534 (75.54). Among 92 crosses, seventeen crosses differed significantly for *sca* effects and the hybrid DH 11-8 x DB 534 (565.35) recorded highest positive *sca* effect.

4.1.1.3.2.2 Plant height (cm)

The estimates of general combining ability effects among hirsutum testers recorded significant negative value in the tester DH 75- 23 (-21.36) and the highest positive *gca* effect was exhibited by the tester DH 45-23 (9.60). All four barbadense lines exhibited not significant *gca* effects and the line DB 531 showed highest positive *gca* effect (2.88). Four crosses differed significantly for *sca* effects, of these two had positive *sca* effects showed by the crosses DH 18-31 x DB 532 (52.60) and DH 31-2 x DB 531 (43.87), whereas the crosses DH 23-4 x DB 533 (-44.04) and DH 18-31 x DB 531 (-67.46) recorded significant negative *sca* effects for plant height.

4.1.1.3.2.3 Number of sympodia per plant

The estimates of general combining ability effects indicated not significant differences among all hirsutum testers and four barbadense lines. Three crosses expressed significant *sca* effects, of these one hybrid exhibited positive *sca* effect showed by the cross DH 31-2 x DB 532 (5.06) and two hybrids recorded negative *sca* effects DH 23-4 x DB 533 (-5.64) and DH 31-2 x DB 534 (-5.97).

4.1.1.3.2.4 Number of bolls per plant

Out of the 23 testers, 15 testers showed significant *gca* effects for number of bolls per plant. ZCH 8 (2.02), DH 37-4 (1.62), DH 8-7 (1.85), DH 29-1 (1.33), DH 35-17 (5.29), DH 13-7 (1.49) and DH 23-21 (5.18) exhibited significant positive *sca* effects in the desirable direction, whereas testers DH 18-31 (-3.25), 178-24 (-3.34), DH 24-4 (-2.38), DH 11-8 (- 1.03), DH 23-4 (-3.19), DH 75- 23 (-2.63), DH 91-1 (-2.38) and DH 45-23 (-1.23) showed significant negative *gca* effects in desirable direction. Out of 4 lines, three lines exhibited significant *gca* effects in desirable direction, the lines DB 534 and DB 532 exhibited positive significant *gca* effects 1.06 and 0.52 respectively. While the line DB 533 (-1.51) recorded significant negative *gca* effect. Out of 92 crosses, fifty three crosses recorded significant *sca* effects in desirable direction. Twenty five crosses showed positive significant *sca* effects and the cross DH 23-1 x DB 532 (8.61) exhibited higher value of positive significant *sca* effect.Whereas twenty eight crosses recorded negative significant *sca* effects.

4.1.1.3.2.5 Mean boll weight (g)

The estimates of *gca* effects of tester parents in the population based crosses were found to be significant in twelve testers, out of which six were positive significant and other were negative significant differences, shown the highest values by the testers DH 49-1 (0.34) and DH 18-31 (0.25). Among the lines, three showed significant differences of *gca* effects and the line DB 534 had significant positive of *gca* effect (0.16). Ninteen crosses expressed significant *sca* effects, out of which nine recorded positive significant *sca* effects and the cross DH 31-2 x DB 533 (0.77) had higher value of positive significant *sca* effect.

4.1.1.3.2.6 Seed index (g)

Nine tester parents exhibited significant *gca* effects, four testers had significant *gca* in positive direction and highest was recorded in DH 13-7 (1.18). Among the lines, DB 534 showed positive significant *gca* effect (0.27). Thirteen crosses revealed significant *sca* effects, of these six crosses showed positive *sca* effects and the highest was displayed by the cross DH 23-21 x DB 532 (2.61).

4.1.1.3.2.7 Ginning outturn (%)

Six hirsutum tester parents displayed significant *gca* effects, of which three testers exhibited significant positive *gca* effects and highest value was recorded by DH 98-27 (2.87). Among the barbadense lines, DB 532 (-0.61) exhibited significant negative *gca* effect. Eighteen crosses expressed significant *sca* effects, of these eight crosses showed positive *sca* effects and the hybrid 178-24 x DB 533 recorded highest positive *sca* effect (6.70).

4.1.1.3.2.8 Lint index (g)

Seven hirsutum testers showed significant *gca* effects, of which four testers had positive *gca* effects and the tester DH 13-7 (0.84) recorded highest value of *gca* effect. There are no significant differences among all barbadense lines and DB 534 (0.14) exhibited highest value of *gca* effect. Out of 92 crosses studied, seven crosses recorded significant *sca* effects for this character, of which five showed significant in positive direction and the cross 178-24 x DB 533 recorded highest significant positive *sca* effect (1.91).

Table 6. Estimates of general combining ability effects of parents for different quantitative characters included in line x tester inter specific crosses (YHB)

Sl. No	Parents	Seed cotton yield (kg/ha)	Plant height (cm)	No. of sympodia	No. of bolls	Mean boll weight (g)	Seed index (g)	Ginning outturn (%)	Lint index (g)	
		Value	Rank	2	3	4	5	6	7	8
	Hirsutum Testers									
1	**DH 98-27**	333.42**	1	-7.07	1.57	0.14	-0.05	0.20	2.87**	0.77**
2	**DH 18-31**	329.65**	2	3.98	-1.64	-3.25**	0.25**	1.01	-0.93	0.13
3	DH 35-17	307.44**	3	9.23	1.53	5.29**	-0.39**	-0.80**	0.03	-0.32
4	DH 13-7	271.47**	4	-4.98	-0.39	1.49**	0.07	1.18**	1.48*	0.84**
5	DH 23-4	269.95**	5	2.52	-0.39	-3.19**	-0.15*	0.654*	-0.45	0.16
6	DH 24-4	257.55**	6	-1.36	-1.39	-2.38**	-0.01	-0.48	-0.49	-0.31
7	**178-24**	236.63**	7	3.77	-0.22	-3.34**	0.12	-0.13	-0.30	-0.03
8	**ZCH 8**	216.37**	8	6.81	0.53	2.02**	-0.17*	-1.40**	1.30	-0.30
9	DH46-1	192.11*	9	-6.36	-1.39	-0.40	0.00	0.35	-3.99**	-0.81**
10	DH 49-1	164.65*	10	-3.90	0.24	0.91	0.34**	-0.07	-2.16**	-0.53*
11	DH 11-8	149.00	11	-19.32	-1.64	-1.03*	-0.07	0.672 *	0.99	0.47*
12	DH 37-4	144.46	12	6.14	-1.93	1.62**	-0.10	-0.96**	0.86	-0.19
13	DH 82-3	142.20	13	-2.81	-0.35	-0.05	-0.28**	-0.32	1.23	0.14
14	DH 91-1	67.27	14	7.10	1.49	-2.38**	-0.15*	-0.19	-0.94	-0.30
15	DH 53-2	57.15	15	-2.57	-0.22	-0.55	0.17*	-0.69*	0.83	-0.09
16	DH 23-1	32.61	16	-2.69	1.24	0.47	0.04	0.07	0.03	0.01
17	DH 45-23	25.64	17	9.60	2.07	-1.23*	0.15*	1.17**	-0.31	0.40

Contd....

Sl.No	Parents	Seed cotton yield (kg/ha)		Plant height (cm)	No. of sympodia	No. of bolls	Mean boll weight (g)	Seed index (g)	Ginning outturn (%)	Lint index (g)
		Value	Rank	2	3	4	5	6	7	8
18	DH 23-21	-458.05**	18	1.64	1.03	5.18**	-0.3**	0.51	1.447*	0.547*
19	DH 31-2	-486.73**	19	9.31	0.28	-0.82	0.17*	-0.02	0.52	0.12
20	DH 14-2	-538.49**	20	4.77	0.61	0.93	-0.09	0.02	0.14	0.07
21	DH 75- 23	-557.05**	21	-21.36*	-1.56	-2.63**	0.17*	-1.047**	0.87	-0.21
22	DH 29-1	-577.69**	22	0.89	0.44	1.33**	0.14	0.22	-3.64**	-0.73**
23	DH 8-7	-579.54**	23	6.64	0.11	1.85**	0.14	0.05	0.63	0.19
	SE (gi)	77.00		10.20	1.24	0.49	0.07	0.30	0.66	0.21
	SEd (gi-gj)	108.90		14.42	1.75	0.70	0.10	0.43	0.93	0.30
	CD at 5%	215.62		20.25	2.46	1.38	0.21	0.61	1.30	0.42
	CD at 1%	286.40		26.82	3.26	1.83	0.27	0.80	1.73	0.56
	Barbadense Lines									
1	**DB 533**	242.92**	1	1.748	-0.118	-1.51**	0	-0.236	0.24	-0.027
2	**DB 534**	75.54*	2	-5.774	-0.111	1.06**	0.16**	0.265*	0.23	0.142
3	DB 532	-4.92	3	1.146	0.194	0.52*	-0.08*	-0.014	-0.613*	-0.14
4	DB 531	-313.54**	4	2.879	0.034	-0.07	-0.09**	-0.015	0.15	0.025
	SE (gi)	32.11		4.25	0.52	0.21	0.03	0.13	0.27	0.09
	SEd (gi-gj)	45.41		6.01	0.73	0.29	0.04	0.18	0.39	0.13
	CD at 5%	89.92		8.45	1.03	0.58	0.09	0.25	0.54	0.18
	CD at 1%	119.44		11.19	1.36	0.76	1.83	0.33	0.72	0.23

* Significant at P = 0.05 ** Significant at P = 0.01

Table 7. Estimates of specific combining ability effects of line x tester inter specific crosses (YHB) for different quantitative characters

Sl.No	Crosses	Seed cotton yield (kg/ha)	Plant height (cm)	No. of sympodia	No. of bolls	Mean boll weight (g)	Seed index (g)	Ginning outturn (%)	Lint index (g)
		1	2	3	4	5	6	7	8
1	DH 18-31 x DB 533	528.15**	11.50	2.12	-3.7**	0.65**	-0.93	0.53	-0.15
2	DH 49-1 x DB 533	179.83	-2.12	-0.76	0.86	0.16	-0.71	-1.80	-0.60
3	DH 23-1 x DB 533	-20.16	-6.17	3.25	-1.78	0.24	-1.07	1.50	-0.07
4	DH 98-27 x DB 533	-78.91	10.05	2.58	8.47**	-0.20	0.69	-1.21	-0.04
5	178-24 x DB 533	-19.90	-7.29	3.87	3.78**	0.41**	0.57	6.70**	1.91**
6	DH46-1 x DB 533	345.00*	-0.17	1.21	4.26**	0.26	-0.51	-1.20	-0.35
7	ZCH 8 x DB 533	380.94*	20.00	-0.38	-2.49*	0.55**	-0.70	1.95	0.09
8	DH 37-4 x DB 533	226.05	-4.33	-0.26	-5.76**	-0.16	0.07	3.384*	0.78
9	DH 24-4 x DB 533	-301.61	4.84	0.20	-0.51	-0.06	-0.62	1.17	0.03
10	DH 8-7 x DB 533	-93.50	2.67	-4.13	-6.33**	-0.27	-1.708**	-0.42	-0.80
11	DH 11-8 x DB 533	-336.54*	30.80	0.45	-0.95	0.09	1.18	-1.77	-0.01
12	DH 29-1 x DB 533	-35.57	14.09	2.53	4.03**	0.01	-0.33	1.44	0.19
13	DH 53-2 x DB 533	149.72	2.71	3.03	-2.18*	0.16	0.69	0.96	0.47
14	DH 35-17 x DB 533	-473.08**	15.08	-3.38	0.74	0.17	1.53*	-2.79*	-0.04
15	DH 23-4 x DB 533	-288.10	-44.038*	-5.635*	-6.37**	-0.26	0.23	-2.17	-0.45
16	DH 31-2 x DB 533	-124.58	-33.33	-2.30	-7.41**	-0.77**	0.86	0.57	0.50
17	DH 13-7 x DB 533	505.24**	14.29	-0.63	7.61**	-0.23	-1.12	1.19	-0.15
18	DH 75- 23 x DB 533	-152.41	6.84	-0.13	-1.10	-0.53**	0.46	-2.39	-0.36
19	DH 91-1 x DB 533	-175.63	-9.46	-3.51	0.57	-0.25	1.20	-0.52	0.29

Contd...

Sl.No	Crosses	Seed cotton yield (kg/ha)	Plant height (cm)	No. of sympodia	No. of bolls	Mean boll weight (g)	Seed index (g)	Ginning outturn (%)	Lint index (g)
		1	2	3	4	5	6	7	8
20	DH 45-23 x DB 533	8.79	-14.96	0.74	0.34	-0.22	-0.91	-0.64	-0.52
21	DH 14-2 x DB 533	-148.42	4.04	2.03	3.09**	0.17	1.06	-4.13**	-0.61
22	DH 82-3 x DB 533	-20.24	-0.54	0.32	3.24**	0.03	0.22	2.06	0.57
23	DH 23-21 x DB 533	-55.07	-14.50	-1.22	1.59	0.05	-0.12	-2.42	-0.69
24	DH 18-31 x DB 532	-69.82	52.601*	3.14	-0.59	-0.27	1.39*	-2.80*	-0.24
25	DH 49-1 x DB 532	58.74	-5.19	2.93	1.76	0.29	-0.30	0.92	0.07
26	DH 23-1 x DB 532	177.96	-8.23	0.76	8.61**	-0.09	0.37	0.29	0.16
27	DH 98-27 x DB 532	352.59*	-13.36	-1.57	-3.72**	0.13	-1.09	1.39	-0.16
28	178-24 x DB 532	-67.85	10.81	-3.44	-0.66	0.26	-0.40	-1.86	-0.66
29	DH46-1 x DB 532	4.30	-17.23	-1.45	-4.85**	-0.32*	-2.07**	0.68	-0.51
30	ZCH 8 x DB 532	311.09*	2.10	-1.69	-3.35**	-0.15	0.60	0.17	0.30
31	DH 37-4 x DB 532	-6.46	9.27	-0.57	4.21**	0.08	0.08	-3.51**	-0.73
32	DH 24-4 x DB 532	155.18	-2.73	-0.28	0.30	-0.07	-0.55	1.44	0.10
33	DH 8-7 x DB 532	10.32	-15.23	0.72	-0.27	-0.15	-0.31	-1.89	-0.57
34	DH 11-8 x DB 532	-214.96	-10.94	-0.36	-5.56**	0.15	-0.78	2.10*	0.43
35	DH 29-1 x DB 532	-15.83	-25.31	-2.44	-3.16**	-0.06	-0.11	-3.46**	-0.74
36	DH 53-2 x DB 532	321.29*	-8.86	-3.61	-0.21	-0.15	-0.26	1.94	0.31
37	DH 35-17 x DB 532	35.66	7.86	1.97	-1.45	0.13	-0.47	3.71**	0.63
38	DH 23-4 x DB 532	-276.01	1.73	0.39	5.27**	0.31*	0.85	2.30	0.90*
39	DH 31-2 x DB 532	-64.25	24.77	5.055*	1.32	0.23	-0.81	-1.03	-0.57
40	DH 13-7 x DB 532	-328.12*	-15.94	0.89	-2.5*	-0.17	2.04**	-0.81	0.56

Contd...

Sl.No	Crosses	Seed cotton yield (kg/ha)	Plant height (cm)	No. of sympodia	No. of bolls	Mean boll weight (g)	Seed index (g)	Ginning outturn (%)	Lint index (g)
		1	2	3	4	5	6	7	8
41	DH 75- 23 x DB 532	-15.60	5.77	2.06	3.3**	-0.11	-0.56	1.84	0.16
42	DH 91-1 x DB 532	136.03	1.65	-2.98	-3.04**	0.13	0.13	-2.51	-0.49
43	DH 45-23 x DB 532	-67.75	-1.35	0.77	-1.10	-0.27	0.59	3.73**	1.19**
44	DH 14-2 x DB 532	-258.54	8.31	-1.94	-5.6**	0.12	-1.285*	-1.33	-0.79
45	DH 82-3 x DB 532	-96.81	-14.44	-1.15	4.29**	0.23	0.34	-2.76*	-0.52
46	DH 23-21 x DB 532	-81.17	13.94	2.81	6.98**	-0.25	2.606**	0.57	1.19**
47	DH 18-31 x DB 531	-285.70	-67.46**	-5.20	6.08**	0.25	-0.84	2.24	0.23
48	DH 49-1 x DB 531	14.05	8.91	-0.57	-2.91**	-0.45**	0.40	0.00	0.13
49	DH 23-1 x DB 531	143.83	11.71	-1.24	0.36	-0.17	0.60	-1.92	-0.19
50	DH 98-27 x DB 531	-73.59	-15.92	-1.74	-3.31**	-0.21	-0.23	-0.60	-0.26
51	178-24 x DB 531	345.95*	-4.92	-1.95	-4.91**	-0.13	-0.50	-4.10**	-1.35**
52	DH46-1 x DB 531	39.28	9.21	-2.45	1.82	-0.16	0.15	2.66*	0.64
53	ZCH 8 x DB 531	-198.08	-24.63	-1.20	4.32**	-0.01	0.56	-1.65	-0.13
54	DH 37-4 x DB 531	-25.34	-21.29	-0.58	-0.95	0.05	0.34	-1.02	-0.11
55	DH 24-4 x DB 531	293.36	-2.30	-0.79	2.05*	0.05	0.49	0.06	0.22
56	DH 8-7 x DB 531	-48.61	5.54	1.21	-0.26	0.35*	0.96	1.34	0.70
57	DH 11-8 x DB 531	-13.86	-1.34	-0.53	0.61	-0.21	-1.511*	0.60	-0.45
58	DH 29-1 x DB 531	-113.90	5.29	-0.45	-6.24**	-0.19	-0.56	0.31	-0.15
59	DH 53-2 x DB 531	-456.72**	-5.76	-1.12	-1.78	0.20	-0.18	-3.174*	-0.76
60	DH 35-17 x DB 531	320.86*	-11.05	2.30	8.22**	-0.34*	-0.71	1.07	-0.06
61	DH 23-4 x DB 531	1.94	30.16	1.72	0.45	-0.38*	-0.31	1.07	0.12

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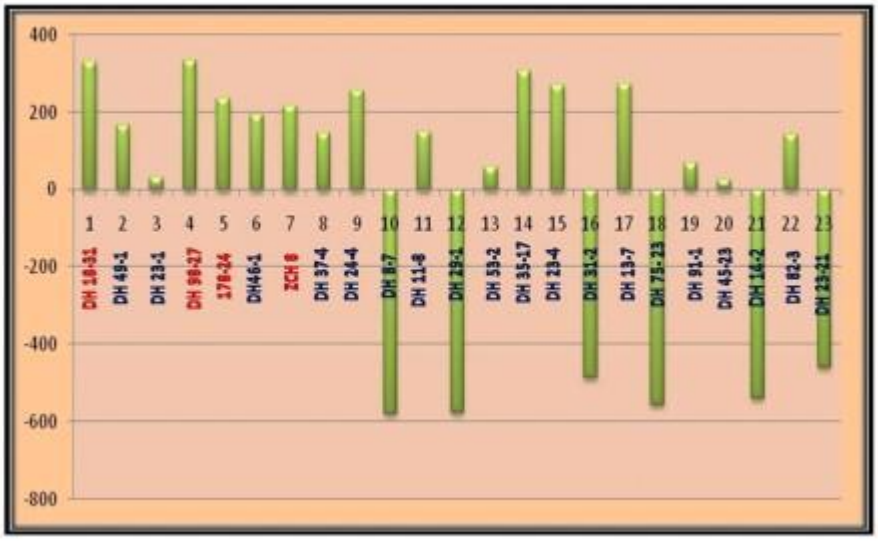
Sl.No	Crosses	Seed cotton yield (kg/ha)	Plant height (cm)	No. of sympodia	No. of bolls	Mean boll weight (g)	Seed index (g)	Ginning outturn (%)	Lint index (g)
		1	2	3	4	5	6	7	8
62	DH 31-2 x DB 531	44.88	43.87*	3.21	4.32**	0.27	0.47	-0.71	0.00
63	DH 13-7 x DB 531	-103.04	11.66	3.38	-2.16*	0.40**	0.05	-0.19	-0.02
64	DH 75- 23 x DB 531	-48.33	10.70	-1.45	-0.12	0.22	0.17	3.52**	0.87*
65	DH 91-1 x DB 531	-56.65	-4.59	2.01	-0.37	-0.04	-0.58	0.78	-0.04
66	DH 45-23 x DB 531	44.73	7.41	-0.24	0.07	0.29	1.272*	-0.67	0.29
67	DH 14-2 x DB 531	202.16	-9.09	1.88	4.82**	-0.12	0.26	2.26	0.62
68	DH 82-3 x DB 531	-133.61	12.50	3.34	-3.45**	-0.25	0.93	-0.45	0.28
69	DH 23-21 x DB 531	106.39	11.37	0.47	-6.68**	0.57**	-1.237*	-0.52	-0.61
70	DH 18-31 x DB 534	-172.64	3.36	-0.06	-1.80	-0.63**	0.38	0.04	0.16
71	DH 49-1 x DB 534	-252.62	-1.60	-1.60	0.29	0.00	0.61	0.88	0.41
72	DH 23-1 x DB 534	-301.62	2.69	-2.77	-7.19**	0.03	0.10	0.13	0.10
73	DH 98-27 x DB 534	-200.10	19.23	0.74	-1.44	0.29	0.64	0.43	0.46
74	178-24 x DB 534	-258.19	1.40	1.53	1.79	-0.54**	0.34	0.16	0.09
75	DH46-1 x DB 534	-388.58*	8.19	2.69	-1.23	0.22	2.43**	-2.15	0.22
76	ZCH 8 x DB 534	-493.95**	2.52	3.28	1.52	-0.39**	-0.46	-0.46	-0.26
77	DH 37-4 x DB 534	-194.25	16.36	1.40	2.5*	0.02	-0.49	1.14	0.06
78	DH 24-4 x DB 534	-146.93	0.19	0.86	-1.83	0.07	0.67	-2.67*	-0.35
79	DH 8-7 x DB 534	131.79	7.02	2.19	6.85**	0.07	1.06	0.97	0.68
80	DH 11-8 x DB 534	565.35**	-18.52	0.44	5.9**	-0.04	1.12	-1.83	0.03
81	DH 29-1 x DB 534	165.29	5.94	0.36	5.37**	0.23	1.00	1.71	0.70
82	DH 53-2 x DB 534	-14.29	11.90	1.69	4.17**	-0.21	-0.26	0.28	-0.03

Contd...

Sl.No	Crosses	Seed cotton yield (kg/ha)	Plant height (cm)	No. of sympodia	No. of bolls	Mean boll weight (g)	Seed index (g)	Ginning outturn (%)	Lint index (g)
		1	2	3	4	5	6	7	8
83	DH 35-17 x DB 534	116.56	-11.89	-0.89	-7.5**	0.04	-0.36	-1.99	-0.53
84	DH 23-4 x DB 534	562.18**	12.15	3.53	0.64	0.34*	-0.77	-1.20	-0.58
85	DH 31-2 x DB 534	143.96	-35.31	-5.971*	1.77	0.27	-0.51	1.16	0.06
86	DH 13-7 x DB 534	-74.07	-10.02	-3.64	-2.96**	0.00	-0.96	-0.19	-0.39
87	DH 75- 23 x DB 534	216.34	-23.31	-0.47	-2.08*	0.42**	-0.06	-2.96*	-0.68
88	DH 91-1 x DB 534	96.26	12.40	4.48	2.83**	0.16	-0.76	2.26	0.24
89	DH 45-23 x DB 534	14.23	8.90	-1.27	0.69	0.21	-0.95	-2.42	-0.96*
90	DH 14-2 x DB 534	204.80	-3.27	-1.97	-2.31*	-0.16	-0.03	3.19*	0.78
91	DH 82-3 x DB 534	250.65	2.48	-2.51	-4.08**	-0.01	-1.492*	1.15	-0.33
92	DH 23-21 x DB 534	29.84	-10.81	-2.05	-1.90	-0.38*	-1.248*	2.37	0.12
	SEd	154.00	20.39	2.48	0.99	0.15	0.61	1.31	0.42
	CD at 5%	431.23	40.50	4.92	2.76	0.41	1.21	2.61	0.84
	CD at 1%	572.80	53.65	6.51	3.67	0.55	1.60	3.46	1.12

* Significant at P = 0.05 ** Significant at P = 0.01

Lines gca effects



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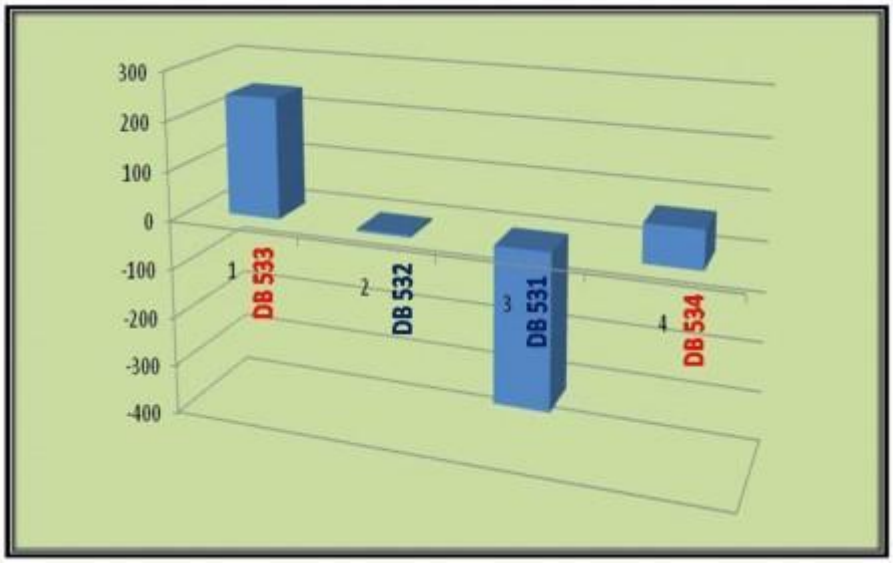

Fig 5 : Estimates of general combining ability effects of parents for seed cotton yield included in Line x Tester inter specific crosses (YHB)

4.1.2 Comparison of hybrids based on heterotic box with checks (Best HB)

The mean performance of 49 best HB inter specific hybrids and three commercial checks (*Bt* check MRC 6918 and non *Bt* checks RAHB 87 and DCH 32) are briefly presented in Appendix 2.

4.1.2.1 Seed cotton yield (kg ha^{-1})

Among 52 hybrids, seed cotton yield values ranged from 2277.81 [ZCH 8 x DB 533] to 1232.69 [DH 11-20 x DB 534]. Fourteen hybrids had high performance with respect to seed cotton yield as compared to RAHB 87 (2087.13), two hybrids exhibited higher seed cotton yield than MRC 6918 (2070.00) and twenty three hybrids had higher values of seed cotton yield than DCH 32 (1767.23).

4.1.2.2 Plant height (cm)

Plant height values ranged from 301.00 [DH 102-23 x DB 534] to 178.00 [DH 18-31 x DB 532] and the results showed that ten hybrids recorded higher plant height than DCH 32 (256.67), thirty hybrids recorded high performance with respect to plant height as compared to RAHB 87 (210.67) and seven hybrids had higher plant height than MRC 6918 (199.00).

4.1.2.3 Number of monopodia per plant

Among 52 hybrids evaluated, number of monopodia per plant values ranged from 4.00 [DH 43-44 x DB 532] to 0.67 [DH 18-31 x DB 533] and twenty six hybrids recorded higher number of monopodia per plant than RAHB 87 (2.00), eight hybrids recorded high performance with respect to number of monopodia per plant as compared to DCH 32 (1.33) and two hybrids DH 57-95 x DB 533 and DH 10-2 x DB 531 exhibited equal performance of number of monopodia per plant to the *Bt* check MRC 6918 (1.00).

4.1.2.4 Number of sympodia per plant

Among all the hybrids evaluated, number of sympodia per plant values ranged from 39.33 [DH 40-29 x DB 532] to 23.00 [DH 18-31 x DB 532] and the results showed that three hybrids recorded high performance with respect to number of sympodia per plant as compared to DCH 32 (34.67), twelve hybrids recorded higher number of sympodia per plant than RAHB 87 (31.33) and seventeen hybrids had higher number of sympodia per plant than MRC 6918 (28.67).

4.1.2.5 Number of bolls per plant

Number of bolls per plant values ranged from 47.33 [DH 22-76 x DB 534] to 21.00 [DH 102-23 x DB 534], seventeen hybrids exhibited high performance with respect to number of bolls per plant as compared to RAHB 87 (33.00), one hybrid DH 18-31 x DB 534 recorded equal value of performance to the *Bt* check MRC 6918 (32.67) and ten hybrids had higher number of bolls per plant than DCH 32 (30.67).

4.1.2.6 Mean boll weight (g)

Mean boll weight values of 52 best HB hybrids ranged from 5.20 [DH 39-84 x DB 531, DH 11-8 x DB 532, DH 53-2 x DB 534, DH 84-7 x DB 533 and DH 8-7 x DB 532] to 3.50 [DH 11-8 x DB 531, 177-24 x DB 531, DH 11-8 x DB 534 and DH 91-1 x DB 531] and the results showed that seven hybrids recorded higher mean boll weight than DCH 32 (5.00), eight hybrids showed high performance with respect to mean boll weight as compared to RAHB 87 (4.60) and two hybrids had higher mean boll weight than MRC 6918 (4.40).

4.1.2.7 Reproductive points on sympodia

Among all hybrids, reproductive points on sympodia values ranged from 7.33 [DH 25-22 x DB 533 and DH 25-3 x DB 533] to 4.33 [DH 21-29 x DB 532 and RAHB 87]. Thirty four hybrids had higher reproductive points on sympodia than MRC 6918 (5.17) and DCH 32 (5.17) and twelve hybrids showed higher reproductive points on sympodia than RAHB 87 (4.33).

4.1.2.8 Sympodial length at 50 per cent plant height (cm)

Sympodial length at 50 per cent plant height values ranged from 89.50 [DH 102-23 x DB 534] to 50.00 [RAHB 87] and the results showed that thirty three hybrids recorded high performance with respect to sympodial length at 50 per cent plant height as compared to DCH 32 (62.33), four hybrids recorded higher sympodial length at 50 per cent plant height than MRC 6918 (60.67) and twelve

hybrids had high performance with respect to sympodial length at 50 per cent plant height as compared to RAHB 87 (50.00).

4.1.2.9 Inter branch distance (cm)

Among 52 hybrids, inter branch distance values ranged from 37.00 [DH 102-23 x DB 534] to 20.67 [DH 11-8 x DB 533] and the results showed that fifteen hybrids recorded high performance with respect to inter branch distance as compared to DCH 32 (30.33), eight hybrids recorded higher inter branch distance than MRC 6918 (29.33) and six hybrids showed higher values of inter branch distance than RAHB 87 (27.67).

4.1.2.10 Seed index (g)

Seed index values of 52 YHB hybrids ranged from 15.00 [DH 28-36 x DB 531, DH 91-1 x DB 531 and DCH 32] to 11.00 [DH 22-76 x DB 534, DH 57-95 x DB 533, DH 47-67 x DB 532, ZCH 8 x DB 533, DH 11-8 x DB 531, 179-20 x DB 532, DH 44-14 x DB 534, DH 25-3 x DB 533 and RAHB 87]. Two hybrids had equal performance of seed index to the check DCH 32 (15.00), twenty one hybrids exhibited high performance with respect to seed index than MRC 6918 (12.00) and eight hybrids showed equal values of seed index to the check RAHB 87 (11.00).

4.1.2.11 Ginning outturn (%)

Ginning outturn values of 52 best HB hybrids ranged from 39.74 [RAHB 87] to 27.76 [DH 39-84 x DB 531]. Twenty one hybrids exhibited high performance with respect to ginning outturn as compared to DCH 32 (34.38) and fourteen hybrids had higher values of ginning outturn than MRC 6918 (32.44).

4.1.2.12 Lint index (g)

Lint index values of all best HB hybrids ranged from 5.16 [DH 28-36 x DB 531 and DCH 32] to 3.50 [177-24 x DB 531] and the results exhibited that eighteen hybrids exhibited higher lint index than RAHB 87 (4.37) and twenty one hybrids had higher values of lint index than MRC 6918 (3.89).

4.1.2.13 2.5% span length (mm)

2.5% span length values of all hybrids ranged from 40.40 [177-24 x DB 531] to 32.40 [DH 8-7 x DB 531]. Six hybrids showed high performance with respect to 2.5% span length as compared to DCH 32 (39.60), twenty nine hybrids exhibited higher 2.5% span length than RAHB 87 (35.40) and four hybrids had higher values of 2.5% span length than MRC 6918 (34.90).

4.1.2.14 Fiber uniformity ratio (%)

Among 52 hybrids, fiber uniformity ratio values ranged from 49.00 [DH 11-8 x DB 533] to 43.00 [DH 28-36 x DB 531, DH 53-2 x DB 534, DH 25-22 x DB 533, DH 18-19 x DB 533 and ZCH 8 x DB 534]. Five hybrids showed higher fiber uniformity ratio than two checks MRC 6918 (46.00) and RAHB 87 (46.00) and fifteen hybrids exhibited equal performance of fiber uniformity ratio to the check DCH 32 (45.00).

4.1.2.15 Fiber micronaire value (μg/inch)

Fiber micronaire values ranged from 3.60 [DH 8-7 x DB 531] to 2.50 [DH 25-22 x DB 533]. The results showed that one hybrid DH 8-7 x DB 531 showed highest value of micronaire than RAHB 87 (3.50) and DCH 32 (3.50) and fourty three hybrids exhibited higher fiber micronaire values than MRC 6918 (2.60).

4.1.2.16 Fiber strength (Tenacity) (g/tex)

The tenacity values ranged from 30.60 [DH 11-8 x DB 531] to 22.70 [DCH 32]. One hybrid DH 11-8 x DB 531 showed higher tenacity value than MRC 6918 (27.40), thirty hybrids exhibited high performance with respect to tenacity value as compared to RAHB 87 (24.90) and sixteen hybrids had higher values of tenacity than DCH 32 (22.70).

4.1.2.17 Fiber elongation (%)

Fiber elongation values ranged from 6.70 [DH 22-76 x DB 534] to 5.60 [177-24 x DB 531], the results recorded that one hybrid DH 22-76 x DB 534 exhibited higher fiber elongation value than RAHB 87 (6.40), ten hybrids had high performance with respect to fiber elongation than DCH 32 (6.10) and twenty hybrids showed higher values of fiber elongation than MRC 6918 (5.80).

Table 8. Analysis of variance for different quantitative characters (RBD) in 53 barbadense lines

Source	d.f.	Mean sum of squares												
		Seed cotton yield (kg/ha)	Plant height (cm)	No. of Mono podia	No. of sym podia	No. of bolls	Mean boll weight (g)	Repro ductive points on sympodia	Length of sympodia at 50% height (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Photosynt hetic rate ($\mu molCO_2 m^{-2} s^{-1}$)	Stomatal conductance ($\mu molm^{-2} s^{-1}$)	Transpiration rate ($mmol H_2Om^{-2} s^{-1}$)
		1	2	3	4	5	6	7	8	9	10	11	12	13	14
Replications	1	109528.60**	241.45**	0.11**	2.62	99.37**	1.25**	2.62**	291.13**	38.45**	73.67**	26.17**	136.94**	0.013	18.12**
Genotypes	52	362766.12**	154.16**	0.46**	12.40**	26.85	0.24**	1.04**	29.81**	2.91**	13.77**	1.24**	35.34**	0.23**	4.79**
Error	52	59269.06	119.91	0.09	7.40	35.90	0.14	0.14	14.85	0.07	3.08	0.14	29.98	0.09	2.70
S.E d		243.45	10.95	0.31	2.72	5.99	0.38	0.37	3.85	0.26	1.75	0.37	5.48	0.30	1.64
CD@ 5%		342.16	15.39	0.43	3.82	8.42	0.53	0.52	5.42	0.37	2.47	0.52	7.70	0.43	2.31
C.D. 1%		455.91	20.51	0.58	5.10	11.22	0.70	0.69	7.22	0.49	3.29	0.69	10.25	0.57	3.08

* Significant at P = 0.05 ** Significant at P = 0.01

4.1.3 Evaluation of 53 F_5 barbadense lines

4.1.3.1 Analysis of variance (RBD)

The preliminary RBD analysis was carried out for fourteen characters under study for 53 barbadense lines (included Suvin as check). Mean sum of squares for fourteen characters are presented in Table 8. 'F' test indicated highly significant variation among the brbadense lines for all the 14 characters except number of bolls per plant.

4.1.3.2 Mean *per se* performance of 53 barbadense lines

The mean performance of 53 barbadense lines included Suvin variety as check, are briefly presented in Appendix 3.

4.1.3.2.1 Seed cotton yield (kg ha^{-1})

The *per se* performance of 53 barbadense lines showed that 13 lines had higher values of seed cotton yield than Suvin line. Maximum seed cotton yield per plant was observed in the line DB 533 x DB 534 F_5 IPS 132 (2175.70) followed by the line DB 533 x DB 534 F_5 IPS 18 (2151.21), while the line DB 533 x DB 534 F_5 IPS 33 recorded minimum seed cotton yield per plant (441.81) followed by the line DB 533 x DB 534 F_5 IPS 24 (585.08).

4.1.3.2.2 Plant height (cm)

The barbadense line DB 533 x DB 534 F_5 IPS 62 recorded the tallest plant height (100.33) followed by the line DB 533 x DB 534 F_5 IPS 105 (97.83), while the line DB 533 x DB 534 F_5 IPS 34 exhibited the shortest plant height (65.33).

4.1.3.2.3 Number of monopodia per plant

Among 53 barbadense lines, the line DB 533 x DB 534 F_5 IPS 6 recorded maximum number of monopodia per plant (2.50) followed by DB 533 x DB 534 F_5 IPS 18 (2.17). On the other hand, the line DB 533 x DB 534 F_5 IPS 19 (0.17) recorded minimum number of monopodia per plant.

4.1.3.2.4 Number of sympodia per plant

Maximum number of sympodia per plant was observed in the line DB 533 x DB 534 F_5 IPS 37 (24.83) followed by DB 533 x DB 534 F_5 IPS 21 (22.50) and DB 533 x DB 534 F_5 IPS 20 (21.83) which are on par with one another. On the other hand, the lines DB 533 x DB 534 F_5 IPS 32 and DB 533 x DB 534 F_5 IPS 1 recorded lowest number of sympodia per plant (13.83) followed by the line DB 533 x DB 534 F_5 IPS 38 (14.17).

4.1.3.2.5 Number of bolls per plant

The *per se* performance of 53 barbadense lines showed that 17 lines had higher values of number of bolls per plant than Suvin line. The barbadense line DB 533 x DB 534 F_5 IPS 62 produced maximum number of bolls per plant (39.33) followed by the lines DB 533 x DB 534 F_5 IPS 48 (38.17), DB 533 x DB 534 F_5 IPS 44 (37.50), DB 534 x DB 533 F_5 IPS 22 (37.33) and DB 533 x DB 534 F_5 IPS 88 (35.33). On the other hand, the line DB 533 x DB 534 F_5 IPS 96 produced minimum number of bolls per plant (22.50) followed by DB 533 x DB 534 F_5 IPS 35 (24.33).

4.1.3.2.6 Mean boll weight (g)

Among all barbadense lines, 16 lines recorded higher value than Suvin line. The line DB 533 x DB 534 F_5 IPS 30 exhibited heaviest bolls (3.23) followed by the barbadense lines DB 533 x DB 534 F_5 IPS 132 (3.17), DB 533 x DB 534 F_5 IPS 37 (2.93) and DB 533 x DB 534 F_5 IPS 18 (2.93), while the line DB 533 x DB 534 F_5 IPS 33 had minimum mean boll weight (1.67) followed by the line DB 533 x DB 534 F_5 IPS 38 (1.73).

4.1.3.2.7 Reproductive points on sympodia

The line DB 533 x DB 534 F_5 IPS 62 exhibited maximum value of reproductive points on sympodia (5.25) followed by the barbadense lines DB 533 x DB 534 F_5 IPS 48 (5.08), DB 534 x DB 533 F_5 IPS 22 (4.98) and DB 533 x DB 534 F_5 IPS 71 (4.93), while the line DB 533 x DB 534 F_5 IPS 101 had minimum value of reproductive points on sympodia (2.58) followed by the lines DB 533 x DB 534 F_5 IPS 65 (2.67), DB 533 x DB 534 F_5 IPS 20 (2.67) and DB 533 x DB 534 F_5 IPS 68 (2.67).

4.1.3.2.8 Sympodial length at 50 per cent plant height (cm)

The barbadense line DB 533 x DB 534 F_5 IPS 62 exhibited maximum value of sympodial length at 50 per cent plant height (39.75) followed by the barbadense lines DB 533 x DB 534 F_5 IPS 71 (35.92), DB 533 x DB 534 F_5 IPS 105 (35.83) and DB 533 x DB 534 F_5 IPS 14 (35.42), while the line DB 533 x DB 534 F_5 IPS 27 had minimum value of sympodial length at 50 per cent plant height (21.67) followed by the lines DB 533 x DB 534 F_5 IPS 11 (22.42) and DB 533 x DB 534 F_5 IPS 101 (22.83).

4.1.3.2.9 Inter branch distance (cm)

The barbadense line DB 533 x DB 534 F_5 IPS 27 exhibited maximum value of inter branch distance (9.83) followed by the lines DB 533 x DB 534 F_5 IPS 6 (9.33) and DB 533 x DB 534 F_5 IPS 112 (9.17), while the barbadense line DB 533 x DB 534 F_5 IPS 16 had minimum value of inter branch distance (6.17) followed by the lines DB 533 x DB 534 F_5 IPS 1 (6.50) and DB 533 x DB 534 F_5 IPS 25 (6.67).

4.1.3.2.10 Seed index (g)

Among all lines, the line DB 533 x DB 534 F_5 IPS 101 recorded maximum seed index (12.00) followed by the lines DB 533 x DB 534 F_5 IPS 132 (11.00), DB 533 x DB 534 F_5 IPS 34 (10.94) and the line DB 533 x DB 534 F_5 IPS 52 (10.06). On the other hand, the line DB 533 x DB 534 F_5 IPS 62 recorded minimum seed index (6.41) followed by the line DB 533 x DB 534 F_5 IPS 44 (6.49).

4.1.3.2.11 Ginning outturn (%)

The line DB 533 x DB 534 F_5 IPS 57 possessed maximum ginning out turn (35.23) followed by the lines DB 533 x DB 534 F_5 IPS 18 (35.13), DB 533 x DB 534 F_5 IPS 65 (34.76), DB 533 x DB 534 F_5 IPS 10 (34.64) and the line DB 534 x DB 533 F_5 IPS 22 (34.00), while the line DB 533 x DB 534 F_5 IPS 49 recorded minimum ginning out turn (24.77).

4.1.3.2.12 Lint index (g)

The line DB 533 x DB 534 F_5 IPS 18 had maximum lint index (5.41) followed by the line DB 533 x DB 534 F_5 IPS 101 (5.28) and DB 533 x DB 534 F_5 IPS 132 (4.96) which are on par with one another, while the line DB 533 x DB 534 F_5 IPS 62 recorded minimum lint index (2.03) followed by DB 533 x DB 534 F_5 IPS 36 (2.86).

4.1.3.2.13 Photosynthetic rate ($\mu molCO_2m^{-2}s^{-1}$)

The line DB 533 x DB 534 F_5 IPS 13 had maximum value of photosynthetic rate (27.15) followed by the line DB 533 x DB 534 F_5 IPS 49 (26.80) and DB 533 x DB 534 F_5 IPS 16 (26.69) which are on par with one another, while the line DB 533 x DB 534 F_5 IPS 132 recorded minimum value of photosynthetic rate (9.52) followed by DB 533 x DB 534 F_5 IPS 109 (11.96).

4.1.3.2.14 Stomatal conductance ($\mu molm^{-2}s^{-1}$)

The line DB 533 x DB 534 F_5 IPS 55 had maximum value of stomatal conductance (2.38) followed by the line DB 533 x DB 534 F_5 IPS 10 (2.03) and DB 533 x DB 534 F_5 IPS 16 (1.29), while the line DB 533 x DB 534 F_5 IPS 132 (0.30) recorded minimum value of stomatal conductance followed by DB 533 x DB 534 F_5 IPS 19 (0.42).

4.1.3.2.15 Transpiration rate (mmol $H_2Om^{-2}s^{-1}$)

The barbadense line DB 533 x DB 534 F_5 IPS 105 had maximum value of transpiration rate (16.66) followed by the line DB 533 x DB 534 F_5 IPS 10 (13.62) and DB 533 x DB 534 F_5 IPS 112 (11.72), while the line DB 533 x DB 534 F_5 IPS 132 recorded minimum value of transpiration rate (7.13) followed by DB 533 x DB 534 F_5 IPS 19 (7.23).

4.1.3.2.16 2.5% S L (mm)

The line DB 533 x DB 534 F_5 IPS 34 had maximum value of 2.5% S L (38.16) followed by the lines DB 533 x DB 534 F_5 IPS 112 (38.08), DB 533 x DB 534 F_5 IPS 80 (37.42) and DB 533 x DB 534 F_5 IPS 21 (37.42), while the line DB 533 x DB 534 F_5 IPS 4 recorded minimum value of 2.5% S L (28.78) followed by DB 533 x DB 534 F_5 IPS 25 (30.54). The *per se* performance of 53 barbadense lines showed that 27 lines had higher values of 2.5 % SL than Suvin line.

4.1.3.2.17 Fibre uniformity ratio (%)

The barbadense line DB 533 x DB 534 F_5 IPS 19 had maximum value of fibre uniformity ratio (47.54) followed by the lines DB 533 x DB 534 F_5 IPS 4 (47.48) and DB 533 x DB 534 F_5 IPS 11 (46.91), while the line DB 533 x DB 534 F_5 IPS 34 recorded minimum value of fibre uniformity ratio (42.64) followed by DB 533 x DB 534 F_5 IPS 23 (42.69).

4.1.3.2.18 Fibre micronaire value (μg/inch)

The line DB 533 x DB 534 F_5 IPS 101 had maximum value of fibre micronaire value (4.47) followed by the lines DB 533 x DB 534 F_5 IPS 19 (4.39) and DB 533 x DB 534 F_5 IPS 18 (4.14), while the line DB 533 x DB 534 F_5 IPS 44 (2.42) recorded minimum value of fibre micronaire followed by DB 533 x DB 534 F_5 IPS 38 (2.49). Among all barbadense lines, 10 lines exhibited higher value than Suvin line for fiber micronaire.

4.1.3.2.19 Fiber maturity ratio (%)

The barbadense line DB 533 x DB 534 F_5 IPS 19 had maximum value of fibre maturity ratio (0.70) followed by the line DB 533 x DB 534 F_5 IPS 101 (0.69), while the lines DB 533 x DB 534 F_5 IPS 44, DB 533 x DB 534 F_5 IPS 38 and DB 533 x DB 534 F5 IPS 32 recorded minimum value of fibre maturity ratio (0.55) followed by DB 533 x DB 534 F_5 IPS 34 (0.56) and DB 533 x DB 534 F_5 IPS 6 (0.56).

4.1.3.2.20 Fibre strength (Tenacity) (g/tex)

The barbadense line DB 533 x DB 534 F_5 IPS 88 had maximum value of fibre strength (31.67) followed by the lines DB 533 x DB 534 F_5 IPS 57 (30.80) and DB 533 x DB 534 F_5 IPS 10 (30.75), while the line DB 533 x DB 534 F_5 IPS 52 recorded minimum value of fibre strength (26.52) followed by DB 533 x DB 534 F_5 IPS 2 (27.08). The *per se* performance of 53 barbadense lines showed that 29 lines had higher values of fiber strength than Suvin line.

4.1.3.2.21 Fibre elongation (%)

The lines DB 533 x DB 534 F_5 IPS 101 and DB 533 x DB 534 F_5 IPS 57 had maximum values of fibre elongation (6.94) followed by the lines DB 533 x DB 534 F_5 IPS 79 (6.91), DB 533 x DB 534 F_5 IPS 19 (6.91) and DB 533 x DB 534 F_5 IPS 11 (6.91), while the line DB 533 x DB 534 F_5 IPS 2 (6.18) recorded minimum value of fibre elongation followed by DB 533 x DB 534 F_5 IPS 27 (6.24).

4.1.3.2.22 S/L ratio (%)

The line DB 533 x DB 534 F_5 IPS 4 had maximum value of S/L ratio (1.01) followed by the lines DB 533 x DB 534 F_5 IPS 96 (0.96) and DB 533 x DB 534 F_5 IPS 88 (0.96), while the line DB 533 x DB 534 F_5 IPS 52 (0.75) recorded minimum value of S/L. Among all barbadense lines, 27 lines showed higher value than Suvin barbadense line.

4.2 Evaluation of recombinational variability for combining ability

The two barbadense lines DB 533 and DB 534 were selected for creating recombinational variability for combining ability. Twenty eight F_4 lines derived from this cross were utilized to assess recombinational variability for combining ability by crossing them with 4 hirsutum testers. These results are presented below.

4.2.1 Analysis of variance (RBD) for crosses population

The preliminary RBD analysis was carried out for fourteen characters under study for all genotypes involved in the present investigation viz., 112 crosses (Line x Tester), 28 lines, 4 testers , two commercial checks (MRC 6918 *Bt* check and DCH 32 non *Bt* check) and eight bench mark crosses. Mean sum of squares for fourteen characters are presented in Table 9. 'F' test indicated highly significant variation among the genotypes for all the characters and only significant for number of sympodia per plant.

4.2.2 Mean *per se* performance and estimation of heterosis

Mean *per se* performance of four hirsutum females and 28 barbadense males (Appendix 3) and derived F_1 crosses and commercial checks (Appendix 4). Further, results of heterosis values over mid parent and commercial checks for various characters were studied to assess the variability for combining ability were given in Appendix 5, 6 and 7.

Table 9. Analysis of variance for different quantitative characters (RBD) in derived F1 crosses

Source	d.f.	Mean sum of squares												
		Seed cotton yield (kg/ha)	Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympodia at %50 height (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Photosynthetic rate (µmol $CO_2 m^{-2} s^{-1}$)	Stomatal conductance (µmol $m^{-2} s^{-1}$)	Transpiration rate (mmol $H_2O m^{-2} s^{-1}$)
		1	2	3	4	5	6	7	8	9	10	11	12	13	14
Replications	1	470122.81	889.05*	1.71**	172.17**	866.91**	8.00**	2.72**	23.55	100.61**	3.91	93.74**	35.94*	0.00009	18.10**
Geotypes	153	575226.37**	633.89**	0.45**	13.82*	170.21**	0.59**	1.06**	58.04**	3.85**	16.65**	1.96**	75.21**	0.16**	8.16**
Error	153	134348.79	214.41	0.05	9.37	77.05	0.26	0.23	38.98	0.73	9.06	0.57	5.94	0.01	1.36
S.E d		273.03	10.91	0.17	2.07	6.39	0.37	0.35	4.64	0.67	2.20	0.57	1.64	0.05	0.55
CD@ 5%		765.14	30.58	0.48	6.93	12.54	0.89	0.98	13.00	1.87	6.17	1.60	4.60	0.14	1.55
C.D. 1%		1011.98	40.45	0.64	9.21	16.66	1.18	1.29	17.20	2.48	8.16	2.12	6.09	0.18	2.05

* Significant at P = 0.05 ** Significant at P = 0.01

4.2.2.1 Seed cotton yield (kg ha^{-1})

Seed cotton yield values ranged from 1368.15 [DB 533 x DB 534 F_5 IPS 49] to 441.81 [DB 533 x DB 534 F_5 IPS 33] among males/ lines, 2503.93 [DH 98-27] to 1870.91 [178-24] among females/testers and 2884.26 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 49)] to 1146.20 [178-24 X (DB 533 x DB 534 F_4 IPS 33)] among derived F_1 crosses.

Per cent heterosis of F_1 crosses over their respective mid parental values ranged from 108.16 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 49)] to -38.94 [178-24 X (DB 533 x DB 534 F_4 IPS 33)]. Thirty crosses showed significant positive heterosis and only one cross showed significant negative heterosis over their mid parent. The cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 49) (39.97) recorded highest significant positive heterosis over MRC 6918 and the cross 178-24 X (DB 533 x DB 534 F_4 IPS 33) (-44.37) exhibited lowest significant negative heterosis over MRC 6918. Two crosses showed significant heterosis in positive direction and two crosses showed significant heterosis in negative direction over MRC 6918. In case of DCH 32 non *Bt* check, the cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 49) (44.31) showed highest significant positive heterosis over this check, but the cross 178-24 X (DB 533 x DB 534 F_4 IPS 33) (-42.65) recorded lowest significant negative heterosis value over DCH 32. Two crosses exhibited significant positive heterosis over DCH 32 and only one cross showed significant negative heterosis.

4.2.2.2 Plant height (cm)

Plant height values ranged from 100.33 [DB 533 x DB 534 F_5 IPS 62] to 65.33 [DB 533 x DB 534 F_5 IPS 34] among males/ lines, 100.67 [DH 18-31] to 93.50 [178-24] among females/testers and 143.83 [DH 98-27 X (DB 533 X DB 534 F_4 IPS 24)] to 84.67 [DH 18-31 X (DB 533 X DB 534 F_4 IPS 24)] among derived F_1 crosses.

Per cent heterosis of F_1 crosses over their respective mid parental values ranged from 68.57 [ZCH 8 X (DB 533 x DB 534 F_4 IPS 14)] to -6.96 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 14)]. Majority of the crosses exhibited significant heterosis over mid parent in positive direction. Significant positive heterosis was revealed by 51crosses.

The cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 17) (33.80) showed highest significant positive heterosis over MRC 6918, the cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 14) (-21.24) exhibited lowest heterosis over MRC 6918 and only three crosses showed significant heterosis in positive direction. In case of DCH 32 non *Bt* check, the cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 17) (23.46) showed highest positive heterosis over this check, but the cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 14) (-27.33) recorded lowest significant negative heterosis value over DCH 32. Only one cross had significant negative heterosis over DCH 32.

4.2.2.3 Number of monopodia per plant

Number of monopodia per plant values ranged from 2.50 [DB 533 x DB 534 F_5 IPS 6] to 0.33 [DB 533 x DB 534 F_5 IPS 12] among males/ lines, 1.90 [ZCH 8] to 0.50 [DH 18-31] among females/testers and 2.44 [178-24 X (DB 533 x DB 534 F_4 IPS 71)] to 1.11 [ZCH 8 X (DB 533 x DB 534 F_4 IPS 15) and ZCH 8 X (DB 533 x DB 534 F_4 IPS 26)] among derived F_1 crosses.

Per cent heterosis of F_1 crosses over their respective mid parental values ranged from 446.82 [178-24 X (DB 533 x DB 534 F_4 IPS 38)] to -41.58 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 62)]. Majority of the crosses exhibited significant heterosis over mid parent in positive direction. Seventy two crosses showed significant positive heterosis and three crosses revealed significant negative heterosis over their mid parent.

The cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 23) (22.00) recorded highest positive heterosis over MRC 6918, the crosses DH 98-27 X (DB 533 x DB 534 F_4 IPS 62) (-44.50) and DH 98-27 X (DB 533 x DB 534 F_4 IPS 34) (-44.50) exhibited lowest negative significant heterosis over MRC 6918 and twenty eight crosses showed significant negative heterosis. In case of DCH 32 check, the cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 23) (46.55) showed highest significant positive heterosis over this check, but the crosses DH 98-27 X (DB 533 x DB 534 F_4 IPS 62) (-33.33) and DH 98-27 X DB 533 x DB 534 F_4 IPS 34 (-33.33) recorded lowest significant negative heterosis value over DCH 32. Six crosses had significant negative heterosis and eighteen crosses exhibited significant positive heterosis over DCH 32.

4.2.2.4 Number of sympodia per plant

Number of sympodia per plant values ranged from 21.17 [DB 533 x DB 534 F_5 IPS 62] to 13.83 [DB 533 x DB 534 F_5 IPS 32] among males/ lines, 22.83 [DH18-31] to 18.33 [178-24] among females/testers and 25.17 [178-24 X (DB 533 x DB 534 F_4 IPS 14) and DH 18-31 X (DB 533 x DB 534 F_4 IPS 13)] to 16.00 [DH 18-31 X (DB 533 x DB 534 F_4 IPS 17)] among derived F_1 crosses.

Per cent heterosis of F_1 crosses over their respective mid parental values ranged from 52.83 [DH 18-31 X (DB 533 x DB 534 F_4 IPS 15)] to -17.95 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 71)]. Thirteen crosses showed significant positive heterosis over their mid parent.

The crosses DH 98-27 X (DB 533 x DB 534 F_4 IPS 30) (29.08) and DH 18-31 X (DB 533 x DB 534 F_4 IPS 71) (29.08) recorded highest positive heterosis over MRC 6918 and the cross 178-24 X (DB 533 x DB 534 F_4 IPS 15) (-17.95) exhibited lowest negative heterosis over MRC 6918. There is no significant heterosis with respect to this trait over MRC 6918 (*Bt* commercial check) between crosses. In case of DCH 32 non *Bt* check, the crosses DH 98-27 X (DB 533 x DB 534 F_4 IPS 30) (17.07) and DH 18-31 X (DB 533 x DB 534 F_4 IPS 71) (17.07) showed highest positive heterosis over this check, but the cross 178-24 X (DB 533 x DB 534 F_4 IPS 15) (-25.58) recorded lowest negative heterosis value over DCH 32. There is no significant heterosis with respect to this trait over DCH 32 (commercial check) between crosses.

4.2.2.5 Number of bolls per plant

Number of bolls per plant values ranged from 39.33 [DB 533 x DB 534 F_5 IPS 62] to 24.67 [DB 533 x DB 534 F_5 IPS 34] among males/ lines, 34.67 [DH 98-27] to 24.50 [178-24] among females/testers and 66.17 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 36)] to 34.50 [ZCH 8 X (DB 533 x DB 534 F_4 IPS 14)] among derived F_1 crosses.

Per cent heterosis of F_1s over their respective mid parent values ranged from 135.61 [ZCH 8 X (DB 533 x DB 534 F_4 IPS 30)] to -5.27 [DH 18-31 X (DB 533 x DB 534 F_4 IPS 33)]. Sixty nine crosses showed significant positive heterosis over their mid parent.

The cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 30) (40.78) recorded highest significant positive heterosis over MRC 6918 and the cross DH 18-31 X (DB 533 x DB 534 F_4 IPS 33) (-26.60) exhibited lowest negative heterosis over MRC 6918. Only one cross showed significant heterosis over MRC 6918 in positive direction. In case of DCH 32 check, the cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 30) (59.45) showed highest significant positive heterosis over this check, but the cross DH 18-31 X (DB 533 x DB 534 F_4 IPS 33) (-16.86) recorded lowest negative heterosis value over DCH 32. Two crosses exhibited significant positive heterosis respect to this trait over DCH 32 between crosses.

4.2.2.6 Mean boll weight (g)

Mean boll weight values ranged from 3.23 [DB 533 x DB 534 F_5 IPS 30] to 1.67 [DB 533 x DB 534 F_5 IPS 33] among males/ lines, 4.45 [178-24 and DH 18-31] to 3.95 [ZCH 8] among females/testers and 4.20 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 33)] to 2.35 [178-24 X (DB 533 x DB 534 F_4 IPS 12)] among derived F_1 crosses.

Per cent heterosis of F_1 crosses over their respective mid parent values ranged from 32.28 [ZCH 8 X (DB 533 x DB 534 F_4 IPS 49)] to -34.94 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 38)]. Five crosses showed significant negative heterosis and one cross recorded significant positive heterosis over their mid parent.

The cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 49) (15.07) recorded highest positive heterosis over MRC 6918 and the cross 178-24 X (DB 533 x DB 534 F_4 IPS 33) (-35.62) exhibited lowest significant negative heterosis over MRC 6918. Eight crosses showed significant heterosis over MRC 6918 in negative direction. In case of DCH 32 check, the cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 49) (27.27) showed highest positive heterosis over this check, but the cross 178-24 X (DB 533 x DB 534 F_4 IPS 33) (-28.79) recorded lowest negative heterosis value over DCH 32. The crosses exhibited non significant heterosis respect to this trait over DCH 32 non *Bt* check.

4.2.2.7 Reproductive points on sympodia

Reproductive points on sympodia values ranged from 5.25 [DB 533 x DB 534 F_5 IPS 62] to 3.08 [DB 533 x DB 534 F_5 IPS 1] among males/ lines, 3.89 [DH18-31] to 3.08 [178-24] among females/testers and 5.28 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 25)] to 1.92 [DH 18-31 X (DB 533 x DB 534 F_4 IPS 48)] among derived F_1 crosses.

Per cent heterosis of F_1 crosses over their respective mid parent values ranged from 59.75 [DH 18-31 X (DB 533 x DB 534 F_4 IPS 6)] to -57.53 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 49)]. Twenty three crosses showed significant negative heterosis and twelve recorded significant positive heterosis over their mid parent.

The cross 178-24 X (DB 533 x DB 534 F_4 IPS 12) (81.30) recorded highest significant positive heterosis over MRC 6918 and the cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 13) (-34.31) exhibited lowest significant negative heterosis over MRC 6918. Thirty six crosses showed significant heterosis over MRC6918 in positive direction, while three crosses recorded significant heterosis in negative direction. In case of DCH 32 check, the cross 178-24 X (DB 533 x DB 534 F_4 IPS 12) (51.00) showed highest significant positive heterosis over this check, but the cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 13) (-45.29) recorded lowest significant negative heterosis value over DCH 32. Thirteen crosses exhibited significant positive heterosis and nine recorded significant negative heterosis with respect to this trait over DCH 32.

4.2.2.8 Sympodial length at 50 per cent plant height (cm)

Sympodial length at 50 per cent plant height values ranged from 39.75 [DB 533 x DB 534 F_5 IPS 62] to 24.17 [DB 533 x DB 534 F_5 IPS 8] among males/ lines, 38.92 [DH 18-31] to 28.50 [DH 98-27] among females/testers and 54.92 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 44)] to 24.42 [DH 18-31 X (DB 533 x DB 534 F_4 IPS 8)] among derived F_1 crosses.

Per cent heterosis of F_1 crosses over their respective mid parent values ranged from 84.71 [ZCH 8 X (DB 533 x DB 534 F_4 IPS 23)] to -32.74 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 30)]. Eleven crosses showed significant positive heterosis and only two crosses recorded significant negative heterosis over their mid parent.

The cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 38) (75.25) recorded highest significant positive heterosis over MRC 6918 and the cross DH 18-31 X (DB 533 x DB 534 F_4 IPS 16) (-22.08) exhibited lowest negative heterosis over MRC 6918. Five crosses showed significant heterosis over MRC 6918 in positive direction. In case of DCH 32 check, the cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 38) (36.43) showed highest significant positive heterosis over this check, but the cross DH 18-31 X (DB 533 x DB 534 F_4 IPS 16) (-39.34) recorded lowest significant negative heterosis value over DCH 32. Eleven crosses exhibited significant negative heterosis and only two recorded significant positive heterosis respect to this trait over DCH 32.

4.2.2.9 Inter branch distance (cm)

Inter branch distance values ranged from 9.33 [DB 533 x DB 534 F_5 IPS 6] to 6.17 [DB 533 x DB 534 F_5 IPS 16] among males/ lines, 9.17 [178-24 and DH 18-31] to 8.67 [DH 98-27 and ZCH 8] among females/testers and 9.50 [178-24 X (DB 533 x DB 534 F_4 IPS 13)] to 5.33 [ZCH 8 X (DB 533 x DB 534 F_4 IPS 17)] among derived F_1 crosses.

4.2.2.10 Seed index (g)

Seed index values ranged from 10.94 [DB 533 x DB 534 F_5 IPS 34] to 6.41 [DB 533 x DB 534 F_5 IPS 62] among males/ lines, 11.67 [178-24] to 9.72 [DH 98-27] among females/testers and 17.50 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 32)] to 7.00 [[DH 98-27 X (DB 533 x DB 534 F_4 IPS 13)] among derived F_1 crosses.

Per cent heterosis of F_1s over their respective mid parent values ranged from 80.45 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 32)] to -29.96 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 13)]. Twenty five crosses showed significant positive heterosis and seven crosses recorded significant negative heterosis over their mid parent.

The cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 32) (83.87) recorded highest significant positive heterosis over MRC 6918 and the cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 13) (-26.43) exhibited significant negative heterosis over MRC 6918. Fourteen crosses showed significant heterosis in positive direction and two crosses recorded significant negative heterosis over MRC 6918. In case of DCH 32 check, the cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 32) (84.16) showed highest significant positive heterosis over this check, but the cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 13) (-26.32) recorded lowest significant negative heterosis value over DCH 32. Fourteen crosses exhibited significant positive heterosis and only two recorded significant negative heterosis respect to seed index over DCH 32.

4.2.2.11 Ginning outturn (%)

The values of ginning outturn ranged from 34.00 [DB 534 x DB 533 F_5 IPS 22] to 24.77 [DB 533 x DB 534 F_5 IPS 49] among males/ lines, 39.14 [DH 18-31] to 34.25 [178-24] among females/testers and 35.31 [178-24 X (DB 533 x DB 534 F_4 IPS 44)] to 13.81 [ZCH 8 X (DB 533 x DB 534 F_4 IPS 33)] among derived F_1 crosses.

Per cent heterosis of F_1 crosses over their respective mid parent values ranged from 11.31 [DH 18-31 X (DB 533 x DB 534 F_4 IPS 105)] to -58.48 [ZCH 8 X (DB 533 x DB 534 F_4 IPS 33)]. Twenty five crosses showed significant negative heterosis over their mid parent. The cross DH 18-31 X (DB 533 x DB 534 F_4 IPS 105) (25.65) recorded highest significant positive heterosis over MRC 6918 and the cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 33) (-51.63) exhibited lowest significant negative heterosis over MRC 6918. One cross showed significant heterosis in negative direction and two crosses recorded significant positive heterosis over MRC 6918. In case of DCH 32 check, the cross DH 18-31 X (DB 533 x DB 534 F_4 IPS 105) (6.74) showed highest positive heterosis over this check, but the cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 33) (-58.91) recorded lowest significant negative heterosis value over DCH 32 non *Bt* check. Sixteen crosses exhibited significant negative heterosis over DCH 32.

4.2.2.12 Lint index (g)

Lint index values ranged from 4.72 [DB 533 x DB 534 F_5 IPS 25] to 2.03 [DB 533 x DB 534 F_5 IPS 62] among males/ lines, 6.56 [DH 18-31] to 6.14 [DH 98-27] among females/testers and 7.40 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 32)] to 2.71 [ZCH 8 X (DB 533 x DB 534 F_4 IPS 30)] among derived F_1 crosses.

Per cent heterosis of F_1 crosses over their respective mid parent values ranged from 53.71 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 32)] to -44.65 [ZCH 8 X (DB 533 x DB 534 F_4 IPS 30)]. Twenty four crosses showed significant negative heterosis and four crosses showed significant positive heterosis over their mid parent. The cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 32) (82.61) recorded highest significant positive heterosis over MRC 6918 and the cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 30) (-33.29) exhibited lowest negative heterosis over MRC 6918. Twenty one crosses showed significant heterosis in positive direction over MRC 6918. In case of DCH 32, the cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 32) (45.34) showed highest significant positive heterosis over this check, but the cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 30) (-46.91) recorded lowest significant negative heterosis value over DCH 32. Seventeen crosses exhibited significant negative heterosis over DCH 32 and only one cross showed significant positive heterosis.

4.2.2.13 Photosynthetic rate ($\mu molCO_2m^{-2}s^{-1}$)

The values of photosynthetic rate ranged from 27.15 [DB 533 x DB 534 F_5 IPS 13] to 16.49 [DB 533 x DB 534 F_5 IPS 8] among males/ lines, 29.62 [178-24] to 21.20 [DH18-31] among females/testers and 34.25 [ZCH 8 X (DB 533 x DB 534 F_4 IPS 52)] to 3.15 [ZCH 8 X (DB 533 x DB 534 F_4 IPS 33)] among derived F_1 crosses.

Per cent heterosis of F_1s over their respective mid parent values ranged from 74.56 [ZCH 8 X (DB 533 x DB 534 F_4 IPS 52)] to -84.91 [ZCH 8 X (DB 533 x DB 534 F_4 IPS 33)]. Fourty four crosses showed significant positive heterosis and twenty crosses showed significant negative heterosis over their mid parent. The cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 52) (18.97) recorded highest significant positive heterosis over MRC 6918 and the cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 33) (-89.07) exhibited lowest significant negative heterosis over MRC 6918. Thirty nine crosses showed significant heterosis in negative direction and only one cross showed significant heterosis in positive direction over MRC 6918. In case of DCH 32 check, the cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 52) (41.83) showed highest significant positive heterosis over this check, but the cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 33) (-86.97) recorded lowest significant negative heterosis value over DCH 32. Thirty crosses exhibited significant positive heterosis over DCH 32 and eighteen crosses showed significant negative heterosis.

4.2.2.14 Stomatal conductance ($\mu molm^{-2}s^{-1}$)

Stomatal conductance values ranged from 2.38 [DB 533 x DB 534 F_5 IPS 55] to 0.55 [DB 533 x DB 534 F_5 IPS 15] among males/ lines, 1.22 [178-24] to 0.78 [DH18-31] among females/testers and 1.17 [ZCH 8 X (DB 533 x DB 534 F_4 IPS 52)] to 0.09 [178-24 X (DB 533 x DB 534 F_4 IPS 15)] among derived F_1 crosses.

Per cent heterosis of F_1 crosses over their respective mid parental values ranged from 75.94 [ZCH 8 X (DB 533 x DB 534 F_4 IPS 52)] to -90.67 [178-24 X (DB 533 x DB 534 F_4 IPS 15)]. Sixty three crosses showed significant negative heterosis and eleven crosses showed significant positive heterosis over their mid parent. The cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 52) (53.95) recorded highest significant positive heterosis over MRC 6918 and the cross 178-24 X (DB 533 x DB 534 F_4 IPS 15) (-88.16) exhibited lowest significant negative heterosis over MRC 6918. Thirty eight crosses showed significant heterosis in negative direction and nine crosses showed significant heterosis in positive direction over MRC 6918. In case of DCH 32 check, the cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 52) (234.29) showed highest significant positive heterosis over this check, but the cross 178-24 X (DB 533 x DB 534 F_4 IPS 15) (-74.29) recorded lowest significant negative heterosis value over DCH 32. Seventy four crosses exhibited significant positive heterosis over DCH 32 and six crosses showed significant negative heterosis.

4.2.2.15 Transpiration rate (mmol $H_2Om^{-2}s^{-1}$)

Transpiration rate values ranged from 16.66 [DB 533 x DB 534 F_5 IPS 105] to 7.92 [DB 533 x DB 534 F_5 IPS 14] among males/ lines, 11.77 [178-24] to 10.09 [DH 98-27] among females/testers and 10.04 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 1)] to 2.07 [178-24 X (DB 533 x DB 534 F_4 IPS 32)] among derived F_1 crosses.

Per cent heterosis of F_1s over their respective mid parent values ranged from -5.85 [178-24 X (DB 533 x DB 534 F_4 IPS 38)] to -79.10 [178-24 X (DB 533 x DB 534 F_4 IPS 32)]. Ninety seven crosses showed significant negative heterosis over their mid parent. The cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 1) (55.26) recorded highest significant positive heterosis over commercial check MRC 6918 and the cross 178-24 X (DB 533 x DB 534 F_4 IPS 32) (-67.93) exhibited lowest significant negative heterosis over MRC 6918. Thirteen crosses showed significant heterosis in negative direction and only one cross showed significant heterosis in positive direction over MRC 6918. In case of DCH 32 check, the cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 1) (93.92) showed highest significant positive heterosis over this check, but the cross 178-24 X (DB 533 x DB 534 F_4 IPS 32) (-59.94) recorded lowest significant negative heterosis value over DCH 32. Two crosses exhibited significant negative heterosis over DCH 32 and seventeen crosses showed significant positive heterosis.

4.2.2.16 2.5% S L (mm)

The values of 2.5% SL ranged from 38.16 [DB 533 x DB 534 F_5 IPS 34] to 30.54 [DB 533 x DB 534 F_5 IPS 25] among males/ lines, 32.52 [178-24] to 27.85 [DH18-31] among females/testers and 36.79 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 16)] to 31.13 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 105)] among derived F_1 crosses.

4.2.2.17 Fiber uniformity ratio (%)

Fiber uniformity ratio values ranged from 46.39 [DB 533 x DB 534 F_5 IPS 62] to 42.64 [DB 533 x DB 534 F_5 IPS 34] among males/ lines, 49.11 [DH 98-27] to 44.31 [178-24] among females/testers and 46.55 [DH 18-31 X (DB 533 x DB 534 F_4 IPS 8)] to 42.60 [178-24 X (DB 533 x DB 534 F_4 IPS 48)] among derived F_1 crosses.

4.2.2.18 Fiber micronaire value (μg/inch)

Fibre micronaire values ranged from 3.43 [DB 533 x DB 534 F_5 IPS 25] to 2.42 [DB 533 x DB 534 F_5 IPS 44] among males/ lines, 4.87 [DH 18-31] to 4.19 [178-24] among females/testers and 3.61 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 105)] to 2.49 [178-24 X (DB 533 x DB 534 F_4 IPS 33)] among derived F_1 crosses.

4.2.2.19 Fiber maturity ratio (%)

The values of fiber maturity ratio ranged from 0.63 [DB 533 x DB 534 F_5 IPS 25] to 0.55 [DB 533 x DB 534 F_5 IPS 44, DB 533 x DB 534 F_5 IPS 32 and DB 533 x DB 534 F_5 IPS 38] among males/ lines, 0.72 [DH18-31] to 0.68 [178-24] among females/testers and 0.67 [MRC6918] followed by the cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 71) (0.65) to 0.54 [DCH32] followed by the cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 30) (0.55) among derived F_1 crosses.

4.2.2.20 Fiber strength (Tenacity) (g/tex)

Fiber strength values ranged from 30.37 [DB 533 x DB 534 F_5 IPS 44] to 26.52 [DB 533 x DB 534 F_5 IPS 52] among males/ lines, 22.90 [DH 98-27] to 20.01 [DH 18-31] among females/testers and

31.22 [ZCH 8 X (DB 533 x DB 534 F_4 IPS 30)] to 22.91 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 105)] among derived F_1s.

4.2.2.21 Fiber elongation (%)

Fiber elongation values ranged from 6.84 [DB 533 x DB 534 F_5 IPS 105] to 6.27 [DB 533 x DB 534 F_5 IPS 62] among males/ lines, 5.88 [ZCH 8] to 5.41 [DH18-31] among females/testers and 6.85 [178-24 X (DB 533 x DB 534 F_4 IPS 49)] to 5.88 [DH 98-27 X (DB 533 x DB 534 F_4 IPS 105)] among derived F_1 crosses.

4.2.3 Combining ability analysis

4.2.3.1 Analysis of variance for combining ability

The analysis of variance for 14 characters studied for this set are presented in Table 10.

Among the lines (males), the mean sum of squares (MSS) were not significant for all the characters except mean boll weight, reproductive points on sympodia and seed cotton yield which showed highly significant differences, while number of bolls per plant and ginning outturn exhibited significant differences.Testers (females) exhibited not significant difference for all the characters except number of bolls per plant and seed cotton yield which recorded highly significant differences, while mean boll weight and transpiration rate showed significant differences. Line x Tester interaction were highly significant differences for number of monopodia per plant, number of bolls per plant, mean boll weight, reproductive points on sympodia, seed index, lint index, photosynthetic rate, stomatal conductance and transpiration rate, while seed cotton yiel had significant differences.

The estimates of variance due to general combining ability (GCA), variance due to specific combining ability (SCA), the magnitude of SCA variances were greater than GCA variance for all 14 characters and the variance ratio was less than half in these traits, indicating that dominance variance was more than additive variance for these characters (Table 11).

4.2.3.2 Combining ability effects

The estimates of general combining ability effects of females and males presented in Table 12, their specific combining ability effects are presented in Table 13 for all the characters.

4.2.3.2.1 Seed cotton yield (kg/ha)

Eight lines recorded significant *gca* effects (Fig. 6), of which five lines exhibited positive significant *gca* effects. The highest *gca* effect was found by the line DB 533 x DB 534 F_4 IPS 8 (363.15). Among the testers, the tester DH 98-27 had positive significant *gca* effect (94.65) and the tester DH 18-31 showed positive *gca* effect (35.44), while 178-24 (-77.43) recorded negative significant *gca* effect (Fig. 6). Two crosses manifested positive significant *sca* effects, of which the cross DH 98-27 X (DB 534 x DB 533 F_4 IPS 22) (680.34) recorded the highest positive *sca* effect.

4.2.3.2.2 Plant height (cm)

The estimates of general combining ability effect indicated significant differences among the line parents, three lines had significant positive *gca* and two had significant negative *gca*. The highest value of *gca* effect was exhibited by DB 533 x DB 534 F_4 IPS 36 (14.29). All four testers exhibited non significant *gca* effects. Seven crosses differed significantly for *sca* effects, of these four had positive *sca* effects. The cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 12) (26.27) had expressed the highest value of *sca* effect.

4.2.3.2.3 Number of monopodia per plant

Nine line parents expressed significant *gca* effects and the line DB 533 x DB 534 F_4 IPS 48 (0.40) was the best general combiner among the line parents. Among the testers, the tester DH 18-31 showed significant positive *gca* effect (0.06) for number of monopodia per plant. Twenty seven crosses expressed significant *sca* effects. Among these, fourteen crosses had positive *sca* effects and the maximum *sca* effect was recorded by the cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 23) (0.53).

4.2.3.2.4 Number of sympodia per plant

Out of 28 male (Line) parents used in the population based crosses, one line showed significant negative *gca* effect was shown by DB 533 x DB 534 F_4 IPS 15 (-2.36). Among the females (testers), there are no significant *gca* effects. Two crosses expressed significant *sca* effects were shown by DH 98-27 X (DB 533 x DB 534 F_4 IPS 71) and 178-24 X (DB 533 x DB 534 F_4 IPS 48) -4.76 and -4.55, respectively.

Table 10. Analysis of variance for combining ability in derived F_1 crosses for different quantitative characters

Source	d.f.	Mean sum of squares												
		Seed cotton yield (kg/ha)	Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympodia at %50height (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Photosynthetic rate (-2^{-1} (µmol CO_2m s))	Stomatal conductance (-2^{-1} ((µmol m s))	Transpiration rate (mmol -2^{-1} H_2Om s)
		1	2	3	4	5	6	7	8	9	10	11	12	13	14
Replications	1	1085229.86**	650.39	1.96**	303.32**	1484.54**	8.37**	5.41**	139.39	69.82**	2.79	77.99**	51.29**	0.034**	74.75**
Crosses	111	215277.08*	350.53*	0.20**	7.96	89.14**	0.28**	1.10**	60.89*	3.61**	15.61**	1.70**	90.50**	0.12**	4.24**
Line Effect	27	422120.75**	428.64	0.18	6.40	64.35*	0.28**	1.86**	72.82	2.66	22.45*	2.13	114.71	0.15	3.44
Tester Effect	3	354355.88**	182.50	0.14	3.65	120.97**	0.07*	0.92	10.10	6.04	11.93	2.25	79.13	0.16	13.04*
Line x Tester Effect	81	141178.12*	330.71	0.21**	8.64	96.23**	0.29**	0.86**	58.79	3.84**	13.46	1.54**	82.85**	0.11**	4.18**
Error	111	149093.70	238.15	0.06	8.58	81.66	0.28	0.24	43.06	0.89	9.69	0.66	5.39	0.00	0.61

* Significant at P = 0.05 ** Significant at P = 0.01

Table 11. Variance due to general and specific combining ability in derived F_1 crosses for different quantitative characters

Characters	Variance Due to GCA	Variance Due to SCA	GCA/SCA
1- Seed cotton yield (kg/ha)	4745.8378	1429428.5000	0.0035
2- Plant height (cm)	2.4440	3348.4453	0.0007
3- Number of monopodia	0.0018	2.1663	0.0010
4- Number of sympodia	0.0488	87.5278	0.0005
5- Number of bolls	1.6200	974.2978	0.0015
6- Mean boll Weight (g)	0.0008	2.8943	0.0003
7- Reproductive points on sympodia	0.0125	8.6920	0.0018
8- Length of sympodia at 50% height (cm)	0.1350	595.2768	0.0000
9-Seed index (g)	0.0810	38.8530	0.0020
10-Ginning outturn (%)	0.1600	136.3290	0.0013
11- Lint index (g)	0.0300	15.5615	0.0018
12- Photosynthetic rate ($\mu molCO_2m^{-2}s^{-1}$)	1.0598	838.8318	0.0013
13- Stomatal conductance ($\mu molm^{-2}s^{-1}$)	0.0020	1.1120	0.0018
14- Transpiration rate ($mmol\ H_2Om^{-2}s^{-1}$)	0.1745	42.3088	0.0035

Table 12. Estimates of general combining ability effects of parents involved in recombinational variability study for different quantitative characters

Sl.No	Parents	Seed cotton yield (kg/ha)	Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympodia at %50height (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Photosynthetic rate (μmol CO_2 m^{-2} s^{-1})	Stomatal conductance (μmol m^{-2} s^{-1})	Transpiration rate (mmol H_2O m^{-2} s^{-1})
		1	2	3	4	5	6	7	8	9	10	11	12	13	14
	Males														
1	DB 533 x DB 534 F4 IPS 44	123.36	0.04	-0.080	-0.2	-3.82*	-0.09	0.04	3.65	-0.61*	1.58	-0.53	0.98	0.03	-1.1**
2	DB 533 x DB 534 F4 IPS 62	219.09	-5.66	0.050	0.43	3.35*	-0.21	-0.45**	-4.06	0.83**	-0.84	0.40	1.57	0.01	-0.56
3	DB 533 x DB 534 F4 IPS 105	-72.66	-4.33	0.19*	-0.86	-1.07	-0.18	0.12	-0.50	0.49	-1.09	-0.19	-7.5**	-0.3**	-0.23
4	DB 533 x DB 534 F4 IPS 26	131.44	5.00	0.19*	0.64	-1.69	-0.19	0.05	2.59	0.82**	1.97	0.46	7.36**	0.31**	0.38
5	DB 533 x DB 534 F4 IPS 71	212.97	-9.87	0.030	0.64	2.02	0.04	-0.58**	-3.14	-0.22	0.08	-0.03	-1.75*	0.02	-0.26
6	DB 533 x DB 534 F4 IPS 30	72.04	10.88*	-0.030	-0.74	-0.19	-0.47*	0.29	6.02**	1.3**	0.77	0.52	-0.79	-0.13**	-1.03*
7	DB 533 x DB 534 F4 IPS 25	118.02	-1.16	-0.21*	0.68	2.10	-0.08	-0.82**	-2.33	-0.52	0.52	0.32	3.92**	0.20**	0.16
8	DB 533 x DB 534 F4 IPS 49	-208.12	6.17	-0.17*	0.68	-1.98	0.14	0.73**	3.38	0.02	-2.53*	-0.56*	-3.46**	-0.09*	-0.46
9	DB 533 x DB 534 F4 IPS 23	-144.82	0.29	0.030	-0.07	2.52	0.21	0.19	0.65	-0.38	-2.41*	-0.52	-7.59**	-0.29**	-1.04*
10	DB 533 x DB 534 F4 IPS 36	-317.54*	14.29**	0.020	0.6	4.81**	0.04	0.62**	5.00*	0.18	-2.41*	-0.26	-3.53**	-0.04	0.32
11	DB 533 x DB 534 F4 IPS 15	-238.08	5.21	0.000	-2.36*	0.98	0.03	0.93**	2.94	-0.83**	-3.8**	-0.87**	-4.08**	-0.09*	-0.27
12	DB 533 x DB 534 F4 IPS 1	-142.35	10.63*	0.120	0.6	3.35*	0.31	-0.48**	-0.19	-0.84**	-0.18	-0.45	-2.91**	-0.03	0.3
13	DB 533 x DB 534 F4 IPS 33	-231.44	-0.87	0.130	0.05	0.39	0.12	0.83**	3.40	-0.15	-1.31	-0.61*	0.09	0.01	-0.33
14	DB 533 x DB 534 F4 IPS 24	-179.34	3.75	-0.23**	1.10	5.52**	-0.07	-0.27	-1.35	-0.03	-1.18	-0.53*	2.55**	0.10*	0.16
15	DB 533 x DB 534 F4 IPS 16	-179.86	-3.83	-0.140	0.01	0.94	-0.19	0.06	-2.54	0.13	2.93**	0.34	2.05*	-0.12**	0.02
16	DB 533 x DB 534 F4 IPS 52	-128.67	5.63	-0.040	1.72	-1.69	0.38*	-0.45**	-2.66	-0.41	1.65	0.38	1.62	0.09*	0.91*
17	DB 533 x DB 534 F4 IPS 12	-291.48*	-15.5**	0.040	-1.95	0.31	0.18	-0.71**	-4.29	-0.28	1.65	0.15	-3.49**	-0.19**	-0.66
18	DB 534 x DB 533 F4 IPS 22	-346.19**	1.50	0.040	-0.16	0.52	-0.06	-0.39*	-2.85	0.08	-0.53	-0.15	-3.57**	-0.01	0.01
19	DB 533 x DB 534 F4 IPS 14	-110.83	9.04	-0.070	0.72	-1.69	0.04	0.11	2.73	-0.86**	-0.65	-0.45	-2.77**	0.04	0.88*
20	DB 533 x DB 534 F4 IPS 34	-239.26	7.54	0.030	0.51	-1.57	-0.11	-0.11	0.21	0.39	-1.69	-0.58*	-3.26**	-0.07*	-0.18

Contd....

	Parents	Seed cotton yield (kg/ha)	Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympodia at %50height (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Photosynthetic rate ($^{-2}$ $^{-1}$ (µmol CO_2m s)	Stomatal conductance ($^{-2}$ $^{-1}$ ((µmol m s)	Transpiration rate (mmol $^{-2}$ $^{-1}$ H_2Om s)
		1	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**
21	DB 533 x DB 534 F4 IPS 55	-86.21	0.33	0.150	-0.11	2.77	0.19	-0.69**	0.86	-0.59	-0.20	0.01	0.49	0.18**	1.98**
22	DB 533 x DB 534 F4 IPS 17	311.05*	-11.29*	-0.100	-0.57	-2.94	0.06	-0.24	-3.46	0.17	2.75*	1.34**	5.21**	0.1**	0.23
23	DB 533 x DB 534 F4 IPS 32	320.04*	-6.50	-0.27**	-0.32	-3.40*	0.18	0.10	-2.60	1.17**	0.66	0.56*	2.78**	-0.01	-0.42
24	DB 533 x DB 534 F4 IPS 38	211.93	-3.08	0.020	0.43	-4.32**	-0.12	0.73**	2.43	0.4	-0.19	0.52	1.61	0.08*	-0.29
25	DB 533 x DB 534 F4 IPS 48	225.48	-6.41	0.4**	0.68	-1.07	-0.31	-0.13	-3.37	-0.19	0.97	0.75**	3.59**	0.00	0.59
26	DB 533 x DB 534 F4 IPS 13	349.48**	-5.79	0.18*	-1.24	-4.9**	0.11	-0.04	-1.60	0.41	0.71	-0.16	4.19**	0.00	0.18
27	DB 533 x DB 534 F4 IPS 6	258.82*	2.33	-0.21*	-0.82	3.64*	-0.02	0.30	2.90	-0.28	1.42	-0.11	3.07**	0.00	0.11
28	DB 533 x DB 534 F4 IPS 8	363.15**	-8.33	-0.090	-0.07	-2.9	0.04	0.25	-1.81	-0.21	1.36	0.25	3.61**	0.2**	0.59
	SE (gi)	**129.59**	**5.18**	**0.08**	**1.08**	**3.10**	**0.18**	**0.17**	**2.21**	**0.30**	**1.06**	**0.27**	**0.86**	**0.04**	**0.41**
	SEd (gi-gj)	**183.27**	**7.32**	**0.12**	**1.53**	**4.39**	**0.25**	**0.24**	**3.12**	**0.43**	**1.51**	**0.38**	**1.22**	**0.05**	**0.58**
	CD at 5%	**378.40**	**15.12**	**0.24**	**2.87**	**8.86**	**0.52**	**0.48**	**6.43**	**0.93**	**3.05**	**0.79**	**2.28**	**0.07**	**0.76**
	CD at 1%	**498.10**	**19.91**	**0.31**	**3.78**	**11.66**	**0.68**	**0.64**	**8.47**	**1.22**	**4.02**	**1.04**	**3.00**	**0.09**	**1.01**
	Females														
1	DH 98-27	94.65**	0.53	-0.05	0.13	1.37**	-0.01	0.09	0.59	0.14	-0.48	0.04	-0.53	-0.02	-0.19
2	ZCH 8	-52.66	1.48	-0.01	-0.14	-0.45	0.03*	-0.17**	-0.38	-0.05	0.15	-0.27**	0.36	0.03 *	0.20
3	178-24	-77.43**	-2.63	0.00	-0.28	-1.87**	-0.05**	0.10	-0.22	0.34**	0.57	0.21*	-1.3**	-0.07 **	-0.56**
4	DH 18-31	35.44	0.62	0.06*	0.29	0.95**	0.02	-0.02	0.02	-0.43**	-0.24	0.02	1.47**	0.05 **	0.55**
	SE (gi)	**48.98**	**1.96**	**0.03**	**0.41**	**1.17**	**0.07**	**0.06**	**0.83**	**0.11**	**0.40**	**0.10**	**0.33**	**0.01**	**0.16**
	SEd (gi-gj)	**69.27**	**2.77**	**0.04**	**0.58**	**1.66**	**0.10**	**0.09**	**1.18**	**0.16**	**0.57**	**0.14**	**0.46**	**0.02**	**0.22**
	CD at 5%	**143.0233**	**5.72**	**0.09**	**1.08**	**3.35**	**0.20**	**0.18**	**2.43**	**0.35**	**1.15**	**0.30**	**0.86**	**0.03**	**0.29**
	CD at 1%	**188.2653**	**7.52**	**0.12**	**1.43**	**4.41**	**0.26**	**0.24**	**3.20**	**0.46**	**1.52**	**0.39**	**1.13**	**0.03**	**0.38**

* Significant at P = 0.05 ** Significant at P = 0.01

Table 13. Estimates of specific combining ability effects of derived F_1 crosses for different quantitative characters

Sl.No	Crosses	Seed cotton yield (kg/ha)	Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympodia at 50% height (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Photosynthetic rate (µmol CO_2 m^{-2} s^{-1})	Stomatal conductance ((µmol m^{-2} s^{-1})	Transpiration rate (mmol H_2O m^{-2} s^{-1})
		1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	[[DH 98-27 x (DB 533 x DB 534 F4 IPS 44)]	23.63	15.35	0.33	-1.80	3.30	-0.04	0.85*	11.1*	-1.25*	-0.32	-1.08*	-11.87**	-0.34**	-2.60**
2	[DH 98-27 x (DB 533 x DB 534 F4 IPS 62)]	-211.61	10.06	-0.57**	0.97	-3.88	-0.33	0.7*	-2.10	0.88	0.21	1.25*	4.96**	0.24**	-0.49
3	[DH 98-27 x (DB 533 x DB 534 F4 IPS 105)]	487.51	-19.50	-0.09	-1.22	0.37	0.15	-0.92**	-2.76	-0.95	-2.92	-1.01	3.26	0.11	1.37
4	[DH 98-27 x (DB 533 x DB 534 F4 IPS 26)]	-299.53	-5.91	0.33	2.05	0.21	0.23	-0.63	-6.25	1.32*	3.03	0.84	3.66*	-0.02	1.72*
5	[DH 98-27 x (DB 533 x DB 534 F4 IPS 71)]	-207.56	-6.94	-0.03	-4.76*	-7.04	-0.13	0.42	-1.27	-0.59	-1.03	0.13	-0.33	-0.14	0.69
6	[DH 98-27 x (DB 533 x DB 534 F4 IPS 30)]	-340.69	0.43	-0.22	3.51	-6.71	0.43	0.19	-4.64	-0.78	0.96	-0.99	-1.04	-0.04	-0.48
7	[DH 98-27 x (DB 533 x DB 534 F4 IPS 25)]	-62.01	-0.78	0.4*	2.15	4.87	-0.29	0.49	9.37*	1.60*	1.29	0.53	-1.53	0.06	-0.34
8	[DH 98-27 x (DB 533 x DB 534 F4 IPS 49)]	610.26*	7.30	-0.16	-0.91	8.88	-0.01	-1.11**	-3.46	-0.24	-1.21	0.32	2.9	0.12	0.13
9	[DH 98-27 x (DB 533 x DB 534 F4 IPS 23)]	45.12	4.56	0.53**	-0.63	6.05	0.00	-0.57	-1.34	0.09	2.65	1.46*	7.76**	0.16*	-0.17
10	[DH 98-27 x (DB 533 x DB 534 F4 IPS 36)]	-22.88	-0.07	0.00	2.80	-4.46	-0.25	-0.14	-0.78	0.00	0.16	-0.56	-9.22**	-0.26**	-2.08*
11	[DH 98-27 x (DB 533 x DB 534 F4 IPS 15)]	-20.33	-1.62	-0.55**	-0.89	-8.55	0.38	0.17	5.55	0.06	-1.57	0.15	-0.97	0.04	-1.32
12	[DH 98-27 x (DB 533 x DB 534 F4 IPS 1)]	-1.91	-2.87	0.02	-1.29	6.96	-0.13	0.54	-3.44	-0.15	-1.24	-1.05	2.44	0.06	3.58**
13	[DH 98-27 x (DB 533 x DB 534 F4 IPS 33)]	-372.07	14.73	0.31	2.70	1.67	-0.09	-0.38	-6.25	-0.15	0.07	-0.29	0.74	0.14	1.01
14	[DH 98-27 x (DB 533 x DB 534 F4 IPS 24)]	-335.87	0.10	0.38*	-1.03	-5.01	-0.28	1.02**	10.22*	-1.77**	0.18	-0.54	-0.76	-0.14	-2.15*
15	[DH 98-27 x (DB 533 x DB 534 F4 IPS 16)]	257.49	13.38	0.01	-2.22	8.58	0.20	0.66	0.39	-0.52	-2.00	-0.17	2.02	0.16*	2.43**
16	[DH 98-27 x (DB 533 x DB 534 F4 IPS 52)]	450.45	-28.20**	-0.7**	0.55	-5.24	0.18	-1.3**	-4.35	2.44**	1.75	0.99	-2	-0.16*	-1.29
17	[DH 98-27 x (DB 533 x DB 534 F4 IPS 12)]	-234.26	26.27*	-0.03	-2.13	-6.70	-0.18	0.41	2.23	0.47	2.30	0.45	4.71**	0.05	-0.55
18	[DH 98-27 x (DB 534 x DB 533 F4 IPS 22)]	680.34*	-12.53	0.38*	0.80	6.12	0.48	-0.60	-5.55	0.16	0.09	0.30	-16.66**	-0.42**	-0.52
19	[DH 98-27 x (DB 533 x DB 534 F4 IPS 14)]	-252.83	-14.58	0.41*	1.11	6.20	-0.09	-0.47	-2.22	0.33	-1.11	-0.89	10.38**	0.42**	1.71*
20	[DH 98-27 x (DB 533 x DB 534 F4 IPS 34)]	-193.25	0.84	-0.76**	0.21	-5.62	-0.21	0.66	5.55	-0.96	-1.27	0.14	1.56	-0.05	-0.64
21	[DH 98-27 x (DB 533 x DB 534 F4 IPS 55)]	119.24	-2.32	-0.19	-0.09	4.17	0.33	-0.32	-10.69*	-1.23*	2.94	0.66	6.70**	0.19*	0.00

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22	[DH 98-27 x (DB 533 x DB 534 F4 IPS 17)]	453.96	19.73	0.00	-0.32	2.49	-0.16	0.01	0.45	-1.84**	-4.67*	-0.97	8.13**	0.28**	1.04
23	[DH 98-27 x (DB 533 x DB 534 F4 IPS 32)]	-306.23	-9.33	-0.06	0.32	-0.76	-0.03	-0.08	-4.38	5.80**	0.25	1.98**	-7.08**	-0.25**	-0.91
24	[DH 98-27 x (DB 533 x DB 534 F4 IPS 38)]	-266.97	-8.08	0.25	0.09	-5.91	-0.15	0.38	14.62**	-2.73**	1.48	-1.67**	-7.75**	-0.22**	-0.13
25	[DH 98-27 x (DB 533 x DB 534 F4 IPS 48)]	380.13	5.22	0.22	-1.67	8.05	0.15	-0.04	4.25	1.04	1.51	0.97	0.11	0.01	1.01
26	[DH 98-27 x (DB 533 x DB 534 F4 IPS 13)]	-16.11	-12.40	0.14	0.76	-5.80	-0.40	-0.61	-3.95	-2.49**	-1.39	-0.94	2.25	0.16*	0.82
27	[DH 98-27 x (DB 533 x DB 534 F4 IPS 6)]	-190.18	-1.46	-0.4*	-1.43	0.95	0.33	-0.20	-4.03	1.06	1.88	-0.34	4.49*	0.10*	0.31
28	[DH 98-27 x (DB 533 x DB 534 F4 IPS 8)]	-173.84	8.63	0.04	2.34	-3.20	-0.08	0.85*	3.73	0.39	-2.00	0.30	-6.85**	-0.26**	-2.14*
29	[ZCH 8 x (DB 533 x DB 534 F4 IPS 44)]	97.75	-3.11	-0.39*	1.49	9.80	0.62	0.58	4.21	-0.72	-4.23*	-1.11*	2.09	0.18*	0.47
30	[ZCH 8 x (DB 533 x DB 534 F4 IPS 62)]	-123.96	-4.90	0.25	-0.90	-6.05	0.13	-0.58	-7.41	-0.20	2.31	0.28	-3.53*	-0.13	0.19
31	[ZCH 8 x (DB 533 x DB 534 F4 IPS 105)]	227.66	8.55	-0.04	-1.76	-7.46	-0.34	-0.60	1.26	0.19	-3.60	-0.88	-4.21*	-0.11*	-0.81
32	[ZCH 8 x (DB 533 x DB 534 F4 IPS 26)]	-201.45	-0.54	0.18	1.17	3.71	-0.41	0.61	1.94	0.73	5.52*	1.71**	5.65**	0.07	0.15
33	[ZCH 8 x (DB 533 x DB 534 F4 IPS 71)]	-63.50	-16.07	-0.12	0.24	2.80	-0.24	-0.22	-7.65	-2.04**	2.82	-0.90	-10.84**	-0.21**	-0.82
34	[ZCH 8 x (DB 533 x DB 534 F4 IPS 30)]	-248.74	9.14	0.21	0.35	17.79**	-0.03	-0.54	6.99	-0.91	-4.48*	-1.2*	-9.57**	-0.27**	-1.34
35	[ZCH 8 x (DB 533 x DB 534 F4 IPS 25)]	-28.41	-5.25	0.03	-1.01	-10.30	-0.60	0.86*	-5.09	1.48*	1.76	1.97**	13.09**	0.32**	1.92*
36	[ZCH 8 x (DB 533 x DB 534 F4 IPS 49)]	340.65	12.17	-0.13	0.42	-10.29	0.88*	-0.10	5.75	1.47*	-0.10	0.13	7.33**	0.16*	0.24
37	[ZCH 8 x (DB 533 x DB 534 F4 IPS 23)]	57.63	14.76	0.10	0.41	3.17	0.22	0.18	13.50**	-0.77	1.03	-0.09	4.65**	0.28**	1.04
38	[ZCH 8 x (DB 533 x DB 534 F4 IPS 36)]	-69.77	9.48	-0.45**	0.35	2.33	-0.22	0.11	-1.28	0.65	-0.13	0.52	4.57**	0.32**	1.97*
39	[ZCH 8 x (DB 533 x DB 534 F4 IPS 15)]	15.10	-2.91	0.37*	0.49	-4.25	0.06	0.50	-2.44	0.42	1.48	0.93	4.68**	-0.08	-0.02
40	[ZCH 8 x (DB 533 x DB 534 F4 IPS 1)]	-2.95	-21.33*	-0.02	-1.25	-1.25	-0.06	-0.79*	-9.77*	-0.29	-2.37	-1.37*	-13.9**	-0.52**	-2.99**
41	[ZCH 8 x (DB 533 x DB 534 F4 IPS 33)]	-256.27	-7.65	-0.30	2.37	4.84	0.23	0.12	1.39	-0.86	-11.79**	-0.70	-16.68**	-0.28**	-1.82*
42	[ZCH 8 x (DB 533 x DB 534 F4 IPS 24)]	-195.07	-14.44	0.34*	-2.03	-2.84	-0.31	0.13	-5.89	0.88	3.71	-0.22	2.71	-0.20**	0.39
43	[ZCH 8 x (DB 533 x DB 534 F4 IPS 16)]	227.40	15.67	0.06	-0.72	-4.59	-0.03	0.36	6.62	-0.24	5.12*	1.26*	1.55	-0.11	-0.46
44	[ZCH 8 x (DB 533 x DB 534 F4 IPS 52)]	223.94	6.42	-0.10	0.38	2.59	0.10	-0.60	-2.12	0.22	2.96	-0.34	12.43**	0.58**	1.90*
45	[ZCH 8 x (DB 533 x DB 534 F4 IPS 12)]	-109.74	-9.74	-0.23	0.58	5.30	-0.29	0.08	-2.47	-1.04	0.85	0.11	-0.53	-0.25**	-1.18
46	[ZCH 8 x (DB 534 x DB 533 F4 IPS 22)]	346.89	-3.52	0.23	0.01	-9.05	0.07	-0.18	0.22	0.58	1.42	0.32	3.08	0.20**	0.38
47	[ZCH 8 x (DB 533 x DB 534 F4 IPS 14)]	-140.29	16.09	0.11	1.99	9.70	0.50	-0.30	3.00	-0.69	0.03	-0.13	-3.65*	-0.02	0.11
48	[ZCH 8 x (DB 533 x DB 534 F4 IPS 34)]	-96.86	-2.83	-0.11	-2.58	-5.95	-0.27	0.40	-0.74	1.16	-2.29	-0.30	1.1	0.07	0.70
49	[ZCH 8 x (DB 533 x DB 534 F4 IPS 55)]	154.92	8.27	-0.18	2.45	-2.08	-0.55	0.22	3.27	-0.53	2.19	0.22	-11.93**	-0.37**	-1.83*
50	[ZCH 8 x (DB 533 x DB 534 F4 IPS 17)]	325.54	-13.19	-0.19	-3.78	0.58	-0.30	-0.09	-0.76	-1.25*	0.64	-0.43	-1.34	-0.15*	-0.21
51	[ZCH 8 x (DB 533 x DB 534 F4 IPS 32)]	-282.53	0.09	0.00	3.03	4.16	0.28	-0.38	0.24	0.48	-2.55	-1.04	8.50**	0.50**	1.43
52	[ZCH 8 x (DB 533 x DB 534 F4 IPS 38)]	-197.94	4.84	0.37*	-1.70	-2.66	0.57	0.25	-2.75	1.3*	-0.28	1.25*	4.77**	0.02	0.62
53	[ZCH 8 x (DB 533 x DB 534 F4 IPS 48)]	204.94	-19.19	0.01	0.41	-3.70	-0.17	-0.67	-7.07	-0.39	0.11	-0.14	-0.44	-0.22**	-0.49

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		1	2	3	4	5	6	7	8	9	10	11	12	13	14
54	[ZCH 8 x (DB 533 x DB 534 F4 IPS 13)]	30.65	14.18	-0.06	2.18	7.12	0.54	0.75*	6.74	-0.98	-1.15	-0.36	5.50**	0.41**	1.63
55	[ZCH 8 x (DB 533 x DB 534 F4 IPS 6)]	-110.07	-6.20	0.50**	-1.68	-8.96	0.02	0.48	2.33	2.18**	-0.30	0.35	0.44	-0.15*	0.3
56	[ZCH 8 x (DB 533 x DB 534 F4 IPS 8)]	-125.52	11.21	-0.45**	-0.91	5.54	-0.40	-0.56	-2.00	-0.82	1.34	0.15	-5.5**	-0.04	-1.44
57	[178-24 x (DB 533 x DB 534 F4 IPS 44)]	175.77	-15.11	0.26	-0.84	5.71	-0.09	-0.26	-3.63	0.78	2.97	1.23*	5.86**	0.05	1.02
58	[178-24 x (DB 533 x DB 534 F4 IPS 62)]	-162.64	3.77	-0.12	-0.07	-4.80	-0.08	0.09	-1.16	-0.62	-0.37	-1.31*	2.32	0.05	0.87
59	[178-24 x (DB 533 x DB 534 F4 IPS 105)]	210.34	6.71	-0.28	0.24	-7.21	0.20	0.06	1.35	-0.01	-2.00	0.46	-3.72*	0.04	-1.27
60	[178-24 x (DB 533 x DB 534 F4 IPS 26)]	-223.47	4.63	0.14	0.67	6.30	-0.02	0.10	3.44	-0.15	-0.60	-0.39	-4.46*	-0.14	-0.62
61	[178-24 x (DB 533 x DB 534 F4 IPS 71)]	-52.56	-15.90	0.11	1.12	2.34	0.43	-1.14**	-3.92	0.10	-1.62	-0.20	0.56	0.08	1.72*
62	[178-24 x (DB 533 x DB 534 F4 IPS 30)]	-292.50	-13.86	-0.38*	-3.11	-8.51	-0.01	-0.06	-4.20	0.79	0.20	0.93	-2.36	-0.14	-2.37**
63	[178-24 x (DB 533 x DB 534 F4 IPS 25)]	63.81	22.75*	0.27	1.70	0.91	-0.38	1.33**	8.39	-1.49*	1.25	-0.39	1.37	-0.12	-0.32
64	[178-24 x (DB 533 x DB 534 F4 IPS 49)]	281.25	7.00	0.00	0.30	5.26	-0.05	-0.13	-0.27	0.60	0.18	-0.34	0.43	0.18*	0.98
65	[178-24 x (DB 533 x DB 534 F4 IPS 23)]	-26.25	-4.11	0.41*	-1.38	-0.32	-0.12	1.09**	2.37	-0.86	2.10	0.00	1.49	-0.08	-0.93
66	[178-24 x (DB 533 x DB 534 F4 IPS 36)]	-103.12	3.77	-0.22	1.22	-1.01	-0.01	-0.72*	-3.32	1.99**	-0.87	0.70	9.21**	0.19*	0.45
67	[178-24 x (DB 533 x DB 534 F4 IPS 15)]	64.07	-2.45	-0.31	-3.14	-6.59	0.47	-0.50	-2.90	-0.61	-1.07	-0.22	-11.53**	-0.28**	-1.26
68	[178-24 x (DB 533 x DB 534 F4 IPS 1)]	65.30	2.79	0.13	3.30	7.92	-0.35	0.13	3.86	-0.52	-0.16	-0.48	0.84	0.16*	1.74**
69	[178-24 x (DB 533 x DB 534 F4 IPS 33)]	-390.43	23.06*	-0.09	0.66	-6.87	-0.68	-0.07	-0.31	1.71*	0.65	0.16	2.22	0.24**	0.20
70	[178-24 x (DB 533 x DB 534 F4 IPS 24)]	-262.54	-2.73	-0.14	-1.24	-7.72	0.58	0.63	2.15	1.24*	-0.94	-0.17	5.78**	-0.08	0.61
71	[178-24 x (DB 533 x DB 534 F4 IPS 16)]	333.95	-6.62	0.35*	-1.43	8.70	-0.29	-0.40	-1.17	-1.14	-1.34	-1.12*	-10.91**	-0.45**	-2.26**
72	[178-24 x (DB 533 x DB 534 F4 IPS 52)]	319.02	-13.71	-0.13	2.01	5.88	0.39	-0.17	-0.67	-1.81**	1.63	1.13*	2.91	0.28**	1.45
73	[178-24 x (DB 533 x DB 534 F4 IPS 12)]	-191.28	12.35	-0.08	-0.71	-7.16	-0.03	1.56**	5.44	0.60	-1.92	0.26	4.61**	-0.25**	-1.89*
74	[178-24 x (DB 534 x DB 533 F4 IPS 22)]	302.35	-17.44	0.31	0.72	-0.01	-0.52	-0.30	0.16	-0.37	4.11	0.92	-0.95	0.19*	1.08
75	[178-24 x (DB 533 x DB 534 F4 IPS 14)]	-69.70	-1.66	-0.21	-1.80	3.24	0.01	-0.9**	-2.93	-1.02	1.36	0.02	-5.54**	-0.02	1.09
76	[178-24 x (DB 533 x DB 534 F4 IPS 34)]	-41.37	6.75	-0.02	1.80	3.92	0.54	-0.36	-2.66	0.79	-3.55	-1.2*	1.88	0.08	-0.27
77	[178-24 x (DB 533 x DB 534 F4 IPS 55)]	255.48	-14.49	-0.58**	-3.17	1.21	0.02	-0.67	-0.13	0.35	1.08	-0.35	-0.64	-0.17*	-0.32
78	[178-24 x (DB 533 x DB 534 F4 IPS 17)]	356.80	0.06	0.21	1.93	13.87*	0.48	-0.07	1.10	0.21	1.23	0.83	1.24	0.12	1.41
79	[178-24 x (DB 533 x DB 534 F4 IPS 32)]	-365.36	-0.83	-0.12	0.90	-7.38	-0.54	-0.26	-0.99	-1.93**	0.66	-0.68	-2.23	-0.25**	-3.33**
80	[178-24 x (DB 533 x DB 534 F4 IPS 38)]	-246.91	15.25	0.50**	0.34	-7.70	0.04	1.00**	0.02	1.37*	-2.97	0.20	1.63	0.30**	2.25**
81	[178-24 x (DB 533 x DB 534 F4 IPS 48)]	184.24	-22.61*	-0.03	-4.55*	0.05	0.22	-0.76*	-4.69	0.17	0.31	0.17	4.35*	0.13	0.83
82	[178-24 x (DB 533 x DB 534 F4 IPS 13)]	38.60	9.60	0.26	2.89	4.37	-0.37	-0.08	1.11	1.55*	0.77	0.68	-0.58	-0.06	0.32
83	[178-24 x (DB 533 x DB 534 F4 IPS 6)]	-94.84	-0.29	-0.59**	0.69	-3.21	0.31	0.23	-5.88	-1.25*	-0.53	-0.32	-1.29	0.05	-0.61
84	[178-24 x (DB 533 x DB 534 F4 IPS 8)]	-127.99	13.30	0.35*	0.96	-1.21	-0.16	0.60	9.46*	-0.47	-0.54	-0.52	-2.48	-0.11	-0.53
85	[DH 18-31 x (DB 533 x DB 534 F4 IPS 44)]	128.75	17.52	0.22	2.08	-0.75	-0.64	0.38	0.87	0.40	0.12	-0.78	-0.19	-0.03	0.12

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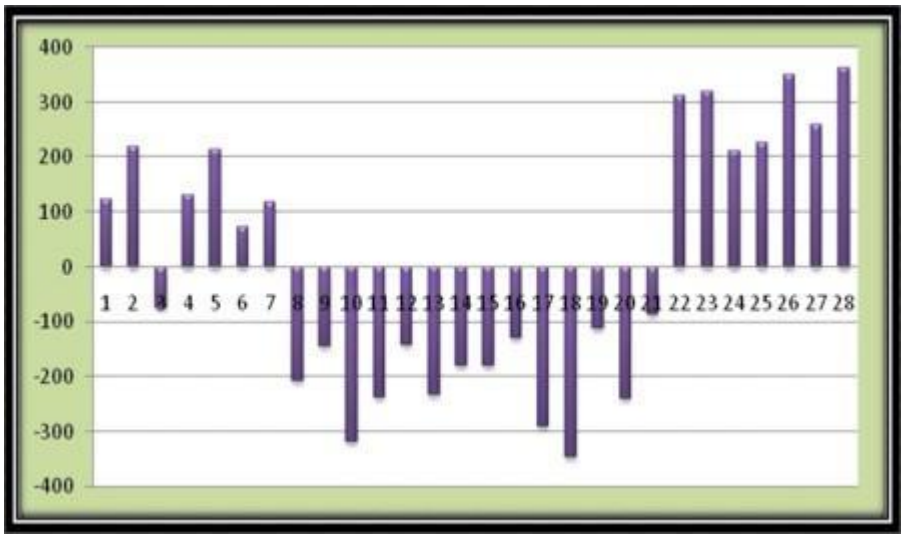
86	[DH 18-31 x (DB 533 x DB 534 F4 IPS 62)]	-194.03	-10.28	-0.32	-1.99	-4.92	0.27	-0.35	-1.66	0.36	-1.61	0.80	-0.56	0.20**	0.12
87	[DH 18-31 x (DB 533 x DB 534 F4 IPS 105)]	175.30	1.17	0.17	-0.18	3.83	0.65	0.06	-0.57	-1.52*	2.67	-0.15	1.88	-0.03	0.83
88	[DH 18-31 x (DB 533 x DB 534 F4 IPS 26)]	-110.02	-8.41	-0.07	0.09	1.84	-0.27	-0.09	1.35	0.76	-1.18	0.13	-1.13	-0.14	-1.07
89	[DH 18-31 x (DB 533 x DB 534 F4 IPS 71)]	56.72	2.06	-0.11	4.00	-6.46	0.18	-0.55	-0.82	1.06	0.28	-0.69	2.67	0.1	0.90
90	[DH 18-31 x (DB 533 x DB 534 F4 IPS 30)]	-224.38	-9.90	0.01	-3.07	0.71	0.39	-0.12	0.56	0.26	-1.25	0.02	-8.16**	-0.12	-1.41
91	[DH 18-31 x (DB 533 x DB 534 F4 IPS 25)]	26.69	3.05	0.33*	0.24	7.95	0.02	0.27	1.93	0.93	-0.45	1.00	4.27*	0.04	0.53
92	[DH 18-31 x (DB 533 x DB 534 F4 IPS 49)]	140.97	4.80	-0.23	-1.16	-2.20	-0.60	0.40	-1.67	-2.25**	1.42	-0.33	1.22	-0.01	-0.02
93	[DH 18-31 x (DB 533 x DB 534 F4 IPS 23)]	16.86	-9.03	0.32	-0.92	-3.53	-0.07	-0.24	-4.60	0.45	0.06	0.51	2.25	0.36**	1.63
94	[DH 18-31 x (DB 533 x DB 534 F4 IPS 36)]	-111.58	24.02*	-0.45**	0.84	-1.22	0.29	-0.08	4.76	1.14	2.30	0.32	3.98*	-0.13	0.84
95	[DH 18-31 x (DB 533 x DB 534 F4 IPS 15)]	63.94	-3.87	0.15	3.32	10.54	-0.18	0.31	3.37	-1.06	-0.81	-0.84	-4.06*	0.02	-0.47
96	[DH 18-31 x (DB 533 x DB 534 F4 IPS 1)]	30.78	-11.12	-0.02	-3.24	-5.79	-0.05	0.02	-3.54	-0.53	-1.55	0.01	-2.17	-0.25**	-2.00**
97	[DH 18-31 x (DB 533 x DB 534 F4 IPS 33)]	-208.73	8.64	-0.28	0.83	-12.12	0.22	0.68*	3.29	0.85	-0.39	-0.43	-1.52	0.11	0.93
98	[DH 18-31 x (DB 533 x DB 534 F4 IPS 24)]	-204.84	3.68	0.01	-0.23	8.20	-0.17	0.69*	4.18	0.30	-0.31	-0.37	0.34	-0.07	-0.38
99	[DH 18-31 x (DB 533 x DB 534 F4 IPS 16)]	203.57	-10.54	0.17	-1.60	-2.72	-0.09	-1**	-6.24	-0.70	-0.09	0.16	-1.34	-0.05	-0.18
100	[DH 18-31 x (DB 533 x DB 534 F4 IPS 52)]	210.00	-1.78	0.10	1.00	6.63	0.04	-0.37	-1.23	-0.44	0.79	0.64	2.51	0.01	-0.38
101	[DH 18-31 x (DB 533 x DB 534 F4 IPS 12)]	-111.83	-14.65	0.25	-0.42	1.88	0.36	-0.15	-2.23	1.77**	-1.59	0.02	0.42	0.04	-0.09
102	[DH 18-31 x (DB 534 x DB 533 F4 IPS 22)]	245.30	6.56	0.22	0.35	6.54	0.32	-0.05	4.40	-0.42	-2.92	-0.39	-0.32	-0.02	0.42
103	[DH 18-31 x (DB 533 x DB 534 F4 IPS 14)]	-69.44	-3.50	-0.46**	0.82	-3.05	-0.35	-0.17	-1.42	-1.81**	2.23	-0.17	2.82	0.08	0.86
104	[DH 18-31 x (DB 533 x DB 534 F4 IPS 34)]	-64.04	11.59	-0.02	-0.75	-5.37	-0.32	0.37	-0.75	0.46	2.28	0.54	-2.91	-0.09	-1.19
105	[DH 18-31 x (DB 533 x DB 534 F4 IPS 55)]	185.14	4.89	-0.17	2.16	-2.16	0.38	0.19	4.85	0.58	-0.95	0.96	3.95*	0.01	0.54
106	[DH 18-31 x (DB 533 x DB 534 F4 IPS 17)]	289.59	2.10	0.00	-0.24	3.50	-0.56	0.51	0.41	-0.17	2.38	-0.29	-1.25	0.03	-0.26
107	[DH 18-31 x (DB 533 x DB 534 F4 IPS 32)]	-279.40	-4.45	-0.04	0.57	-2.76	-0.28	-0.84*	-5.34	0.32	0.31	-0.54	-1.56	0.07	0.59
108	[DH 18-31 x (DB 533 x DB 534 F4 IPS 38)]	-195.33	-2.54	0.21	-2.50	1.42	0.45	0.14	0.09	-0.73	-1.75	-0.13	-1.14	-0.11	-0.87
109	[DH 18-31 x (DB 533 x DB 534 F4 IPS 48)]	138.13	3.22	-0.28	1.58	-1.46	-0.08	-0.7*	0.31	-0.01	-0.19	-0.58	-0.16	0.22**	0.62
110	[DH 18-31 x (DB 533 x DB 534 F4 IPS 13)]	50.32	-1.40	0.16	-1.65	-1.63	0.03	-0.26	-0.72	0.81	-0.56	0.83	2.26	-0.16*	-0.85
111	[DH 18-31 x (DB 533 x DB 534 F4 IPS 6)]	-85.20	8.38	-0.19	1.49	7.79	-0.04	1.21**	4.53	0.12	0.06	0.11	0.87	-0.1	0.10
112	[DH 18-31 x (DB 533 x DB 534 F4 IPS 8)]	-103.25	-10.20	0.30	-1.41	-4.70	0.09	-0.25	-4.12	-0.92	0.70	-0.35	-2.97	0.04	0.13
	SEd	**259.18**	**10.35**	**0.17**	**2.16**	**6.21**	**0.36**	**0.34**	**4.41**	**0.60**	**2.13**	**0.53**	**1.72**	**0.07**	**0.83**
	CD at 5%	**756.81**	**30.25**	**0.48**	**5.74**	**17.71**	**1.04**	**0.97**	**12.86**	**1.85**	**6.10**	**1.59**	**4.55**	**0.13**	**1.53**
	CD at 1%	**996.21**	**39.82**	**0.63**	**7.56**	**23.31**	**1.36**	**1.27**	**16.93**	**2.44**	**8.03**	**2.09**	**5.99**	**0.18**	**2.01**

* Significant at P = 0.05 ** Significant at P = 0.01

Testers gca effects



Lines gca effects

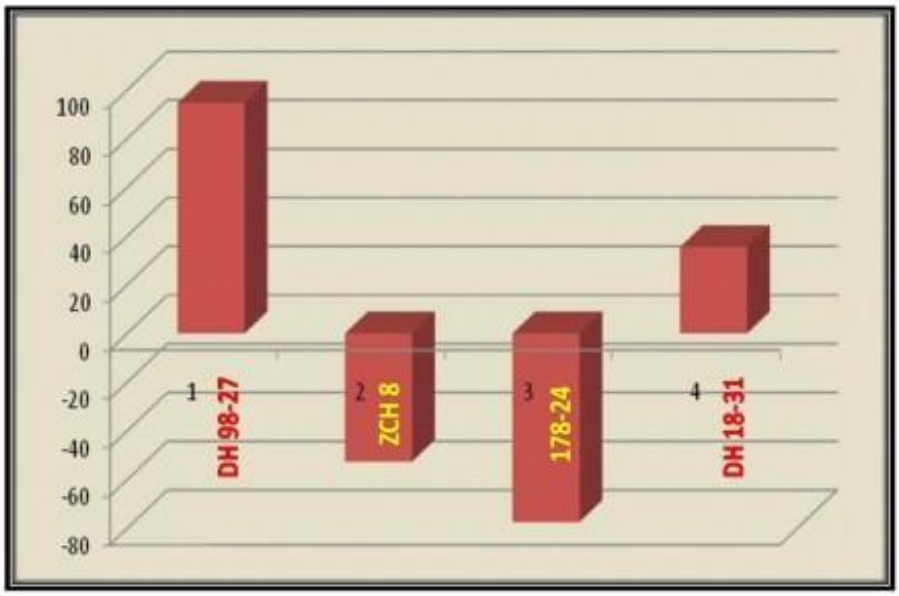


Fig 6 : Estimates of general combining ability effects of parents involved in recombinational variability study for seed cotton yield

4.2.3.2.5 Number of bolls per plant

Among the lines nine lines had significant *gca* effects, out of which five lines recorded positive significant *gca* effects and DB 533 X DB 534 F_4 IPS 24 (5.52) exhibited highest value of *gca* effect. Among the testers, DH 98-27 and DH 18-31 recorded positive significant *gca* effects 1.37 and 0.95, respectively. The tester 178-24 (-1.87) had negative significant *gca* effect. Two crosses differed significantly for *sca* effects, these two crosses had positive *sca* effects and shown by ZCH 8 X (DB 533 x DB 534 F_4 IPS 30) and 178-24 X (DB 533 x DB 534 F_4 IPS 17) 17.97 and 13.87, respectively.

4.2.3.2.6 Mean boll weight (g)

The estimates of *gca* effects of line parents in the population based crosses were found to be significant in two lines, out of which one was positive significant and other was negative significant differences were shown by DB 533 x DB 534 F_4 IPS 52 (0.38) and DB 533 x DB 534 F_4 IPS 30 (-0.47). Among the testers, the tester ZCH 8 recorded positive significant *gca* effect (0.03), while 178-24 had negative significant *gca* effect (-0.05). One cross expressed positive significant *sca* effect, shown by ZCH 8 X (DB 533 x DB 534 F_4 IPS 49) (0.88).

4.2.3.2.7 Reproductive points on sympodia

Out of 28 male (Line) parents used in the population based crosses, thirteen lines recorded significant *gca* effects. Among these, five lines showed significant positive *gca* effects and the cross DB 533 x DB 534 F_4 IPS 15 (0.93) had the highest value of *gca* effect. Among the testers, the tester ZCH 8 (-0.17) exhibited negative significant *gca* effect.Twenty four crosses expressed significant *sca* effects. Among these, thirteen had positive *sca* effects and the maximum *sca* effect was recorded by the cross 178-24 X (DB 533 x DB 534 F_4 IPS 12) (1.56).

4.2.3.2.8 Sympodial length at 50 per cent plant height (cm)

The estimates of *gca* effects of lines revealed positive significant differences for two line parents. These lines are DB 533 x DB 534 F_4 IPS 30 (6.02) and DB 533 x DB 534 F_4 IPS 36 (5.00). Among the testers, there are no significant *gca* effects. The estimates of *sca* effects were significant for eight crosses. Of these, six crosses had positive *sca* effects and the highest *sca* effect was expressed by the cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 38) (14.62).

4.2.3.2.9 Seed index (g)

Eight line parents exhibited significant *gca* effects, four lines had significant *gca* in positive direction and highest was recorded by the line DB 533 x DB 534 F_4 IPS 30 (1.30). Among the testers, the testers 178-24 and DH 18-31 showed positive and negative significant *gca* effects 0.34 and -0.43, respectively. Twenty nine crosses revealed significant *sca* effects, of these fourteen crosses showed positive *sca* effects and the highest was displayed by the cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 32) (5.80).

4.2.3.2.10 Ginning outturn (%)

Six line parents displayed significant *gca* effects, of which two lines exhibited significant positive *gca* effects. Highest *gca* effect was recorded by DB 533 x DB 534 F_4 IPS 16 (2.93). None of the testers depicted significant *gca* effect for this character. Six crosses expressed significant *sca* effects of these, two crosses showed positive *sca* effects. The cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 26) (5.52) recorded highest positive *sca* effect.

4.2.3.2.11 Lint index (g)

Out of twenty eight lines, eight showed significant *gca* effects, of which three lines had positive *gca* effects. The highest *gca* effect was found by the line DB 533 x DB 534 F_4 IPS 17 (1.34). The tester ZCH 8 (-0.27) showed negative significant *gca* effect and the tester 178-24 (0.21) showed positive significant *gca* effect. Of the 112 crosses studied, seventeen crosses recorded significant *sca* effects for this character, of which nine showed significant *gca* effects in positive direction. The cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 32) recorded highest positive *sca* effect (1.98).

4.2.3.2.12 Photosynthetic rate ($\mu molCO_2m^{-2}s^{-1}$)

Out of 28 line parents, twenty one lines are having significant *gca* effects. The male parent DB 533 x DB 534 F_4 IPS 26 (7.36) showed highest positive significant *gca* effect. Among the testers, the tester 178-24 and DH 18-31 had significant negative and positive *gca* effects -1.30 and 1.47, respectively. Fourty eight crosses showed significant *sca* effects, of these twenty six crosses had

positive *sca* effects. The cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 25) expressed the highest *sca* effect (13.09).

4.2.3.2.13 Stomatal conductance ($\mu molm^{-2}s^{-1}$)

Out of twenty eight male lines, sixteen showed significant *gca* effects, of which eight lines exhibited positive *gca* effects and the highest *gca* effect was found by the line DB 533 x DB 534 F_4 IPS 26 (0.31). The tester 178-24 registered significant negative *gca* effect (-0.07), while ZCH 8 and DH 18-31 revealed significant positive *gca* effects 0.03 and 0.05, respectively. Of the 112 crosses, fifty two crosses recorded significant *sca* effects, of which twenty seven showed positive *sca* effects and the cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 52) (0.58) recorded highest positive *sca* effect.

4.2.3.2.14 Transpiration rate (mmol $H_2Om^{-2}s^{-1}$)

The estimates of *gca* effects of lines and testers for transpiration rate trait, six line parents expressed significant *gca* effects. Out of which three lines showed positive significant *gca* effects and the highest *gca* effect was found by the line DB 533 x DB 534 F_4 IPS 55 (1.98). Among the testers, two are with significant *gca* effects, of which DH 18-31 indicated significant positive *gca* effect (0.55) and 178-24 indicated significant negative *gca* effect (-0.56). As regard to *sca* effects, twenty two crosses recorded significant *sca* effects, of which ten were significant positive *gca* and the hybrid DH 98-27 X (DB 533 x DB 534 F_4 IPS 1) registered significant and highest positive *sca* effect (3.58).

4.2.3.3 Pooled score for *gca* effects

Procedure for estimation of pooled scores is described in the chapter Discussion (Section 5.2.2).

In F_4 lines, based on simple pooled *gca* score method (Table 14), the F_4 lines DB 533 x DB 534 F_4 IPS 26, DB 533 x DB 534 F_4 IPS 17, DB 533 x DB 534 F_4 IPS 48 and DB 533 x DB 534 F_4 IPS 8 (Decreasing order) are recognized as the most potential parents. Among the testers, the tester DH 18-31 based on simple pooled *gca* score method showed the most potential parent. Based on per cent *gca* method, the line parents DB 533 x DB 534 F_4 IPS 26, DB 533 x DB 534 F_4 IPS 8, DB 533 x DB 534 F_4 IPS 17 and DB 533 x DB 534 F_4 IPS 55 (Decreasing order) were the most potential combiners (Table 15). Among the testers, the tester DH 18-31 based on per cent *gca* score method showed the most potential parent. Similarly, based on weighted *gca* method the most potential combiners were found to be the lines DB 533 x DB 534 F_4 IPS 26, DB 533 x DB 534 F_4 IPS 17, DB 533 x DB 534 F_4 IPS 8 and DB 533 x DB 534 F_4 IPS 32 . Among the testers, the tester DH 18-31 based on weighted *gca* method is the most potential parent (Table 16).

4.3 Correlation co-efficient analysis

4.3.1 Phenotypic correlation co-efficient in derived F_1 crosses

The phenotypic correlation co-efficients among all characters related to seed cotton yield per plant were estimated and the results are presented in Table 17 & Fig. 7.

4.3.1.1 Seed cotton yield (kg/ha)

It has been observed that seed cotton yield exhibited highly significant positive correlation with plant height (0.3495), number of monopodia per plant (0.4058), number of sympodia per plant (0.3506), number of bolls per plant (0.4013), mean boll weight (0.4200), seed index (0.2999), ginning outturn (0.2154), lint index (0.4448) and photosynthetic rate (0.2327) in derived F_1 crosses. Among these, seed cotton yield exhibited highly significant positive strong association with lint index compare to other characters.

4.3.1.2 Number of monopodia per plant

Number of monopodia per plant recorded highly significant positive strong correlation with plant height (0.3578).

4.3.1.3 Number of sympodia per plant

Number of sympodia per plant exhibited highly significant positive correlation with plant height (0.5250) and number of monopodia per plant (0.2903). Number of sympodia per plant had highly significant positive strong correlation with plant height.

Table 14. Pooled scores of F_4 barbadense lines and hirsutum testers based on simple pooled *gca* score

Sl.No	Parents	Seed cotton yield (kg/ha)	Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympodia at 50% height (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Photosynthetic rate ($\mu mol\ CO_2 m^{-2} s^{-1}$)	Stomatal conductance ($\mu mol\ m^{-2} s^{-1}$)	Transpiration rate ($mmol\ H_2O m^{-2} s^{-1}$)	Pooled gca
	Males	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	
1	DB 533 x DB 534 F4 IPS 44	0	0	0	0	-1	0	0	0	-1	0	0	0	0	-1	**-3**
2	DB 533 x DB 534 F4 IPS 62	0	0	0	0	1	0	-1	0	1	0	0	0	0	0	**1**
3	DB 533 x DB 534 F4 IPS 105	0	0	1	0	0	0	0	0	0	0	0	-1	-1	0	**-1**
4	DB 533 x DB 534 F4 IPS 26	0	0	1	0	0	0	0	0	1	0	0	1	1	0	**4**
5	DB 533 x DB 534 F4 IPS 71	0	0	0	0	0	0	-1	0	0	0	0	-1	0	0	**-2**
6	DB 533 x DB 534 F4 IPS 30	0	1	0	0	0	-1	0	1	1	0	0	0	-1	-1	**0**
7	DB 533 x DB 534 F4 IPS 25	0	0	-1	0	0	0	-1	0	0	0	0	1	1	0	**0**
8	DB 533 x DB 534 F4 IPS 49	0	0	-1	0	0	0	1	0	0	-1	-1	-1	-1	0	**-4**
9	DB 533 x DB 534 F4 IPS 23	0	0	0	0	0	0	0	0	0	-1	0	-1	-1	-1	**-4**
10	DB 533 x DB 534 F4 IPS 36	-1	1	0	0	1	0	1	1	0	-1	0	-1	0	0	**1**
11	DB 533 x DB 534 F4 IPS 15	0	0	0	-1	0	0	1	0	-1	-1	-1	-1	-1	0	**-5**
12	DB 533 x DB 534 F4 IPS 1	0	1	0	0	1	0	-1	0	-1	0	0	-1	0	0	**-1**
13	DB 533 x DB 534 F4 IPS 33	0	0	0	0	0	0	1	0	0	0	-1	0	0	0	**0**
14	DB 533 x DB 534 F4 IPS 24	0	0	-1	0	1	0	0	0	0	0	-1	1	1	0	**1**
15	DB 533 x DB 534 F4 IPS 16	0	0	0	0	0	0	0	0	0	1	0	1	-1	0	**1**

Contd....

Sl.No	Parents	Seed cotton yield (kg/ha)	Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympodia at %50 height (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Photosynthetic rate (µmol $CO_2 m^{-2} s^{-1}$)	Stomatal conductance ((µmol $m^{-2} s^{-1}$)	Transpiration rate (mmol $H_2O m^{-2} s^{-1}$)	Pooled gca
	Males	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	
16	DB 533 x DB 534 F4 IPS 52	0	0	0	0	0	1	-1	0	0	0	0	0	1	1	**2**
17	DB 533 x DB 534 F4 IPS 12	-1	-1	0	0	0	0	-1	0	0	0	0	-1	-1	0	**-5**
18	DB 534 x DB 533 F4 IPS 22	-1	0	0	0	0	0	-1	0	0	0	0	-1	0	0	**-3**
19	DB 533 x DB 534 F4 IPS 14	0	0	0	0	0	0	0	0	-1	0	0	-1	0	1	**-1**
20	DB 533 x DB 534 F4 IPS 34	0	0	0	0	0	0	0	0	0	0	-1	-1	-1	0	**-3**
21	DB 533 x DB 534 F4 IPS 55	0	0	0	0	0	0	-1	0	0	0	0	0	1	1	**1**
22	DB 533 x DB 534 F4 IPS 17	1	-1	0	0	0	0	0	0	0	1	1	1	1	0	**4**
23	DB 533 x DB 534 F4 IPS 32	1	0	-1	0	-1	0	0	0	1	0	1	1	0	0	**2**
24	DB 533 x DB 534 F4 IPS 38	0	0	0	0	-1	0	1	0	0	0	0	0	1	0	**1**
25	DB 533 x DB 534 F4 IPS 48	0	0	1	0	0	0	0	0	0	0	1	1	0	0	**3**
26	DB 533 x DB 534 F4 IPS 13	1	0	1	0	-1	0	0	0	0	0	0	1	0	0	**2**
27	DB 533 x DB 534 F4 IPS 6	1	0	-1	0	1	0	0	0	0	0	0	1	0	0	**2**
28	DB 533 x DB 534 F4 IPS 8	1	0	0	0	0	0	0	0	0	0	0	1	1	0	**3**
	Females															
1	DH 98-27	1	0	0	0	1	0	0	0	0	0	0	0	0	0	**2**
2	ZCH 8	0	0	0	0	0	1	-1	0	0	0	-1	0	1	0	**0**
3	178-24	-1	0	0	0	-1	-1	0	0	1	0	1	-1	-1	-1	**-4**
4	DH 18-31	0	0	1	0	1	0	0	0	-1	0	0	1	1	1	**4**

Table 15. Pooled scores of F_4 barbadense lines and hirsutum testers based on per cent pooled *gca* score

Sl.No	Parents	Seed cotton yield (kg/ha)	Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympodia at %50height (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Photosynthetic rate ($^{-2}$ $^{-1}$ (µmol CO_2m s))	Stomatal conductance ($^{-2}$ $^{-1}$ ((µmol m s))	Transpiration rate ($^{-2}$ $^{-1}$ (mmol H_2Om s))	Pooled gca
	Males	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	
1	DB 533 x DB 534 F4 IPS 44	6.30	0.04	-4.52	-0.94	-8.25	-2.90	1.14	10.62	-6.04	5.31	-11.28	4.02	4.84	-17.92	-19.58
2	DB 533 x DB 534 F4 IPS 62	11.19	-5.07	2.82	2.02	7.24	-6.77	-12.82	-11.82	8.22	-2.82	8.51	6.44	1.61	-9.12	-0.37
3	DB 533 x DB 534 F4 IPS 105	-3.71	-3.88	10.73	-4.03	-2.31	-5.81	3.42	-1.46	4.85	-3.66	-4.04	-30.78	-48.39	-3.75	-92.82
4	DB 533 x DB 534 F4 IPS 26	6.71	4.48	10.73	3.00	-3.65	-6.13	1.42	7.54	8.12	6.62	9.79	30.20	50.00	6.19	135.02
5	DB 533 x DB 534 F4 IPS 71	10.87	-8.83	1.69	3.00	4.36	1.29	-16.52	-9.14	-2.18	0.27	-0.64	-7.18	3.23	-4.23	-24.01
6	DB 533 x DB 534 F4 IPS 30	3.68	9.74	-1.69	-3.47	-0.41	-15.16	8.26	17.52	12.87	2.59	11.06	-3.24	-20.97	-16.78	4
7	DB 533 x DB 534 F4 IPS 25	6.03	-1.04	-11.86	3.19	4.54	-2.58	-23.36	-6.78	-5.15	1.75	6.81	16.09	32.26	2.61	22.51
8	DB 533 x DB 534 F4 IPS 49	-10.63	5.52	-9.60	3.19	-4.28	4.52	20.80	9.84	0.20	-8.50	-11.91	-14.20	-14.52	-7.49	-37.06
9	DB 533 x DB 534 F4 IPS 23	-7.39	0.26	1.69	-0.33	5.44	6.77	5.41	1.89	-3.76	-8.09	-11.06	-31.14	-46.77	-16.94	-104.02
10	DB 533 x DB 534 F4 IPS 36	-16.21	12.79	1.13	2.81	10.39	1.29	17.66	14.55	1.78	-8.09	-5.53	-14.49	-6.45	5.21	16.84
11	DB 533 x DB 534 F4 IPS 15	-12.16	4.66	0.00	-11.07	2.12	0.97	26.50	8.56	-8.22	-12.76	-18.51	-16.74	-14.52	-4.40	-55.57
12	DB 533 x DB 534 F4 IPS 1	-7.27	9.51	6.78	2.81	7.24	10.00	-13.68	-0.55	-8.32	-0.60	-9.57	-11.94	-4.84	4.89	-15.54
13	DB 533 x DB 534 F4 IPS 33	-11.82	-0.78	7.34	0.23	0.84	3.87	23.65	9.90	-1.49	-4.40	-12.98	0.37	1.61	-5.37	10.97
14	DB 533 x DB 534 F4 IPS 24	-9.16	3.36	-12.99	5.16	11.92	-2.26	-7.69	-3.93	-0.30	-3.96	-11.28	10.46	16.13	2.61	-1.93
15	DB 533 x DB 534 F4 IPS 16	-9.18	-3.43	-7.91	0.05	2.03	-6.13	1.71	-7.39	1.29	9.84	7.23	8.41	-19.35	0.33	-22.5
16	DB 533 x DB 534 F4 IPS 52	-6.57	5.04	-2.26	8.07	-3.65	12.26	-12.82	-7.74	-4.06	5.54	8.09	6.65	14.52	14.82	37.89

Contd...

Sl.No	Parents	Seed cotton yield (kg/ha)	Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympodia at %50 height (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Photosynthetic rate (µmol $CO_2 m^{-2} s^{-1}$)	Stomatal conductance ((µmol $m^{-2} s^{-1}$)	Transpiration rate (mmol $H_2O m^{-2} s^{-1}$)	Pooled gca
	Males	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	
17	DB 533 x DB 534 F4 IPS 12	-14.88	-13.87	2.26	-9.15	0.67	5.81	-20.23	-12.49	-2.77	5.54	3.19	-14.32	-30.65	-10.75	-111.64
18	DB 534 x DB 533 F4 IPS 22	-17.68	1.34	2.26	-0.75	1.12	-1.94	-11.11	-8.29	0.79	-1.78	-3.19	-14.65	-1.61	0.16	-55.33
19	DB 533 x DB 534 F4 IPS 14	-5.66	8.09	-3.95	3.38	-3.65	1.29	3.13	7.95	-8.51	-2.18	-9.57	-11.37	6.45	14.33	-0.27
20	DB 533 x DB 534 F4 IPS 34	-12.22	6.75	1.69	2.39	-3.39	-3.55	-3.13	0.61	3.86	-5.67	-12.34	-13.38	-11.29	-2.93	-52.6
21	DB 533 x DB 534 F4 IPS 55	-4.40	0.30	8.47	-0.52	5.98	6.13	-19.66	2.50	-5.84	-0.67	0.21	2.01	29.03	32.25	55.79
22	DB 533 x DB 534 F4 IPS 17	15.88	-10.10	-5.65	-2.67	-6.35	1.94	-6.84	-10.07	1.68	9.23	28.51	21.38	16.13	3.75	56.82
23	DB 533 x DB 534 F4 IPS 32	16.34	-5.82	-15.25	-1.50	-7.34	5.81	2.85	-7.57	11.58	2.22	11.91	11.41	-1.61	-6.84	16.19
24	DB 533 x DB 534 F4 IPS 38	10.82	-2.76	1.13	2.02	-9.33	-3.87	20.80	7.07	3.96	-0.64	11.06	6.61	12.90	-4.72	55.05
25	DB 533 x DB 534 F4 IPS 48	11.51	-5.74	22.60	3.19	-2.31	-10.00	-3.70	-9.81	-1.88	3.26	15.96	14.73	0.00	9.61	47.42
26	DB 533 x DB 534 F4 IPS 13	17.84	-5.18	10.17	-5.82	-10.59	3.55	-1.14	-4.66	4.06	2.38	-3.40	17.19	0.00	2.93	27.33
27	DB 533 x DB 534 F4 IPS 6	13.22	2.09	-11.86	-3.85	7.86	-0.65	8.55	8.44	-2.77	4.77	-2.34	12.60	0.00	1.79	37.85
28	DB 533 x DB 534 F4 IPS 8	18.54	-7.46	-5.08	-0.33	-6.26	1.29	7.12	-5.27	-2.08	4.57	5.32	14.81	32.26	9.61	67.04
	Females															
1	DH 98-27	4.83	0.47	-2.82	0.61	2.96	-0.32	2.56	1.72	1.39	-1.61	0.85	-2.17	-3.23	-3.09	2.15
2	ZCH 8	-2.69	1.32	-0.56	-0.66	-0.97	0.97	-4.84	-1.11	-0.50	0.50	-5.74	1.48	4.84	3.26	-4.7
3	178-24	-3.95	-2.35	0.00	-1.31	-4.04	-1.61	2.85	-0.64	3.37	1.91	4.47	-5.33	-11.29	-9.12	-27.04
4	DH 18-31	1.81	0.55	3.39	1.36	2.05	0.65	-0.57	0.06	-4.26	-0.81	0.43	6.03	8.06	8.96	27.71
	F1 Mean	**1958.45**	**111.73**	**1.77**	**21.32**	**46.29**	**3.10**	**3.51**	**34.36**	**10.10**	**29.78**	**4.70**	**24.37**	**0.62**	**6.14**	

Table 16. Pooled scores of F_4 barbadense lines and hirsutum testers based on weighted percent *gca* method

Sl.No	Parents	Seed cotton yield (kg/ha)	Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympodia at %50height (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Photosynthetic rate ($^{-2}$ $^{-1}$) (µmol CO_2m s)	Stomatal conductance ($^{-2}$ $^{-1}$) ((µmol m s)	Transpiration rate ($^{-2}$ $^{-1}$) (mmol H_2Om s)	Pooled gca
	Males	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	
1	DB 533 x DB 534 F4 IPS 44	63	0.08	-9.04	-2.82	-45.375	-20.3	2.28	26.55	-24.16	29.205	-73.32	16.08	14.52	-17.92	-41.22
2	DB 533 x DB 534 F4 IPS 62	111.9	-10.14	5.64	6.06	39.82	-47.39	-25.64	-29.55	32.88	-15.51	55.315	25.76	4.83	-9.12	144.855
3	DB 533 x DB 534 F4 IPS 105	-37.1	-7.76	21.46	-12.09	-12.705	-40.67	6.84	-3.65	19.4	-20.13	-26.26	-123.12	-145.17	-3.75	-384.705
4	DB 533 x DB 534 F4 IPS 26	67.1	8.96	21.46	9	-20.075	-42.91	2.84	18.85	32.48	36.41	63.635	120.8	150	6.19	474.74
5	DB 533 x DB 534 F4 IPS 71	108.7	-17.66	3.38	9	23.98	9.03	-33.04	-22.85	-8.72	1.485	-4.16	-28.72	9.69	-4.23	45.885
6	DB 533 x DB 534 F4 IPS 30	36.8	19.48	-3.38	-10.41	-2.255	-106.12	16.52	43.8	51.48	14.245	71.89	-12.96	-62.91	-16.78	39.4
7	DB 533 x DB 534 F4 IPS 25	60.3	-2.08	-23.72	9.57	24.97	-18.06	-46.72	-16.95	-20.6	9.625	44.265	64.36	96.78	2.61	184.35
8	DB 533 x DB 534 F4 IPS 49	-106.3	11.04	-19.2	9.57	-23.54	31.64	41.6	24.6	0.8	-46.75	-77.415	-56.8	-43.56	-7.49	-261.805
9	DB 533 x DB 534 F4 IPS 23	-73.9	0.52	3.38	-0.99	29.92	47.39	10.82	4.725	-15.04	-44.495	-71.89	-124.56	-140.31	-16.94	-391.37
10	DB 533 x DB 534 F4 IPS 36	-162.1	25.58	2.26	8.43	57.145	9.03	35.32	36.375	7.12	-44.495	-35.945	-57.96	-19.35	5.21	-133.38
11	DB 533 x DB 534 F4 IPS 15	-121.6	9.32	0	-33.21	11.66	6.79	53	21.4	-32.88	-70.18	-120.315	-66.96	-43.56	-4.4	-390.935
12	DB 533 x DB 534 F4 IPS 1	-72.7	19.02	13.56	8.43	39.82	70	-27.36	-1.375	-33.28	-3.3	-62.205	-47.76	-14.52	4.89	-106.78
13	DB 533 x DB 534 F4 IPS 33	-118.2	-1.56	14.68	0.69	4.62	27.09	47.3	24.75	-5.96	-24.2	-84.37	1.48	4.83	-5.37	-114.22
14	DB 533 x DB 534 F4 IPS 24	-91.6	6.72	-25.98	15.48	65.56	-15.82	-15.38	-9.825	-1.2	-21.78	-73.32	41.84	48.39	2.61	-74.305
15	DB 533 x DB 534 F4 IPS 16	-91.8	-6.86	-15.82	0.15	11.165	-42.91	3.42	-18.475	5.16	54.12	46.995	33.64	-58.05	0.33	-78.935
16	DB 533 x DB 534 F4 IPS 52	-65.7	10.08	-4.52	24.21	-20.075	85.82	-25.64	-19.35	-16.24	30.47	52.585	26.6	43.56	14.82	136.62
17	DB 533 x DB 534 F4 IPS 12	-148.8	-27.74	4.52	-27.45	3.685	40.67	-40.46	-31.225	-11.08	30.47	20.735	-57.28	-91.95	-10.75	-346.655

Contd....

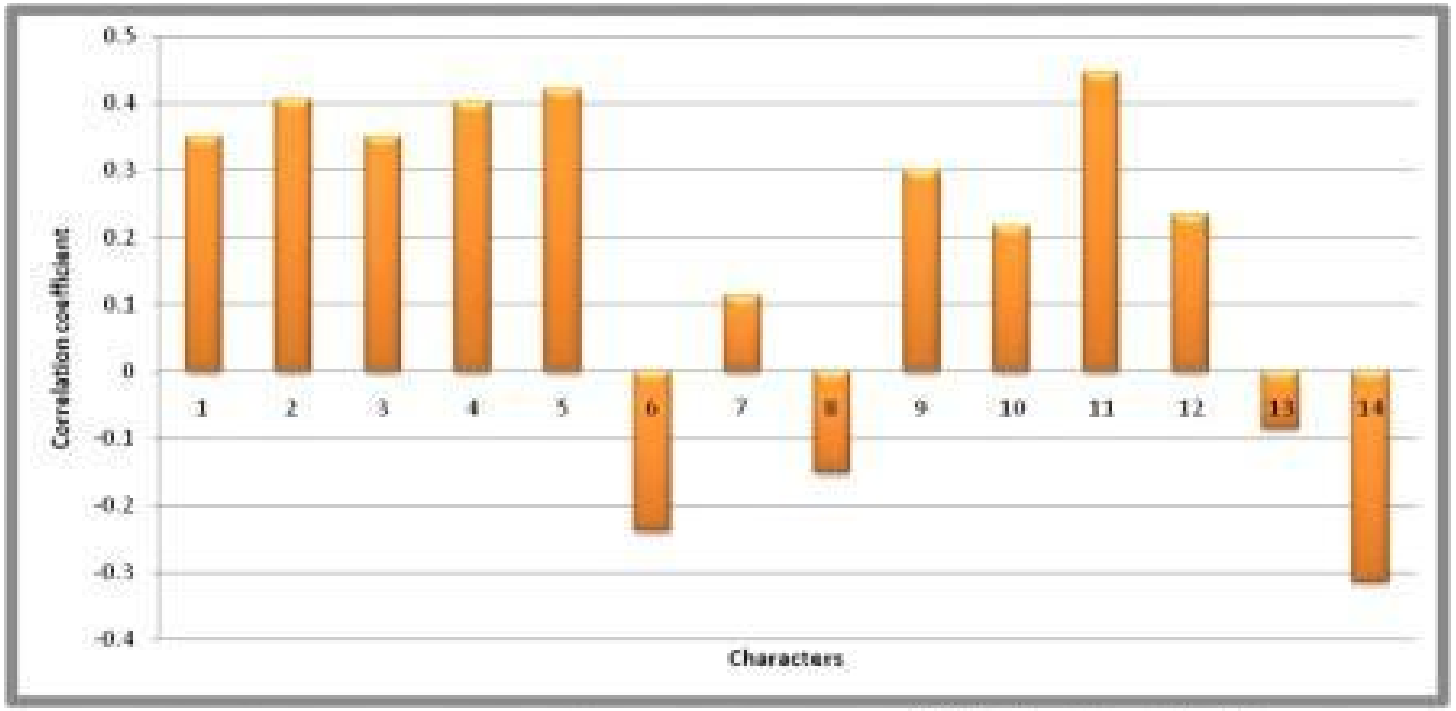
Sl.No	Parents	Seed cotton yield (kg/ha)	Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympodia at %50height (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Photosynthetic rate ($\mu mol\ CO_2 m^{-2} s^{-1}$)	Stomatal conductance ($\mu mol\ m^{-2} s^{-1}$)	Transpiration rate ($mmol\ H_2O m^{-2} s^{-1}$)	Pooled gca
	Males	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**	**11**	**12**	**13**	**14**	
18	DB 534 x DB 533 F4 IPS 22	-176.8	2.68	4.52	-2.25	6.16	-13.58	-22.22	-20.725	3.16	-9.79	-20.735	-58.6	-4.83	0.16	-312.85
19	DB 533 x DB 534 F4 IPS 14	-56.6	16.18	-7.9	10.14	-20.075	9.03	6.26	19.875	-34.04	-11.99	-62.205	-45.48	19.35	14.33	-143.125
20	DB 533 x DB 534 F4 IPS 34	-122.2	13.5	3.38	7.17	-18.645	-24.85	-6.26	1.525	15.44	-31.185	-80.21	-53.52	-33.87	-2.93	-332.655
21	DB 533 x DB 534 F4 IPS 55	-44	0.6	16.94	-1.56	32.89	42.91	-39.32	6.25	-23.36	-3.685	1.365	8.04	87.09	32.25	116.41
22	DB 533 x DB 534 F4 IPS 17	158.8	-20.2	-11.3	-8.01	-34.925	13.58	-13.68	-25.175	6.72	50.765	185.315	85.52	48.39	3.75	439.55
23	DB 533 x DB 534 F4 IPS 32	163.4	-11.64	-30.5	-4.5	-40.37	40.67	5.7	-18.925	46.32	12.21	77.415	45.64	-4.83	-6.84	273.75
24	DB 533 x DB 534 F4 IPS 38	108.2	-5.52	2.26	6.06	-51.315	-27.09	41.6	17.675	15.84	-3.52	71.89	26.44	38.7	-4.72	236.5
25	DB 533 x DB 534 F4 IPS 48	115.1	-11.48	45.2	9.57	-12.705	-70	-7.4	-24.525	-7.52	17.93	103.74	58.92	0	9.61	226.44
26	DB 533 x DB 534 F4 IPS 13	178.4	-10.36	20.34	-17.46	-58.245	24.85	-2.28	-11.65	16.24	13.09	-22.1	68.76	0	2.93	202.515
27	DB 533 x DB 534 F4 IPS 6	132.2	4.18	-23.72	-11.55	43.23	-4.55	17.1	21.1	-11.08	26.235	-15.21	50.4	0	1.79	230.125
28	DB 533 x DB 534 F4 IPS 8	185.4	-14.92	-10.16	-0.99	-34.43	9.03	14.24	-13.175	-8.32	25.135	34.58	59.24	96.78	9.61	352.02
	Females	48.3	0.94	-5.64	1.83	16.28	-2.24	5.12	4.3	5.56	-8.855	5.525				
1	DH 98-27	-26.9	2.64	-1.12	-1.98	-5.335	6.79	-9.68	-2.775	-2	2.75	-37.31	-8.68	-9.69	-3.09	-96.38
2	ZCH 8	-39.5	-4.7	0	-3.93	-22.22	-11.27	5.7	-1.6	13.48	10.505	29.055	5.92	14.52	3.26	-0.78
3	178-24	18.1	1.1	6.78	4.08	11.275	4.55	-1.14	0.15	-17.04	-4.455	2.795	-21.32	-33.87	-9.12	-38.115
4	DH 18-31	48.3	0.94	-5.64	1.83	16.28	-2.24	5.12	4.3	5.56	-8.855	5.525	24.12	24.18	8.96	128.38
	Weightage	**10.00**	**2.00**	**2.00**	**3.00**	**5.50**	**7.00**	**2.00**	**2.50**	**4.00**	**5.50**	**6.50**	**4.00**	**3.00**	**1.00**	

Table 17. Phenotypic correlation co-efficient of seed cotton yield per plant and different quantitative characters in derived F_1 crosses

Characters	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}	X_{15}
X_1	**1.0000**	0.3578**	0.5250**	0.4670**	0.2785**	0.0990	0.5207**	-0.0098	0.1437*	-0.0553	0.1146	0.1022	-0.1133	-0.3070**	0.3495**
X_2		**1.0000**	0.2903**	0.4460**	0.2085**	-0.0621	0.1643**	-0.1048	0.1611**	-0.0416	0.1593**	0.0676	-0.2157**	-0.2338**	0.4058**
X_3			**1.0000**	0.5138**	0.2505**	-0.1216*	0.2397**	0.1068	0.1290*	0.0822	0.1651**	0.0421	-0.0755	-0.2981**	0.3506**
X_4				**1.0000**	0.3010**	-0.1946**	0.1695**	-0.0248	0.0608	-0.0689	0.0739	-0.005	-0.1846**	-0.3779**	0.4013**
X_5					**1.0000**	-0.249**	0.0591	-0.065	0.1788**	0.0791	0.219**	0.0508	-0.0482	-0.1755**	0.4200**
X_6						**1.0000**	0.4939**	0.1008	-0.1014	-0.1283*	-0.1328*	-0.0155	-0.0235	0.1258*	-0.2390
X_7							**1.0000**	0.1296*	-0.0428	-0.1032	-0.0465	-0.0391	-0.0986	-0.1128	0.1125
X_8								**1.0000**	-0.0816	0.0951	-0.0306	-0.0567	0.1498*	0.2563**	-0.1508
X_9									**1.0000**	0.1131	0.4726**	0.2077**	-0.0636	-0.1798**	0.2999**
X_{10}										**1.0000**	0.4501**	0.2323**	0.1265*	0.0728	0.2154**
X_{11}											**1.0000**	0.3031**	0.0279	-0.0646	0.4448**
X_{12}												**1.0000**	0.5401**	0.2858**	0.2327**
X_{13}													**1.0000**	0.5606**	-0.0861
X14														**1.0000**	-0.3150
X15															**1.0000**

* Significant at P = 0.05 ** Significant at P = 0.01

X_1. Plant height (cm)
X_2. Number of monopodia
X_3. Number of sympodia
X_4. Number of bolls
X_5. Mean boll weight (g)
X_6. Reproductive points
X_7. Sympodial length at 50% plant height (cm)
X_8. Inter branch distance (cm)
X_9. Seed index (g)
X_{10}. Ginning outturn (%)
X_{11}. Lint index (g)
X_{12}. Photosynthetic rate ($\mu mol\ CO_2 m^{-2} s^{-1}$)
X_{13}. Stomatal conductance ($\mu mol\ m^{-2} s^{-1}$)
X_{14}. Transpiration rate ($mmol\ H_2O m^{-2} s^{-1}$)
X_{15}. Seed cotton yield (kg/ha)



X1. Plant height (cm)
X2. Number of monopodia
X3. Number of sympodia
X4. Number of bolls
X5. Mean boll weight (g)
X6. Reproductive points
X7. Sympodial length at 50% plant height (cm)
X8. Inter branch distance (cm)
X9. Seed index (g)
X10. Ginning outturn (%)
X11. Lint index (g)
X12. Photosynthetic rate (i mol $CO_2 m^{-2} s^{-1}$)
X13. Stomatal conductance (i mol $m^{-2} s^{-1}$)
X14. Transpiration rate (mmol $H_2Om^{-2} s^{-1}$)
X15. Seed cotton yield (kg/ha)

Fig 7 : Phenotypic correlation co-efficient of seed cotton yield per plant and different quantitative characters in derived F_1 crosses

4.3.1.4 Number of bolls per plant

Number of bolls per plant recorded highly significant positive correlation with plant height (0.4670), number of monopodia per plant (0.4460) and number of sympodia per plant (0.5138). Among these number of bolls per plant had highly significant positive strong correlation with number of sympodia per plant.

4.3.1.5 Mean boll weight (g)

Mean boll weight exhibited highly significant positive correlation with plant height (0.2785), number of monopodia per plant (0.2085), number of sympodia per plant (0.2505) and number of bolls per plant (0.3010). Among these, mean boll weight showed highly significant positive strong correlation with number of bolls per plant.

4.3.1.6 Reproductive points on sympodia

Reproductive points on sympodia showed highly negative significant correlation with number of bolls per plant (-0.1946) and mean boll weight (-0.2490), while reproductive points on sympodia recorded negative significant correlation with number of sympodia per plant (-0.1216).

4.3.1.7 Sympodial length at 50 per cent plant height (cm)

Sympodial length at 50% plant height exhibited highly positive significant correlation with plant height (0.5207), number of monopodia per plant (0.1643), number of sympodia per plant (0.2397), number of bolls per plant (0.1695) and reproductive points on sympodia (0.4939). Among these, sympodial length at 50 % plant height recorded highly significant positive strong correlation with plant height.

4.3.1.8 Inter branch distance (cm)

Inter branch distance exhibited significant positive correlation with sympodial length at 50% plant height (0.1296).

4.3.1.9 Seed index (g)

Seed index recorded significant positive correlation with plant height (0.1437), highly significant positive correlation with number of monopodia per plant (0.1611), significant positive correlation with number of sympodia per plant (0.1290) and highly significant positive correlation with mean boll weight (0.1788). Among these seed index showed highly significant positive strong correlation with mean boll weight.

4.3.1.10 Ginning outturn (%)

Ginning outturn showed significant negative correlation with reproductive points on sympodia (-0.1283).

4.3.1.11 Lint index (g)

Lint index exhibited highly significant positive association with number of monopodia per plant (0.1593), number of sympodia per plant (0.1651), mean boll weight (0.2190), seed index (0.4726) and ginning outturn (0.4501). Among these, lint index showed highly significant positive strong correlation with seed index (0.4726). Lint index recorded significant negative correlation with reproductive points on sympodia (-0.1328).

4.3.1.12 Photosynthetic rate ($\mu molCO_2m^{-2}s^{-1}$)

Photosynthetic rate recorded highly significant positive correlation with seed index (0.2077), ginning outturn (0.2323) and lint index (0.3031). Among these, photosynthetic rate recorded highly significant positive strong correlation with lint index.

4.3.1.13 Stomatal conductance ($\mu molm^{-2}s^{-1}$)

Stomatal conductance showed highly negative significant correlation with number of monopodia per plant (-0.2157) and number of bolls per plant (-0.1846), while stomatal conductance had highly significant positive strong correlation with photosynthetic rate (0.5401). Stomatal conductance exhibited significant positive correlation with inter branch distance (0.1498) and ginning outturn (0.1265).

4.3.1.14 Transpiration rate (mmol $H_2Om^{-2}s^{-1}$)

Transpiration rate had highly significant negative correlation with plant height (-0.3070), number of monopodia per plant (-0.2338), number of sympodia per plant (-0.2981), number of bolls per plant (-0.3779), mean boll weight (-0.1755) and seed index (-0.1798), while transpiration rate recorded highly significant positive correlation with inter branch distance (0.2563), photosynthetic rate (0.2858) and stomatal conductance (0.5606). Among these, transpiration rate showed highly significant positive strong correlation with stomatal conductance. Transpiration rate exhibited significant positive correlation with number of reproductive points (0.1258).

4.3.2 Phenotypic correlation co-efficient in line x tester inter specific crosses (YHB)

The phenotypic correlation co-efficients among all characters related to seed cotton yield per plant were estimated and the results are presented in Table 18 & Fig. 8.

4.3.2.1 Seed cotton yield (kg/ha)

Seed cotton yield exhibited significant positive correlation with mean boll weight (0.1123), ginning outturn (0.1339) and lint index (0.1020). Among these, seed cotton yield recorded significant positive strong correlation with ginning outturn.

4.3.2.2 Number of monopodia per plant

Number of monopodia per plant recorded non significant negative correlation with plant height (-0.1146).

4.3.2.3 Number of sympodia per plant

Number of sympodia per plant exhibited highly significant positive correlation with plant height (0.5141).

4.3.2.4 Number of bolls per plant

Number of bolls per plant recorded highly significant positive correlation with number of sympodia per plant (0.2654).

4.3.2.5 Mean boll weight (g)

Mean boll weight exhibited non significant correlation with other characters.

4.3.2.6 Reproductive points on sympodia

Reproductive points on sympodia showed highly significant positive correlation with plant height (0.2229) and number of sympodia per plant (0.1880). Among these, reproductive points recorded highly significant positive strong correlation with plant height.

4.3.2.7 Sympodial length at 50 per cent plant height (cm)

Sympodial length at 50% plant height exhibited highly significant positive correlation with plant height (0.5214), number of sympodia per plant (0.3137) and reproductive points on sympodia (0.6418). Among these, sympodial length at 50% plant height showed highly significant positive strong correlation with reproductive points on sympodia, while sympodial length at 50 per cent plant height showed highly significant negative correlation with number of monopodia per plant (-0.1895).

4.3.2.8 Inter branch distance (cm)

Inter branch distance exhibited highly significant positive correlation with plant height (0.4779), number of sympodia per plant (0.2179) and sympodial length at 50% plant height (0.3424). Among these, inter branch distance had highly significant positive strong correlation with plant height, while exhibited significant positive correlation with reproductive points on sympodia (0.1441).

4.3.2.9 Seed index (g)

Seed index recorded highly significant positive correlation with number of bolls per plant (0.1939) and highly significant negative correlation with inter branch distance (-0.1896).

4.3.2.10 Ginning outturn (%)

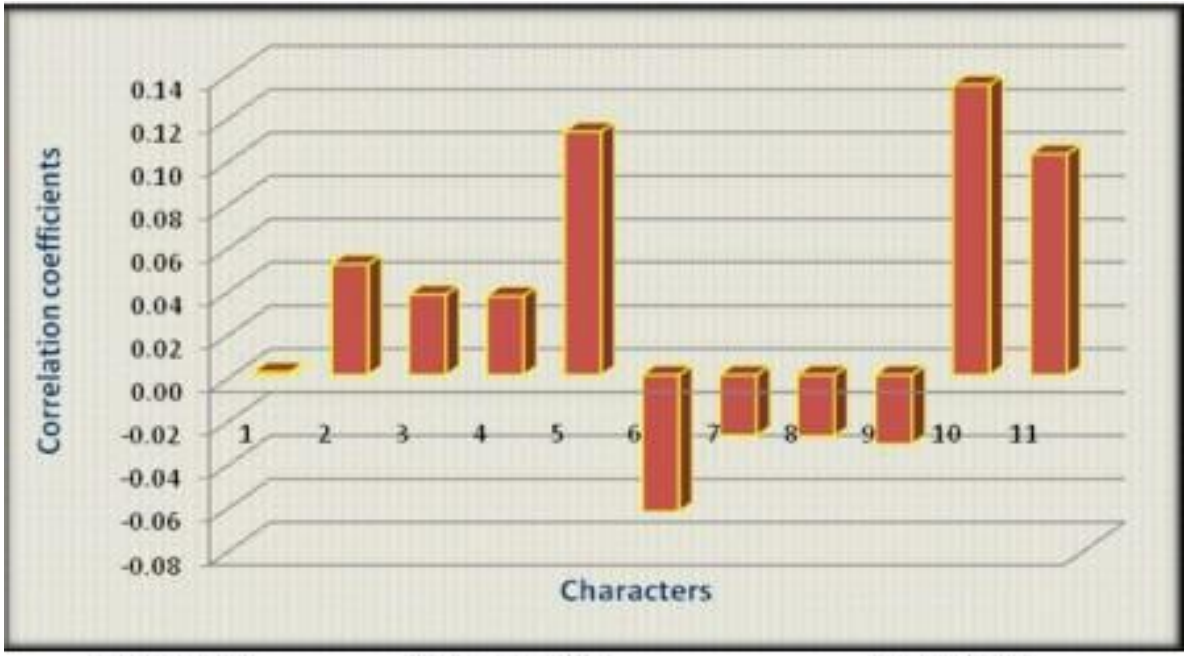
Ginning outturn showed non significant correlation with other characters.

Table 18. Phenotypic correlation co-efficient of seed cotton yield per plant and different quantitative characters in line x tester inter specific crosses (YHB)

Characters	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}
X_1	1.00	-0.1146	0.5141**	0.0296	-0.0346	0.2229**	0.5214**	0.4779**	0.0534	0.0017	0.0222	0.0014
X_2		1.00	-0.0433	0.1383	-0.0381	-0.1000	-0.1895**	-0.1055	-0.0246	0.0270	0.0151	0.0511
X_3			1.00	0.2654**	0.0631	0.1880**	0.3137**	0.2179**	0.0970	0.1053	0.1510*	0.0371
X_4				1.00	0.0848	0.0838	0.0945	-0.0957	0.1939**	0.1336	0.2316**	0.0364
X_5					1.00	-0.0755	-0.0802	-0.0369	0.1198	-0.0634	0.0237	0.1123*
X_6						1.00	0.6418**	0.1441*	-0.0348	-0.0477	-0.0798	-0.0631
X_7							1.00	0.3424**	-0.0397	-0.0573	-0.0953	-0.028
X_8								1.00	-0.1896**	0.0921	-0.0523	-0.0283
X_9									1.00	-0.057	0.5508**	-0.0319
X_{10}										1.00	0.7942**	0.1339*
X_{11}											1.00	0.102*
X12												1.00

* Significant at P = 0.05 ** Significant at P = 0.01

X_1. Plant height (cm)
X_2. Number of monopodia
X_3. Number of sympodia
X_4. Number of bolls
X_5. Mean boll weight (g)
X_6. Reproductive points
X_7. Sympodial length at 50% plant height (cm)
X_8. Inter branch distance (cm)
X_9. Seed index (g)
X_{10}. Ginning outturn (%)
X_{11}. Lint index (g)
X_{12}. Seed cotton yield (kg/ha)



X1. Plant height (cm)
X2. Number of monopodia
X3. Number of sympodia
X4. Number of bolls
X5. Mean boll weight (g)
X6. Reproductive points
X7. Sympodial length at 50% plant height (cm)
X8. Inter branch distance (cm)
X9. Seed index (g)
X10. Ginning outturn (%)
X 11. Lint index (g)
X12. Seed cotton yield (kg/ha)

Fig 8 : Phenotypic correlation co-efficient of seed cotton yield per plant and different quantitative characters in Line x Tester inter specific crosses (YHB)

4.3.2.11 Lint index (g)

Lint index exhibited highly significant positive association with number of bolls per plant (0.2316), seed index (0.5508) and ginning outturn (0.7942). Among these, lint index recorded highly significant positive strong correlation with ginning outturn, while lint index recorded significant positive correlation with number of sympodia per plant (0.1510).

4.3.3 Intergeneration (F_3-F_5) correlation and regression analysis

The simple correlation was worked out between parent F_3 and progeny F_5 mean for all the quality characters by considering same characters in both the generations and the results are presented in Table 19.

Intergeneration correlation values revealed that, the barbadense lines in both generations exhibited highly significant positive correlation for 2.5% SL (0.48) and significant positive correlation for fibre uniformity ratio (0.37) and fibre micronaire value (0.29). Non of barbadense in two generations exhibited significant correlation for fiber maturity ratio, fiber tenacity and fiber elongation.

4.3.4 Narrow sense heritability estimates

The evaluation of parent and progeny provided an opportunity to compute heritability values following parent offspring regression method can be utilized for predicting the response to selection in early and advanced generations. The results obtained from the study are presented in Table 20.

The moderate heritability was noticed for fiber maturity ratio (32 %), fiber tenacity (41 %) and fiber elongation (34 %). The high heritability was noticed for 2.5% SL (89 %), fiber uniformity ratio (74 %) and fiber micronaire value (63 %).

4.4 Path co-efficient analysis

4.4.1 Direct and indirect phenotypic effects of component characters on seed cotton yield in derived F_1 crosses

The phenotypic path co-efficient analysis among all characters related to seed cotton yield per plant were estimated and the results are presented in Table 21 and Fig. 9.

4.4.1.1 Plant height (cm)

The direct effect of this character on seed cotton yield was positive (0.0289), although plant height exhibited highly significant positive association with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through plant height appeared to be positive value in respect of number of monopodia per plant (0.0104), number of sympodia per plant (0.0152), number of bolls per plant (0.0135), mean boll weight (0.0081), reproductive points on sympodia (0.0029), sympodial length at 50% plant height (0.0151), seed index (0.0042), lint index (0.0033) and photosynthetic rate (0.003). The contribution had negative indirect effects *via* inter branch distance (-0.0003), ginning outturn (-0.0016), stomatal conductance (-0.0033), and transpiration rate (-0.0089).

4.4.1.2 Number of monopodia per plant

This character appeared to influence seed cotton yield directly as positive value (0.1771), although number of monopodia per plant recorded highly significant positive correlation with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through number of monopodia per plant appeared to be positive value in respect of plant height (0.0634) , number of sympodia per plant (0.0514), number of bolls per plant (0.079), mean boll weight (0.0369), sympodial length at 50% plant height (0.0291), seed index (0.0285), lint index (0.0282) and photosynthetic rate (0.012). The association recorded negative indirect effects *via* reproductive points on sympodia (-0.011), inter branch distance (-0.0186), ginning outturn (-0.0074), stomatal conductance (-0.0382) and transpiration rate (-0.0414).

4.4.1.3 Number of sympodia per plant

The direct influence of number of sympodia per plant towards seed cotton yield was positive (0.0434), although number of sympodia per plant recorded highly significant positive correlation with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through number of sympodia per plant showed to be positive value in respect of plant height (0.0228), number of monopodia per plant (0.0126), number of bolls per plant (0.0223), mean boll weight (0.0109), sympodial length at 50 % plant height (0.0104), inter branch distance (0.0046), seed index (0.0056),

Table 19. Intergeneration correlation co-efficient between F_3 and F_5 generation for fiber quality

Characters	2.5% SL (mm)	UR %	Micronaire value (µg/inch)	Maturity Ratio (%)	Tenacity (g/tex)	Elongation %
Barbadense lines (F_3/F_5)	0.48**	0.37*	0.29*	-0.03	0.18	-0.18

Table 20. Estimates of heritability (Narrow sense) for fiber quality characters in barbadense lines (F_3/F_5)

Characters	2.5% SL (mm)	UR %	Micronaire value (µg/inch)	Maturity Ratio (%)	Tenacity (g/tex)	Elongation %
Barbadense lines (F_3/F_5)	89	74	63	32	41	34

Table 21. Direct and indirect phenotypic effects of seed cotton yield and different quantitative characters in derived F_1 crosses

Characters	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	X_{12}	X_{13}	X_{14}	Phenotypic correlation with seed cotton yield
X_1	**0.0289**	0.0104	0.0152	0.0135	0.0081	0.0029	0.0151	-0.0003	0.0042	-0.002	0.0033	0.003	-0.0033	-0.0089	0.3495**
X_2	0.0634	**0.1771**	0.0514	0.079	0.0369	-0.011	0.0291	-0.0186	0.0285	-0.007	0.0282	0.012	-0.0382	-0.0414	0.4058**
X_3	0.0228	0.0126	**0.0434**	0.0223	0.0109	-0.0053	0.0104	0.0046	0.0056	0.0036	0.0072	0.0018	-0.0033	-0.0129	0.3506**
X_4	0.0492	0.047	0.0541	**0.1053**	0.0317	-0.0205	0.0179	-0.0026	0.0064	-0.007	0.0078	-0.0005	-0.0194	-0.0398	0.4013**
X_5	0.0516	0.0386	0.0464	0.0557	**0.1852**	-0.0461	0.0109	-0.012	0.0331	0.0146	0.0406	0.0094	-0.0089	-0.0325	0.4200**
X_6	-0.014	0.0088	0.0172	0.0275	0.0351	**-0.1411**	-0.0697	-0.0142	0.0143	0.0181	0.0187	0.0022	0.0033	-0.0178	-0.2390
X_7	0.0621	0.0196	0.0286	0.0202	0.007	0.0589	**0.1192**	0.0155	-0.005	-0.012	-0.0055	-0.005	-0.0118	-0.0135	0.1125
X_8	0.0007	0.0078	-0.008	0.0018	0.0049	-0.0075	-0.0097	**-0.0746**	0.0061	-0.007	0.0023	0.0042	-0.0112	-0.0191	-0.1508
X_9	0.0056	0.0063	0.0051	0.0024	0.007	-0.004	-0.0017	-0.0032	**0.0393**	0.0044	0.0186	0.0082	-0.0025	-0.0071	0.2999**
X_{10}	-0.0043	-0.003	0.0065	-0.005	0.0062	-0.0101	-0.0081	0.0075	0.0089	**0.0786**	0.0354	0.0183	0.0099	0.0057	0.2154**
X_{11}	0.0274	0.0381	0.0395	0.0177	0.0524	-0.0318	-0.0111	-0.0073	0.1131	0.1078	**0.2394**	0.0726	0.0067	-0.0155	0.4448**
X_{12}	0.0162	0.0107	0.0067	-0.0008	0.0081	-0.0025	-0.0062	-0.009	0.033	0.0369	0.0481	**0.1588**	0.0858	0.0454	0.2327**
X_{13}	0.0035	0.0067	0.0023	0.0057	0.0015	0.0007	0.003	-0.0046	0.002	-0.004	-0.0009	-0.017	**-0.0309**	-0.0173	-0.0861
X_{14}	0.0595	0.0453	0.0577	0.0732	0.034	-0.0244	0.0218	-0.0496	0.0348	-0.014	0.0125	-0.055	-0.1086	**-0.1937**	-0.3150

Residual effect = 0.7086

X_1. Plant height (cm)
X_2. Number of monopodia
X_3. Number of sympodia
X_4. Number of bolls
X_5. Mean boll weight (g)
X_6. Reproductive points
X_7. Sympodial length at 50% plant height (cm)
X_8. Inter branch distance (cm)
X_9. Seed index (g)
X_{10}. Ginning outturn (%)
X_{11}. Lint index (g)
X_{12}. Photosynthetic rate ($\mu mol\ CO_2 m^{-2}\ s^{-1}$)
X_{13}. Stomatal conductance ($\mu mol\ m^{-2}\ s^{-1}$)
X_{14}. Transpiration rate ($mmol\ H_2O m^{-2}\ s^{-1}$)

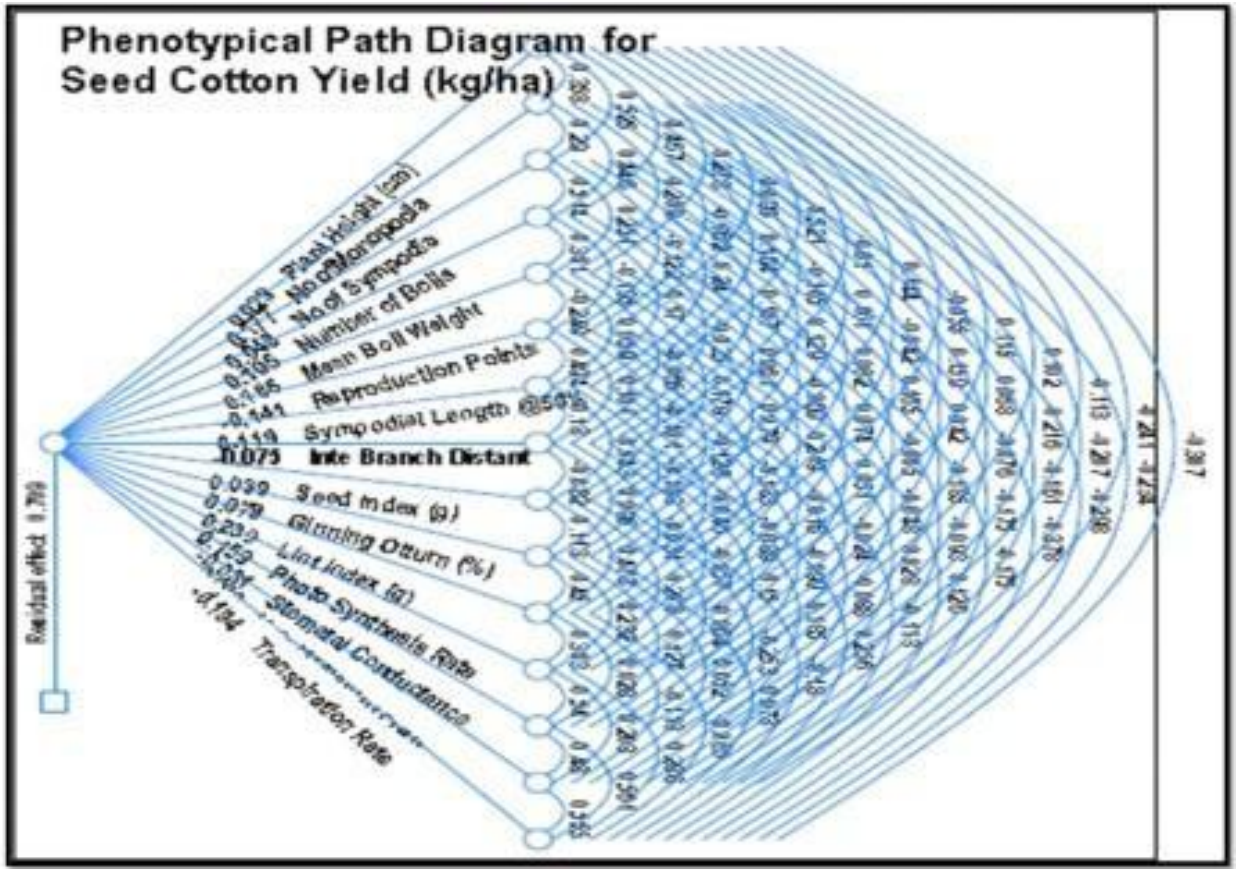


Fig 9 : Direct and indirect phenotypic effects of seed cotton yield and different quantitative characters in derived F_1 crosses

ginning outturn (0.0036), lint index (0.0072) and photosynthetic rate (0.0018). The contribution showed negative indirect effects *via* reproductive points on sympodia (-0.0053), stomatal conductance (-0.0033) and transpiration rate (-0.0129).

4.4.1.4 Number of bolls per plant

The direct effect of number of bolls per plant on seed cotton yield was positive (0.1053), although number of bolls per plant exhibited highly significant positive association with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through number of bolls per plant appeared to be positive value in respect of plant height (0.0492), number of monopodia per plant (0.047), number of sympodia per plant (0.0541), mean boll weight (0.0317), sympodial length at 50% plant height (0.0179), seed index (0.0064) and lint index (0.0078). The contribution exhibited negative indirect effects *via* reproductive points on sympodia (-0.0205), inter branch distance (-0.0026), ginning outturn (-0.0073), photosynthetic rate (-0.0005), stomatal conductance (-0.0194) and transpiration rate (-0.0398).

4.4.1.5 Mean boll weight (g)

The direct contribution of mean boll weight on seed cotton yield was positive (0.1852), although mean boll weight showed highly significant positive association with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through mean boll weight appeared to be positive value in respect of plant height (0.0516), number of monopodia per plant (0.0386), number of sympodia per plant (0.0464), number of bolls per plant (0.0557), sympodial length at 50% plant height (0.0109), seed index (0.0331), ginning outturn (0.0146), lint index (0.0406) and photosynthetic rate (0.0094). The association exhibited negative indirect effects *via* reproductive points on sympodia (-0.0461), inter branch distance (-0.012), stomatal conductance (-0.0089) and transpiration rate (-0.0325).

4.4.1.6 Reproductive points on sympodia

It was observed that this character appeared to influence seed cotton yield directly as negative value (-0.1411), reproductive points on sympodia recorded non significant negative correlation with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through reproductive points on sympodia to be positive value in respect of number of monopodia per plant (0.0088), number of sympodia per plant (0.0172), number of bolls per plant (0.0275), mean boll weight (0.0351), seed index (0.0143), ginning outturn (0.0181), lint index (0.0187), photosynthetic rate (0.0022) and stomatal conductance (0.0033). The association exhibited negative indirect effects *via* plant height (-0.014), sympodial length at 50% plant height (-0.0697), inter branch distance (-0.0142) and transpiration rate (-0.0178).

4.4.1.7 Sympodial length at 50%plant height (cm)

The direct effect of sympodial length at 50% plant height on seed cotton yield was positive (0.1192), although sympodial length at 50 % plant height recorded non significant positive correlation with seed cotton yield. The indirect contribution to seed cotton yield through sympodial length at 50% plant height was positive value in respect of plant height (0.0621), number of monopodia per plant (0.0196), number of sympodia per plant (0.0286), number of bolls per plant (0.0202), mean boll weight (0.007), reproductive points on sympodia (0.0589) and inter branch distance (0.0155). The association exhibited negative indirect effects *via* seed index (-0.0051), ginning outturn (-0.0123), lint index (-0.0055), photosynthetic rate (-0.0047), stomatal conductance (-0.0118) and transpiration rate (-0.0135).

4.4.1.8 Inter branch distance (cm)

It expressed a considerably negative direct effect of inter branch distance on seed cotton yield (-0.0746) and had non significant negative correlation with seed cotton yield. The indirect effect of inter branch distance was positive through plant height (0.0007), number of monopodia per plant (0.0078), number of bolls per plant (0.0018), mean boll weight (0.0049), seed index (0.0061), lint index (0.0023) and photosynthetic rate (0.0042). The association recorded negative indirect effects *via* number of sympodia per plant (-0.008), reproductive points on sympodia (-0.0075), sympodial length at 50% plant height (-0.0097), ginning outturn (-0.0071), stomatal conductance (-0.0112) and transpiration rate (-0.0191).

4.4.1.9 Seed index (g)

It was observed that this character appeared to influence seed cotton yield directly as positive value (0.0393), seed index recorded highly significant positive correlation with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through seed index to be positive value in respect of plant height (0.0056), number of monopodia per plant (0.0063), number of sympodia per plant (0.0051), number of bolls per plant (0.0024), mean boll weight (0.007), ginning outturn (0.0044), lint index (0.0186) and photosynthetic rate (0.0082). The association exhibited negative indirect effects *via* reproductive points on sympodia (-0.004), sympodial length at 50 % plant height (-0.0017), inter branch distance (-0.0032), stomatal conductance (-0.0025) and transpiration rate (-0.0071).

4.4.1.10 Ginning outturn (%)

The direct effect of ginning outturn on seed cotton yield was positive (0.0786), ginning outturn recorded highly significant positive correlation with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through ginning outturn to be positive value in respect of number of sympodia per plant (0.0065), mean boll weight (0.0062), inter branch distance (0.0075), seed index (0.0089), lint index (0.0354), photosynthetic rate (0.0183), stomatal conductance (0.0099) and transpiration rate (0.0057). The association exhibited negative indirect effects *via* plant height (-0.0043), number of monopodia per plant (-0.0033), number of bolls per plant (-0.0054), reproductive points on sympodia (-0.0101) and sympodial length at 50% plant height (-0.0081).

4.4.1.11 Lint index (g)

It expressed a considerably positive direct effect of lint index on seed cotton yield (0.2394) and had highly significant positive correlation with seed cotton yield. The indirect effect of lint index was positive through plant height (0.0274), number of monopodia per plant (0.0381), number of sympodia per plant (0.0395), number of bolls per plant (0.0177), mean boll weight (0.0524), seed index (0.1131), ginning outturn (0.1078), photosynthetic rate (0.0726) and stomatal conductance (0.0067). The association recorded negative indirect effects *via* reproductive points on sympodia (-0.0318), sympodial length at 50 % plant height (-0.0111), inter branch distance (-0.0073) and transpiration rate (-0.0155).

4.4.1.12 Photosynthetic rate ($\mu molCO_2m^{-2}s^{-1}$)

The direct contribution of photosynthetic rate on seed cotton yield was positive (0.1588), although photosynthetic rate showed highly significant positive association with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through photosynthetic rate appeared to be positive value in respect of plant height (0.0162), number of monopodia per plant (0.0107), number of sympodia per plant (0.0067), mean boll weight (0.0081), seed index (0.0330), ginning outturn (0.0369), lint index (0.0481), stomatal conductance (0.0858) and transpiration rate (0.0454). The association exhibited negative indirect effects *via* number of bolls per plant (-0.0008) reproductive points on sympodia (-0.0025), sympodial length at 50 % plant height (-0.0062) and inter branch distance (-0.009).

4.4.1.13 Stomatal conductance ($\mu molm^{-2}s^{-1}$)

It was observed that this character appeared to influence seed cotton yield directly as negative value (-0.0309), stomatal conductance recorded non significant negative correlation with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through stomatal conductance to be positive value in respect of plant height (0.0035), number of monopodia per plant (0.0067), number of sympodia per plant (0.0023), number of bolls per plant (0.0057), mean boll weight (0.0015), reproductive points on sympodia (0.0007), sympodial length at 50 % plant height (0.003) and seed index (0.002). The association exhibited negative indirect effects *via* inter branch distance (-0.0046), ginning outturn (-0.0039), lint index (-0.0009), photosynthetic rate (-0.0167) and transpiration rate (-0.0173).

4.4.1.14 Transpiration rate (mmol $H_2Om^{-2}s^{-1}$)

It expressed a considerably negative direct effect of transpiration rate on seed cotton yield (-0.1937) and had non significant negative correlation with seed cotton yield. The indirect effect of transpiration rate was positive through plant height (0.0595), number of monopodia per plant (0.0453), number of sympodia per plant (0.0577), number of bolls per plant (0.0732), mean boll weight (0.0340), sympodial length at 50 % plant height (0.0218), seed index (0.0348) and lint index (0.0125). The association recorded negative indirect effects *via* reproductive points on sympodia (-0.0244), inter

branch distance (-0.0496), ginning outturn (-0.0141), photosynthetic rate (-0.0553) and stomatal conductance (-0.1086).

4.4.2 Direct and indirect phenotypic effects of component characters on seed cotton yield in line x tester inter specific crosses (YHB)

The phenotypic path co-efficient analysis among all characters related to seed cotton yield per plant were estimated and the results are presented in Table 22 and Fig. 10.

4.4.2.1 Plant height (cm)

The direct effect of this character on seed cotton yield was positive (0.0274), although plant height exhibited non significant positive association with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through plant height appeared to be positive value in respect of number of sympodia per plant (0.0141), number of bolls per plant (0.0008), reproductive points on sympodia (0.0061), sympodial length at 50 % plant height (0.0143), inter branch distance (0.0131), seed index (0.0015), ginning outturn (0.000) and lint index (0.0006). The contribution had negative indirect effects *via* number of monopodia per plant (-0.0031) and mean boll weight (-0.0009).

4.4.2.2 Number of monopodia per plant

It was observed that this character appeared to influence seed cotton yield directly as positive value (0.0480), although number of monopodia per plant recorded non significant positive correlation with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through number of monopodia per plant appeared to be positive value in respect of number of bolls per plant (0.0066), ginning outturn (0.0013) and lint index (0.0007). The association recorded negative indirect effects *via* plant height (-0.0055), number of sympodia per plant (-0.0021), mean boll weight (-0.0018), reproductive points on sympodia (-0.0048), sympodial length at 50 % plant height (-0.0091), inter branch distance (-0.0051) and seed index (-0.0012).

4.4.2.3 Number of sympodia per plant

The direct influence of number of sympodia per plant towards seed cotton yield was positive (0.0103), although number of sympodia per plant recorded non significant positive correlation with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through number of sympodia per plant showed to be positive value in respect ofplant height (0.0053), number of bolls per plant (0.0027), mean boll weight (0.0007), reproductive points on sympodia (0.0019), sympodial length at 50 % plant height (0.0032), inter branch distance (0.0022), seed index (0.0010), ginning outturn (0.0011) and lint index (0.0016). The contribution showed negative indirect effect *via* number of monopodia per plant (-0.0004).

4.4.2.4 Number of bolls per plant

The direct effect of number of bolls per plant on seed cotton yield was negative (-0.0024), although number of bolls per plant exhibited non significant positive association with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through number of bolls per plant appeared to be positive value in respect of inter branch distance (0.0002). The contribution exhibited negative indirect effects *via* plant height (-0.0001), number of monopodia per plant (-0.0003), number of sympodia per plant (-0.0006), mean boll weight (-0.0002), reproductive points on sympodia (-0.0002), sympodial length at 50 % plant height (-0.0002), seed index (-0.0005), ginning outturn (-0.0003) and lint index (-0.0005).

4.4.2.5 Mean boll weight (g)

The direct contribution of mean boll weight on seed cotton yield was positive (0.1241), although mean boll weight showed significant positive association with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through mean boll weight appeared to be positive value in respect of number of sympodia per plant (0.0078), number of bolls per plant (0.0105), seed index (0.0149) and lint index (0.0029). The association exhibited negative indirect effects *via* plant height (-0.0043), number of monopodia per plant (-0.0047), reproductive points on sympodia (-0.0094), sympodial length at 50 % plant height (-0.010), inter branch distance (-0.0046) and ginning outturn (-0.0079).

Table 22. Direct and indirect phenotypic effects of seed cotton yield and different quantitative characters in line x tester inter specific crosses (YHB)

Characters	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8	X_9	X_{10}	X_{11}	Phenotypic correlation with seed cotton yield
X_1	**0.0274**	-0.0031	0.0141	0.0008	-0.0009	0.0061	0.0143	0.0131	0.0015	0.0000	0.0006	0.0014
X_2	-0.0055	**0.0480**	-0.0021	0.0066	-0.0018	-0.0048	-0.0091	-0.0051	-0.0012	0.0013	0.0007	0.0511
X_3	0.0053	-0.0004	**0.0103**	0.0027	0.0007	0.0019	0.0032	0.0022	0.0010	0.0011	0.0016	0.0371
X_4	-0.0001	-0.0003	-0.0006	**-0.0024**	-0.0002	-0.0002	-0.0002	0.0002	-0.0005	-0.0003	-0.0005	0.0364
X_5	-0.0043	-0.0047	0.0078	0.0105	**0.1241**	-0.0094	-0.0100	-0.0046	0.0149	-0.0079	0.0029	0.1123*
X_6	-0.0153	0.0069	-0.0129	-0.0058	0.0052	**-0.0687**	-0.0441	-0.0099	0.0024	0.0033	0.0055	-0.0631
X_7	0.0313	-0.0114	0.0189	0.0057	-0.0048	0.0386	**0.0601**	0.0206	-0.0024	-0.0034	-0.0057	-0.028
X_8	-0.0273	0.0060	-0.0124	0.0055	0.0021	-0.0082	-0.0195	**-0.0571**	0.0108	-0.0053	0.0030	-0.0283
X_9	-0.0247	0.0114	-0.0448	-0.0896	-0.0554	0.0161	0.0184	0.0876	**-0.4620**	0.0263	-0.2545	-0.0319
X_{10}	-0.0007	-0.0116	-0.0451	-0.0572	0.0271	0.0204	0.0245	-0.0394	0.0244	**-0.4280**	-0.3400	0.1339*
X_{11}	0.0153	0.0104	0.1039	0.1594	0.0163	-0.0549	-0.0656	-0.0360	0.3792	0.5468	**0.6884**	0.102*

Residual effect = 0.9754

X_1. Plant height (cm)
X_2. Number of monopodia
X_3. Number of sympodia
X_4. Number of bolls
X_5. Mean boll weight (g)
X_6. Reproductive points
X_7. Sympodial length at 50% plant height (cm)
X_8. Inter branch distance (cm)
X_9. Seed index (g)
X_{10}. Ginning outturn (%)
X_{11}. Lint index (g)

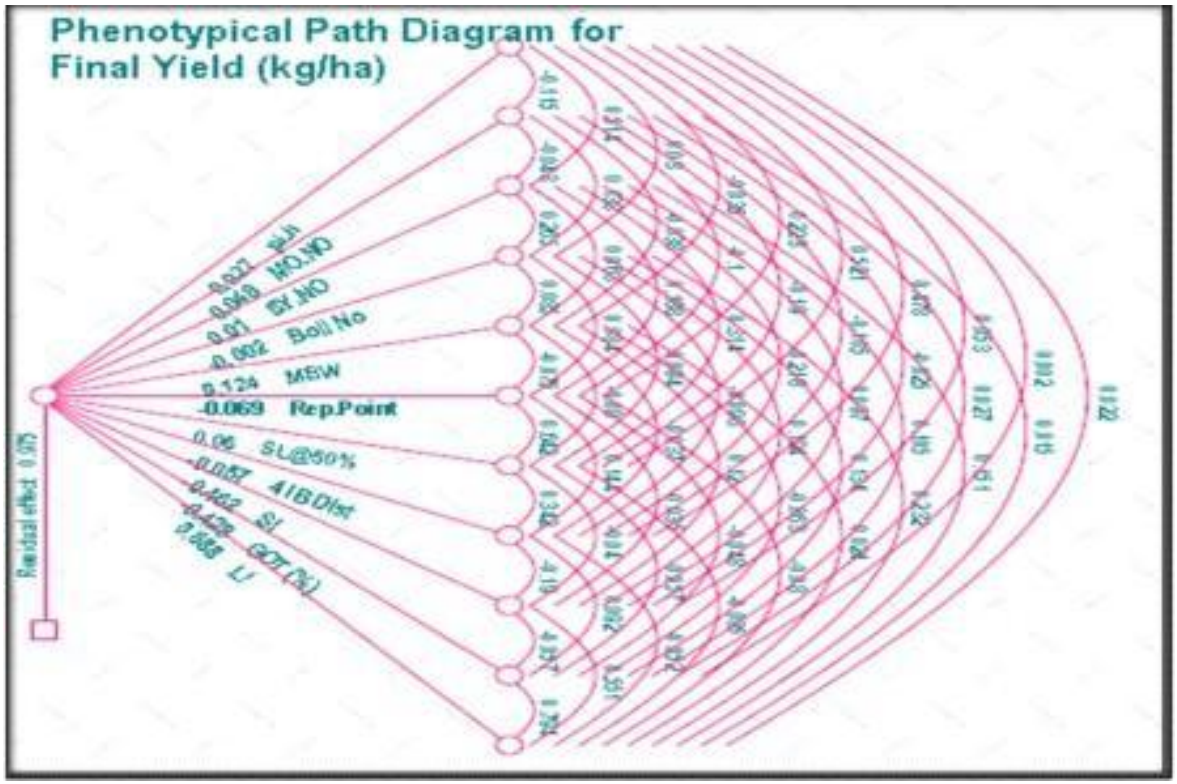


Fig 10 : Direct and indirect phenotypic effects of seed cotton yield and different quantitative characters in Line x Tester inter specific crosses (YHB)

4.4.2.6 Reproductive points on sympodia

It was observed that this character appeared to influence seed cotton yield directly as negative value (-0.0687), reproductive points on sympodia recorded non significant negative correlation with seed cotton yield.The contribution of other characters indirectly on seed cotton yield through reproductive points on sympodia to be positive value in respect of number of monopodia per plant (0.0069), mean boll weight (0.0052), seed index (0.0024), ginning outturn (0.0033) and lint index (0.0055). The association showed negative indirect effects *via* plant height (-0.0153), number of sympodia per plant (-0.0129), number of bolls per plant (-0.0058), sympodial length at 50 % plant height (-0.0441) and inter branch distance (-0.0099).

4.4.2.7 Sympodial length at 50 %plant height (cm)

The direct effect of sympodial length at 50 % plant height on seed cotton yield was positive (0.0601), although sympodial length at 50 % plant height recorded non significant negative correlation with seed cotton yield. The indirect contribution to seed cotton yield through sympodial length at 50 % plant height was positive value in respect of plant height (0.0313), number of sympodia per plant (0.0189), number of bolls per plant (0.0057), reproductive points on sympodia (0.0386) and inter branch distance (0.0206). The association exhibited negative indirect effects *via* number of monopodia per plant (-0.0114), mean boll weight (-0.0048), seed index (-0.0024), ginning outturn (-0.0034) and lint index (-0.0057).

4.4.2.8 Inter branch distance (cm)

It expressed a considerably negative direct effect of inter branch distance on seed cotton yield (-0.0571) and had non significant negative correlation with seed cotton yield. The indirect effect of inter branch distance was positive through number of monopodia per plant (0.0060), number of bolls per plant (0.0055), mean boll weight (0.0021), seed index (0.0108) and lint index (0.0030). The association recorded negative indirect effects *via* plant height (-0.0273), number of sympodia per plant (-0.0124), reproductive points on sympodia (-0.0082), sympodial length at 50 % plant height (-0.0195) and ginning outturn (-0.0053).

4.4.2.9 Seed index (g)

It was observed that this character appeared to influence seed cotton yield directly as negative value (-0.4620), seed index recorded non significant negative correlation with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through seed index to be positive value in respect of number of monopodia per plant (0.0114), reproductive points on sympodia (0.0161), sympodial length at 50 % plant height (0.0184), inter branch distance (0.0876) and ginning outturn (0.0263). The association recorded negative indirect effects *via* plant height (-0.0247), number of sympodia per plant (-0.0448), number of bolls per plant (-0.0896), mean boll weight (-0.0554) and lint index (-0.2545).

4.4.2.10 Ginning outturn (%)

The direct effect of ginning outturn on seed cotton yield was negative (-0.4280), ginning outturn recorded significant positive correlation with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through ginning outturn to be positive value in respect of mean boll weight (0.0271), reproductive points on sympodia (0.0204), sympodial length at 50% plant height (0.0245) and seed index (0.0244). The association exhibited negative indirect effects *via* plant height (-0.0007), number of monopodia per plant (-0.0116), number of sympodia per plant (-0.0451), number of bolls per plant (-0.0572), inter branch distance (-0.0394) and lint index (-0.3400).

4.4.2.11 Lint index (g)

It expressed a considerably positive direct effect of lint index on seed cotton yield (0.6884) and had significant positive correlation with seed cotton yield. The indirect effect of lint index was positive through plant height (0.0153), number of monopodia per plant (0.0104), number of sympodia per plant (0.1039), number of bolls per plant (0.1594), mean boll weight (0.0163), seed index (0.3792) and ginning outturn (0.5468). The association recorded negative indirect effects *via* reproductive points on sympodia (-0.0549), sympodial length at 50 % plant height (-0.0656) and inter branch distance (-0.0360).

4.5 Molecular marker study in cotton

4.5.1 Marker polymorphism

Analysis of microsatellites (SSR's) in 32 parents (28 barbadense lines and 4 hirsutum testers) using 40 primers. Of these, 23 primers revealed a high DNA polymorphism among parents, these 23 primers produced a total of 134 amplified profiles (Table 23). Among these, 93 were polymorphic with an average of 68.65 per cent polymorphism. Primers viz., BNL 3871, BNL 3867 and BNL 1611 gave highest (100%) polymorphism. The number of bands ranged from two (BNL 3871, BNL 1034, BNL 1227 and BNL 3867) to ten (BNL 2655, BNL 3145, BNL 1440, BNL 3171 and BNL 3994) with an average of 3.35 bands per primer. The primers viz., BNL 1034, BNL 1227, BNL 1059 and CIR 246 showed the least polymorphism (50%). DNA amplification pattern of 32 parents is shown in Plate 7.

4.5.2 Molecualr marker diversity among the parents

The similarity co-efficients (Table 24) involved in the line x tester study ranged from 57% to 96 %, with an average of 81%. Among the parental lines, the lines DB 533 x DB 534 F_4 IPS 8 and DB 533 x DB 534 F_4 IPS 1 showed highest similarity co-efficient value (96%).While, the lines DB 533 x DB 534 F_4 IPS 48 and DB 533 x DB 534 F_4 IPS 16 exhibited lowest similarity co-efficient value (57%). All the 32 genotypes showed diversity among themselves indicating that there is a considerable amount of variation, which can be exploited through appropriate breeding programme.

The dendrogram constructed from the pooled data is presented in Fig. 11, revealed three distinct clusters. One cluster involved testers and in other clusters all barbadense lines were placed which are already having proven record in giving good hybrids.

The similarity co-efficient values between the line DB 533 x DB 534 F_4 IPS 49 and the tester DH 98-27 showed 67%. It revealed that DB 533 x DB 534 F_4 IPS 49 was closely related to DH 98-27 with 67 % similarity between parents. The hybrid between DB 533 x DB 534 F_4 IPS 49 and DH 98-27 exhibited the highest yield of 2884.26 kg/ha. Similarity co-efficient (88%) value between lines and testers showed between the

line DB 533 x DB 534 F_4 IPS 52 and the tester ZCH8, the hybrid between these recorded an yield of 2040.757 kg/ha. Lowest similarity co-efficient value was noticed between the line DB 533 x DB 534 F_4 IPS 16 and tester DH 98-27 which revealed that they are far distinct from each other.This combination exhibited 2384.62 kg/ha yield.

4.5.3 Correlation between genetic distance and hybrid performance and heterosis

Genetic distance (GD) based on SSR markers were computed in Table 25. Genetic distance (GD) ranged from 0.041 to 0.429, with an average of 0.183. The result implied that each cluster dendrogram substantially reflected its own genetic relationship among parents. Overall, a low significant correlation of GD with hybrid performance and heterosis was detected in Table 26. Highly significant positive correlation were found between genetic distance (GD) and ginning outturn for F_1 performance (0.277) and heterosis over MRC 6918 (0.279) and DCH 32 (0.279), while significant positive correlation were found between genetic distance (GD) and ginning outturn for mid parent heterosis (0.237). Highly significant positive correlation were found between genetic distance (GD) and seed cotton yield for F_1 performance (0.359) and heterosis over *Bt* check MRC 6918 (0.336) and over non *Bt* check DCH 32 (0.362), while significant positive correlation were found between genetic distance (GD) and seed cotton yield for mid parent heterosis (0.226). Significant positive correlation were found between genetic distance (GD) and lint index for mid parent heterosis (0.227), F_1 performance (0.251) and heterosis over MRC 6918 (0.250) and DCH 32 (0.250), while significant positive correlation were found only between genetic distance (GD) and fiber micronaire value for F_1 performance (0.241).

4.6 *In planta* genetic transformation

Cotton breeding for insect resistance has been limited by a lack of sufficient genetic variation in the existing germplasms. Therefore, genetic engineering provides the possibility of creating varieties carrying new properties coming even from heterologous source (Lycett and Grierson 1990; Dhaliwal *et al.,* 1998). Exogenous pesticidal transgenes can be introduced into plants. *Agrobacterium* mediated plant transformation offers advantages like reducing copy number of the transgene and little co-suppression (Konez *et al.,* 1994; Hansen *et al.,* 1997).

Table 23. Analysis of SSR patterns generated using 40 primers in cotton genotypes

Sl. No.	SSR Name	Number of bands			Polymorphism
		Total	Monomorphic	Polymorphic	
1	BNL3627	0	0	0	0
2	BNL3147	0	0	0	0
3	BNL2921	0	0	0	0
4	BNL4082	0	0	0	0
5	BNL3871	2	0	2	100
6	BNL1034	2	1	1	50
7	BNL1227	2	1	1	50
8	BNL341	0	0	0	0
9	BNL1231	0	0	0	0
10	BNL1878	0	0	0	0
11	BNL3867	2	0	2	100
12	BNL116	4	1	3	75
13	BNL3511	8	2	6	75
14	BNL3031	0	0	0	0
15	BNL3085	0	0	0	0
16	BNL3569	0	0	0	0
17	BNL1421	7	2	5	71
18	BNL1495	5	2	3	60
19	BNL1521	7	3	4	57
20	BNL2655	10	3	7	70
21	BNL3145	10	2	8	80
22	BNL580	0	0	0	0
23	BNL542	0	0	0	0
24	BNL686	0	0	0	0
25	BNL3383	0	0	0	0
26	BNL1611	6	0	6	100
27	BNL1531	7	3	4	57
28	BNL2920	0	0	0	0
29	BNL2882	3	1	2	67
30	BNL1059	4	2	2	50
31	BNL3418	0	0	0	0
32	BNL3259	5	2	3	60
33	BNL1440	10	3	7	70
34	BNL3171	10	2	8	80
35	BNL3408	5	2	3	60
36	BNL3994	10	3	7	70
37	CIR246	4	2	2	50
38	CIR381	6	2	4	67
39	CIR070	0	0	0	0
40	CIR100	5	2	3	60
		134		**93**	**68.65**

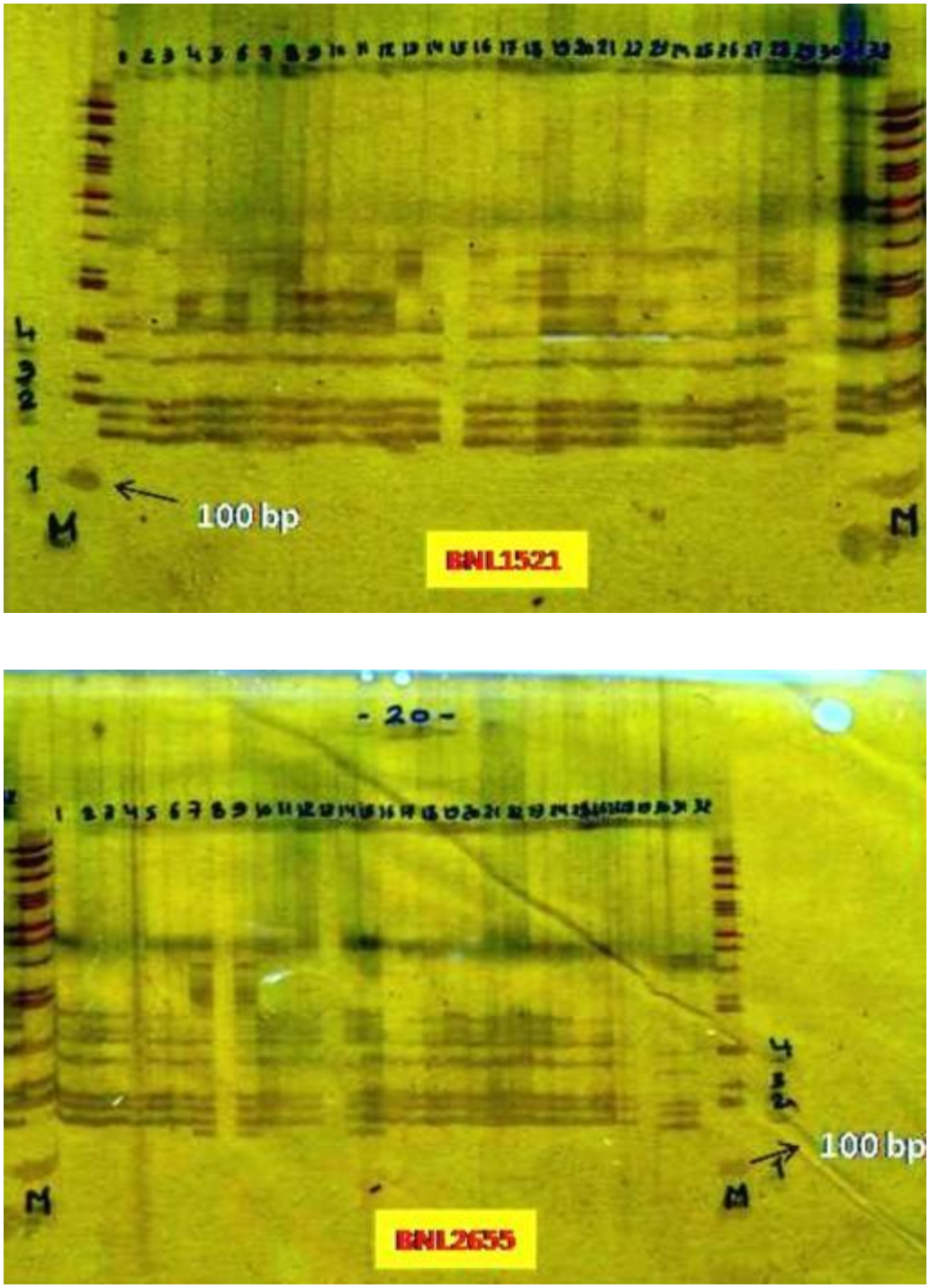


Plate 7 : DNA amplification pattern of 32 parents genotypes

Table 24. Similarity co-efficients for 32 parents computed from SSR molecular marker data

	L_1	L_2	L_3	L_4	L_5	L_6	L_7	L_8	L_9	L_{10}	L_{11}	L_{12}	L_{13}	L_{14}	L_{15}	L_{16}	L_{17}	L_{18}	L_{19}	L_{20}	L_{21}	L_{22}	L_{23}	L_{24}	L_{25}	L_{26}	L_{27}	L_{28}	T_1	T_2	T_3	T_4
L_1	**1**	0.88	0.90	0.78	0.87	0.82	0.77	0.80	0.82	0.84	0.84	0.93	0.77	0.78	0.64	0.85	0.82	0.78	0.79	0.76	0.82	0.77	0.82	0.78	0.75	0.82	0.82	0.88	0.63	0.79	0.74	0.68
L_2		**1**	0.90	0.84	0.84	0.85	0.79	0.77	0.79	0.81	0.84	0.90	0.82	0.81	0.68	0.88	0.82	0.75	0.82	0.82	0.82	0.74	0.85	0.78	0.78	0.85	0.85	0.85	0.63	0.79	0.77	0.68
L_3			**1**	0.87	0.91	0.90	0.85	0.80	0.85	0.80	0.86	0.89	0.82	0.83	0.68	0.93	0.85	0.81	0.84	0.87	0.90	0.82	0.84	0.84	0.81	0.87	0.90	0.87	0.73	0.87	0.82	0.74
L_4				**1**	0.84	0.85	0.79	0.80	0.77	0.78	0.84	0.87	0.82	0.81	0.68	0.88	0.82	0.75	0.79	0.79	0.82	0.74	0.85	0.81	0.78	0.82	0.88	0.88	0.70	0.85	0.77	0.80
L_5					**1**	0.93	0.90	0.85	0.85	0.83	0.92	0.86	0.87	0.86	0.68	0.90	0.79	0.81	0.87	0.87	0.90	0.82	0.87	0.84	0.81	0.87	0.85	0.85	0.73	0.87	0.82	0.71
L_6						**1**	0.86	0.89	0.83	0.90	0.90	0.88	0.86	0.87	0.67	0.89	0.81	0.85	0.85	0.89	0.92	0.84	0.89	0.85	0.85	0.92	0.89	0.86	0.72	0.85	0.81	0.73
L_7							**1**	0.87	0.83	0.79	0.88	0.82	0.86	0.85	0.77	0.86	0.75	0.80	0.85	0.83	0.86	0.81	0.83	0.79	0.79	0.83	0.81	0.81	0.75	0.83	0.81	0.67
L_8								**1**	0.84	0.90	0.91	0.88	0.84	0.82	0.61	0.81	0.84	0.88	0.88	0.81	0.87	0.82	0.86	0.83	0.89	0.87	0.87	0.89	0.67	0.83	0.78	0.76
L_9									**1**	0.85	0.88	0.88	0.81	0.87	0.67	0.83	0.89	0.88	0.91	0.89	0.89	0.87	0.86	0.85	0.85	0.89	0.86	0.86	0.72	0.83	0.81	0.73
L_{10}										**1**	0.92	0.89	0.79	0.83	0.64	0.82	0.82	0.86	0.84	0.81	0.87	0.82	0.84	0.84	0.84	0.90	0.85	0.87	0.60	0.81	0.79	0.74
L_{11}											**1**	0.92	0.88	0.83	0.69	0.88	0.85	0.87	0.92	0.85	0.88	0.86	0.87	0.84	0.87	0.88	0.85	0.90	0.68	0.87	0.85	0.77
L_{12}												**1**	0.85	0.83	0.66	0.90	0.90	0.87	0.87	0.82	0.88	0.83	0.90	0.84	0.84	0.88	0.90	0.96	0.68	0.84	0.80	0.77
L_{13}													**1**	0.87	0.77	0.89	0.81	0.85	0.91	0.86	0.83	0.81	0.89	0.79	0.77	0.83	0.81	0.81	0.79	0.85	0.78	0.75
L_{14}														**1**	0.75	0.90	0.79	0.86	0.84	0.93	0.90	0.85	0.84	0.84	0.78	0.87	0.85	0.82	0.73	0.84	0.79	0.74
L_{15}															**1**	0.73	0.60	0.66	0.67	0.69	0.67	0.67	0.69	0.68	0.57	0.67	0.60	0.60	0.78	0.70	0.67	0.63
L_{16}																**1**	0.86	0.85	0.85	0.91	0.89	0.87	0.86	0.82	0.79	0.86	0.89	0.89	0.75	0.88	0.83	0.78
L_{17}																	**1**	0.88	0.88	0.83	0.83	0.84	0.86	0.82	0.88	0.86	0.92	0.92	0.72	0.83	0.78	0.81
L_{18}																		**1**	0.90	0.90	0.88	0.91	0.82	0.84	0.87	0.90	0.88	0.85	0.74	0.82	0.77	0.80
L_{19}																			**1**	0.88	0.85	0.86	0.85	0.79	0.85	0.85	0.83	0.85	0.72	0.87	0.85	0.75
L_{20}																				**1**	0.91	0.93	0.82	0.88	0.85	0.91	0.89	0.80	0.78	0.85	0.83	0.75
L_{21}																					**1**	0.90	0.89	0.91	0.88	0.94	0.92	0.89	0.72	0.85	0.81	0.73
L_{22}																						**1**	0.78	0.83	0.89	0.87	0.84	0.84	0.76	0.83	0.81	0.73
L_{23}																							**1**	0.88	0.82	0.89	0.89	0.89	0.75	0.80	0.74	0.72
L_{24}																								**1**	0.84	0.91	0.91	0.82	0.77	0.82	0.77	0.77
L_{25}																									**1**	0.88	0.88	0.88	0.70	0.79	0.74	0.71
L_{26}																										**1**	0.94	0.86	0.72	0.83	0.78	0.75
L_{27}																											**1**	0.92	0.72	0.83	0.78	0.81
L_{28}																												**1**	0.66	0.83	0.78	0.78
T_1																													**1**	0.75	0.66	0.69
T_2																														**1**	0.91	0.86
T_3																															**1**	0.84
T_4																																**1**

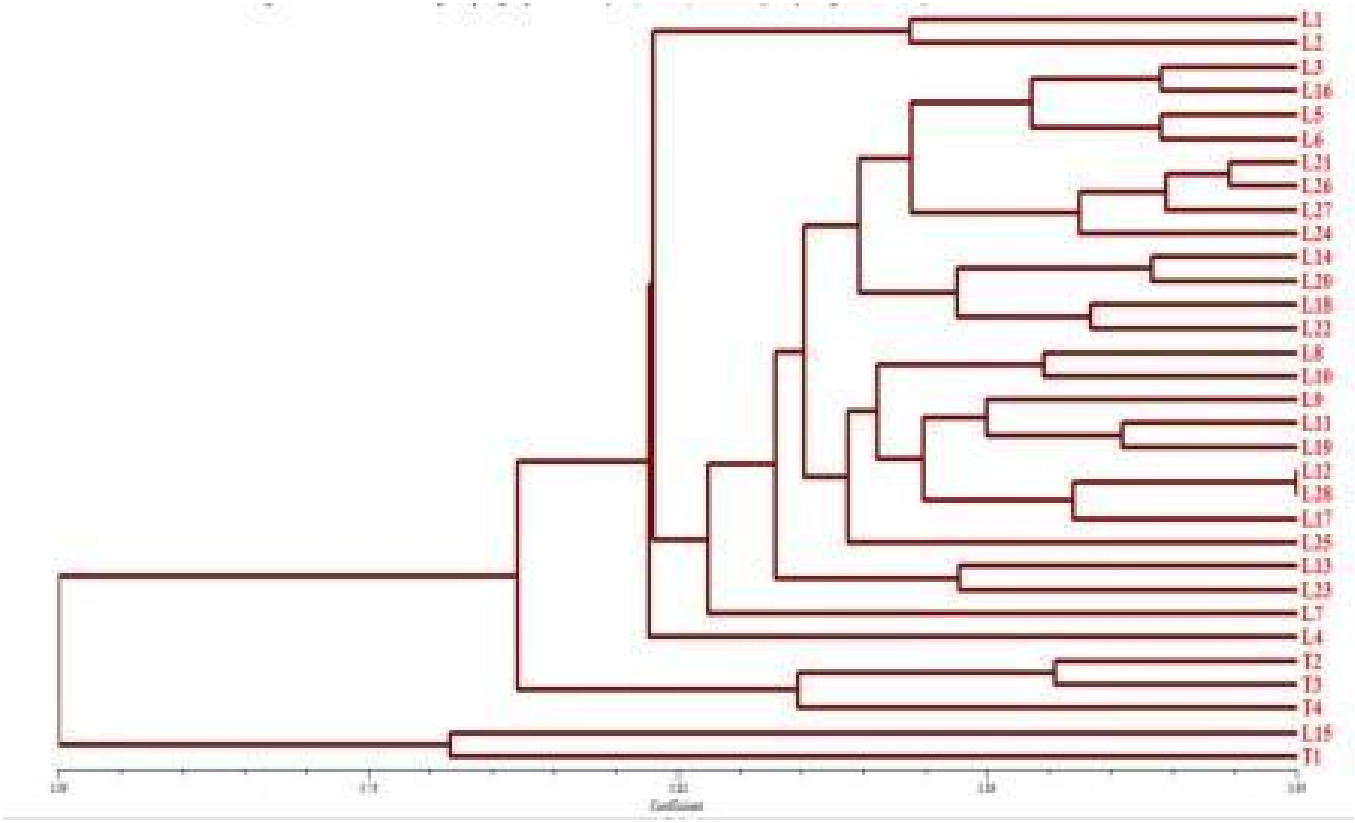


Fig 11 : Dendrograms derived from an unweighted pair group method analysis (UPGMA) cluster analysis by using Nei's similarity co-efficient based on SSR markers

Table 25. Genetic distance for 32 parents computed from SSR molecular marker data

	L_1	L_2	L_3	L_4	L_5	L_6	L_7	L_8	L_9	L_{10}	L_{11}	L_{12}	L_{13}	L_{14}	L_{15}	L_{16}	L_{17}	L_{18}	L_{19}	L_{20}	L_{21}	L_{22}	L_{23}	L_{24}	L_{25}	L_{26}	L_{27}	L_{28}	T_1	T_2	T_3	T_4
L_1	**1**	0.13	0.10	0.22	0.13	0.18	0.24	0.20	0.18	0.16	0.16	0.07	0.24	0.22	0.36	0.15	0.18	0.22	0.21	0.24	0.18	0.23	0.18	0.22	0.25	0.18	0.18	0.12	0.37	0.21	0.27	0.32
L_2		**1**	0.10	0.16	0.16	0.15	0.21	0.23	0.21	0.19	0.16	0.10	0.18	0.19	0.32	0.12	0.18	0.25	0.18	0.18	0.18	0.26	0.15	0.22	0.22	0.15	0.15	0.15	0.37	0.21	0.24	0.32
L_3			**1**	0.13	0.09	0.10	0.16	0.21	0.16	0.20	0.14	0.11	0.18	0.17	0.32	0.07	0.16	0.19	0.16	0.13	0.10	0.18	0.16	0.16	0.19	0.13	0.10	0.13	0.27	0.14	0.18	0.27
L_4				**1**	0.16	0.15	0.21	0.20	0.24	0.22	0.16	0.13	0.18	0.19	0.32	0.12	0.18	0.25	0.21	0.21	0.18	0.26	0.15	0.19	0.22	0.18	0.12	0.12	0.30	0.16	0.24	0.20
L_5					**1**	0.07	0.10	0.15	0.16	0.17	0.08	0.14	0.13	0.14	0.32	0.10	0.21	0.19	0.14	0.13	0.10	0.18	0.13	0.16	0.19	0.13	0.16	0.16	0.27	0.14	0.18	0.29
L_6						**1**	0.14	0.11	0.17	0.10	0.10	0.12	0.14	0.13	0.33	0.11	0.19	0.15	0.15	0.11	0.08	0.16	0.11	0.15	0.15	0.08	0.11	0.14	0.28	0.15	0.19	0.28
L_7							**1**	0.14	0.17	0.21	0.12	0.18	0.14	0.16	0.23	0.14	0.25	0.21	0.15	0.17	0.14	0.19	0.17	0.21	0.21	0.17	0.19	0.19	0.25	0.17	0.19	0.33
L_8								**1**	0.16	0.10	0.09	0.12	0.16	0.18	0.39	0.19	0.16	0.12	0.12	0.19	0.14	0.18	0.14	0.17	0.11	0.14	0.14	0.11	0.33	0.17	0.22	0.24
L_9									**1**	0.16	0.12	0.12	0.19	0.13	0.33	0.17	0.11	0.12	0.09	0.11	0.11	0.13	0.14	0.15	0.15	0.11	0.14	0.14	0.28	0.17	0.19	0.28
L_{10}										**1**	0.08	0.11	0.21	0.17	0.36	0.18	0.18	0.14	0.16	0.19	0.13	0.18	0.16	0.16	0.16	0.10	0.16	0.13	0.40	0.19	0.21	0.27
L_{11}											**1**	0.08	0.12	0.17	0.31	0.12	0.15	0.14	0.08	0.16	0.12	0.14	0.13	0.16	0.13	0.12	0.15	0.10	0.32	0.13	0.15	0.23
L_{12}												**1**	0.15	0.17	0.34	0.10	0.10	0.14	0.13	0.18	0.12	0.17	0.10	0.16	0.16	0.12	0.10	0.04	0.32	0.16	0.21	0.23
L_{13}													**1**	0.13	0.23	0.11	0.19	0.15	0.09	0.14	0.17	0.19	0.11	0.21	0.24	0.17	0.19	0.19	0.21	0.15	0.22	0.25
L_{14}														**1**	0.25	0.10	0.21	0.14	0.16	0.07	0.10	0.15	0.16	0.16	0.22	0.13	0.16	0.18	0.27	0.16	0.21	0.27
L_{15}															**1**	0.27	0.40	0.34	0.33	0.31	0.33	0.33	0.31	0.32	0.43	0.33	0.40	0.40	0.22	0.30	0.33	0.37
L_{16}																**1**	0.14	0.15	0.15	0.09	0.11	0.13	0.14	0.18	0.21	0.14	0.11	0.11	0.25	0.12	0.17	0.22
L_{17}																	**1**	0.12	0.12	0.17	0.17	0.16	0.14	0.18	0.12	0.14	0.08	0.08	0.28	0.17	0.22	0.19
L_{18}																		**1**	0.11	0.10	0.12	0.09	0.18	0.16	0.13	0.10	0.12	0.15	0.26	0.18	0.23	0.20
L_{19}																			**1**	0.12	0.15	0.14	0.15	0.21	0.16	0.15	0.17	0.15	0.28	0.13	0.15	0.25
L_{20}																				**1**	0.09	0.08	0.18	0.12	0.15	0.09	0.11	0.20	0.22	0.15	0.17	0.25
L_{21}																					**1**	0.10	0.11	0.09	0.12	0.06	0.08	0.11	0.28	0.15	0.19	0.28
L_{22}																						**1**	0.22	0.17	0.11	0.13	0.16	0.16	0.24	0.17	0.19	0.27
L_{23}																							**1**	0.12	0.18	0.11	0.11	0.11	0.25	0.21	0.26	0.28
L_{24}																								**1**	0.16	0.09	0.09	0.18	0.23	0.18	0.24	0.23
L_{25}																									**1**	0.12	0.12	0.12	0.30	0.21	0.27	0.29
L_{26}																										**1**	0.06	0.14	0.28	0.17	0.22	0.25
L_{27}																											**1**	0.08	0.28	0.17	0.22	0.19
L_{28}																												**1**	0.34	0.17	0.22	0.22
T_1																													**1**	0.25	0.34	0.31
T_2																														**1**	0.09	0.14
T_3																															**1**	0.16
T_4																																**1**

Table 26. Correlation co-efficient of genetic distance (GD) with F_1 performance and heterosis

Sl. No	Traits	Mid Parent heterosis	F_1 perfor mance	Heterosis over MRC 6918 check	Heterosis over DCH32 check
1	Seed cotton yield (kg/ha)	0.226*	0.359**	0.336**	0.362**
2	Number of bolls per plant	-0.347	-0.181	-0.177	-0.177
3	Mean boll weight (g)	-0.222	-0.297	-0.290	-0.290
4	Seed index (g)	0.193	0.170	0.164	0.164
5	Ginning outturn (%)	0.237*	0.277**	0.279**	0.279**
6	Lint index (g)	0.227*	0.251*	0.250*	0.250*
7	Fibre length (mm)	-	0.120	-	-
8	Fibre strength (g/tex)	-	-0.130	-	-
9	Fibre micronair value (µg/inch)	-	0.241*	-	-
10	Fibre uniformity ratio %	-	-0.056	-	-
11	Fibre maturity ratio (%)	-	0.141	-	-
12	Fibre elongation %	-	-0.119	-	-

* Significant at P = 0.05 ** Significant at P = 0.01

4.6.1 *Agrobacterium* strain and binary vectors

The disarmed *Agrobacterium* strain LBA 4402 harbouring binary vector pCAMBIA, carrying *Cry1Ac-Cry1Ec* genes linked to the CaMV35S promoter, the *nos* transcription terminator (amplified from Pb 101.1 with *MfeI* and *EcoRI* restriction sites at the ends) and *npt*-II gene under the control of nopaline synthase (nos) promoter and terminator was used in transformation studies. Hygromycin resistance as selection marker. *Cry1Ac-Cry1Ec* genes is to control *Helicoverpa armigera* and *Spodoptera litura*.

The *Agrobacterium* LBA 4402 containing above mentioned genes was maintained on solid Yeast Extract Mannitol Agar (YEM) medium (Appendix 10) containing kanamycin at 50 mg/ml and 25 mg/ml rifampicin. It was subcultured once in every 30-40 days on fresh medium and incubated at 28 ^{0}C temperature for 48 hours followed by 4-6 ^{0}C for rest of the period.

A colony of bacteria grown for 48 hours was taken from petridish and was inoculated in 150 ml of liquid YEM medium containing 50 mg/l of Kanamycin and 25 mg/l rifampicin and incubated for 45-48 hours at 22 ^{0}C under orbital shaker with 150 rpm.When bacterium growth reached to OD (600 nm) of 0.6 g pellet of bacterium obtained after centrifuge at 8000 rpm for 5 minute. It was resuspended in 150 ml of MS medium and 150 µM of acetosyringone was added to the *Agrobacterium* culture before 30 minute of its use.

4.6.2 Designing and chemical synthesis of the chimeric *Cry1 Ac* and *Cry1EC* genes

A 1.9 kbp double stranded DNA was theoretically designed (Fig. 12) by modifying the sequence of natural *Cry1Ea* gene, to encode the chimeric d-endotoxin *Cry1EC*. Plant-preferred translation initiation context (Sawant *et al*., 2001) and codons were used in designing the gene. The putative transcription termination signals (AAUAAA and its variants), mRNA instability elements (ATTTA) and potential splice sites were eliminated and long hairpin loops were avoided. The whole sequence was synthesised as 58 overlapping oligonucleotides. The oligonucleotides were synthesised on Gene Assembler Special DNA synthesiser, purified on urea – polyacrylamide gel and assembled in four parts (Fig. 13) by assembly polymerase chain reaction (Singh *et al*., 1996). Eight oligonucleotides were assembled into a BamHI – XhoI fragment (340 bp long), 12 into a XhoI – AccI fragment (511 bp long), 24 into a AccI – ApaI fragment (680 bp long) and 14 into a ApaI – EcoRI fragment (519 bp long). These were cloned in pBluescript SK+ cloning vector.

At least four clones were sequenced in each case to locate the errors in synthesis. Sequencing was done on model 373 automatic DNA sequencer using fluorescent – dye termination cycle sequencing kit. The errors were corrected by exchanging the regions containing mutations with those from correct clones. Finally, the error-free DNA fragments were stepwise ligated to give about 1.9 kbp full length gene.

Cry1Ac protein (endotoxin) produced in *Bt* transgenic cotton is effective in controlling *Helicoverpa armigera*. The *Cry1Ac* (1915bp) gene cloned earlier from native *B. thuringiensis* at UAS, Dharwad was considered for modification (Fig. 14) (Kumaraswamy, 2005). The purpose of redesigning *Cry1Ac* was to create a synthetic gene that would be expressed at high level in plant cells.

4.6.3 PCR amplification

DNA extracted from leaves of transformants was used as template DNA. Taq DNA polymerase, Taq Buffer, dNTPs, Mgcl2 and *Primers* were used for cyclic amplification of DNA. Following *Cry1Ac-Cry1Ec* specific primers were used for confirming transgenic.

Sequence of *Cry1Ac-Cry1Ec* primers:

Forward 5^{I} CCAGAGAACGAGATC TTGGAC 3^{1}

Reverse 3^{1} AGTATTGTACCATCTAACAGCGTA 5^{I}

Sequence of *npt*-II primers:

Forward 5^{I} GAG GCD ATT CGG CTA TGA CTG 3^{I}

Reverse 3^{I} ATC GGG AGG GGC GAT ACC GAT 5^{I}

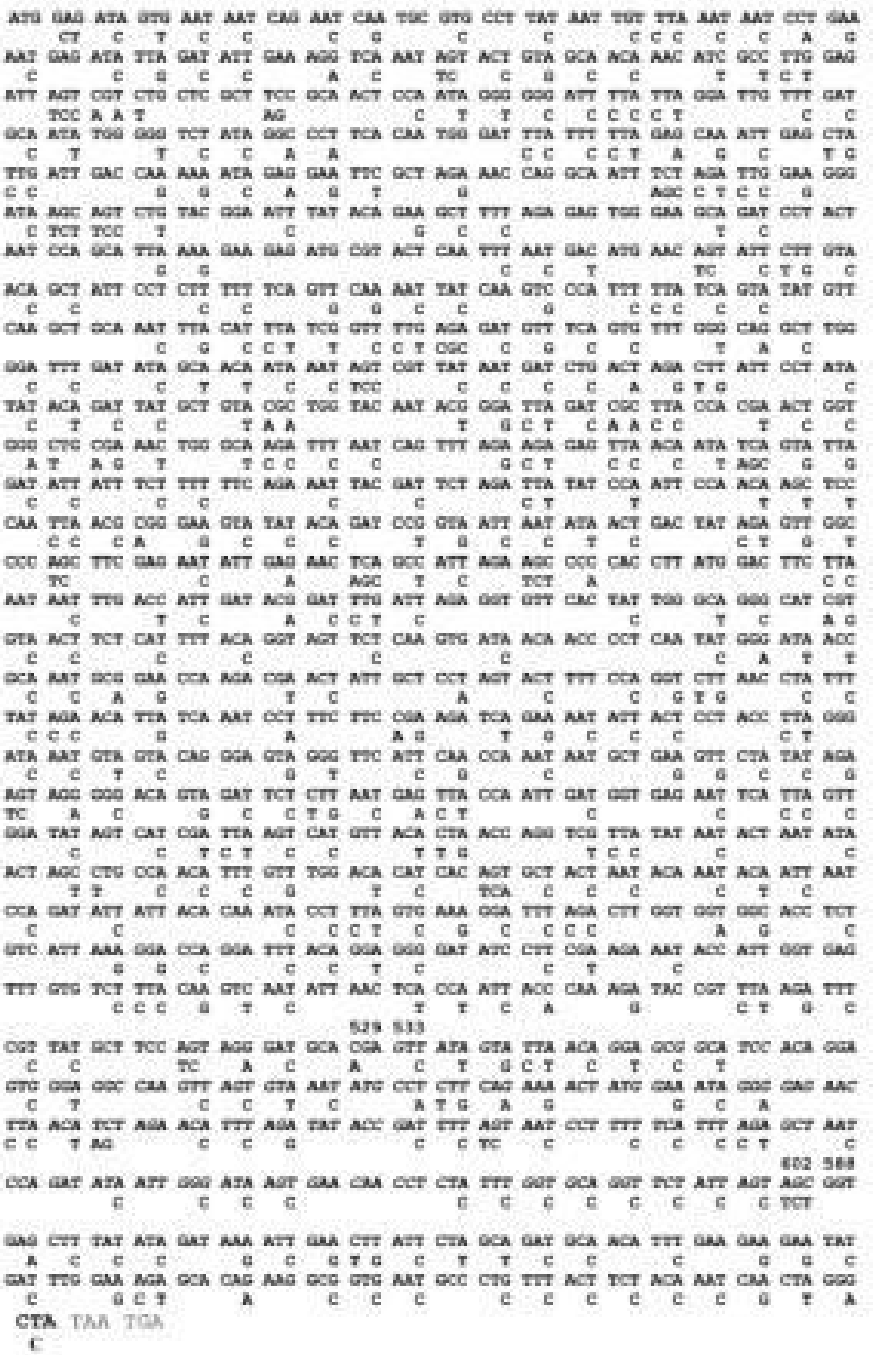


Fig 12 : Designing of the gene coding for chimeric d-endotoxin *Cry1Ec*

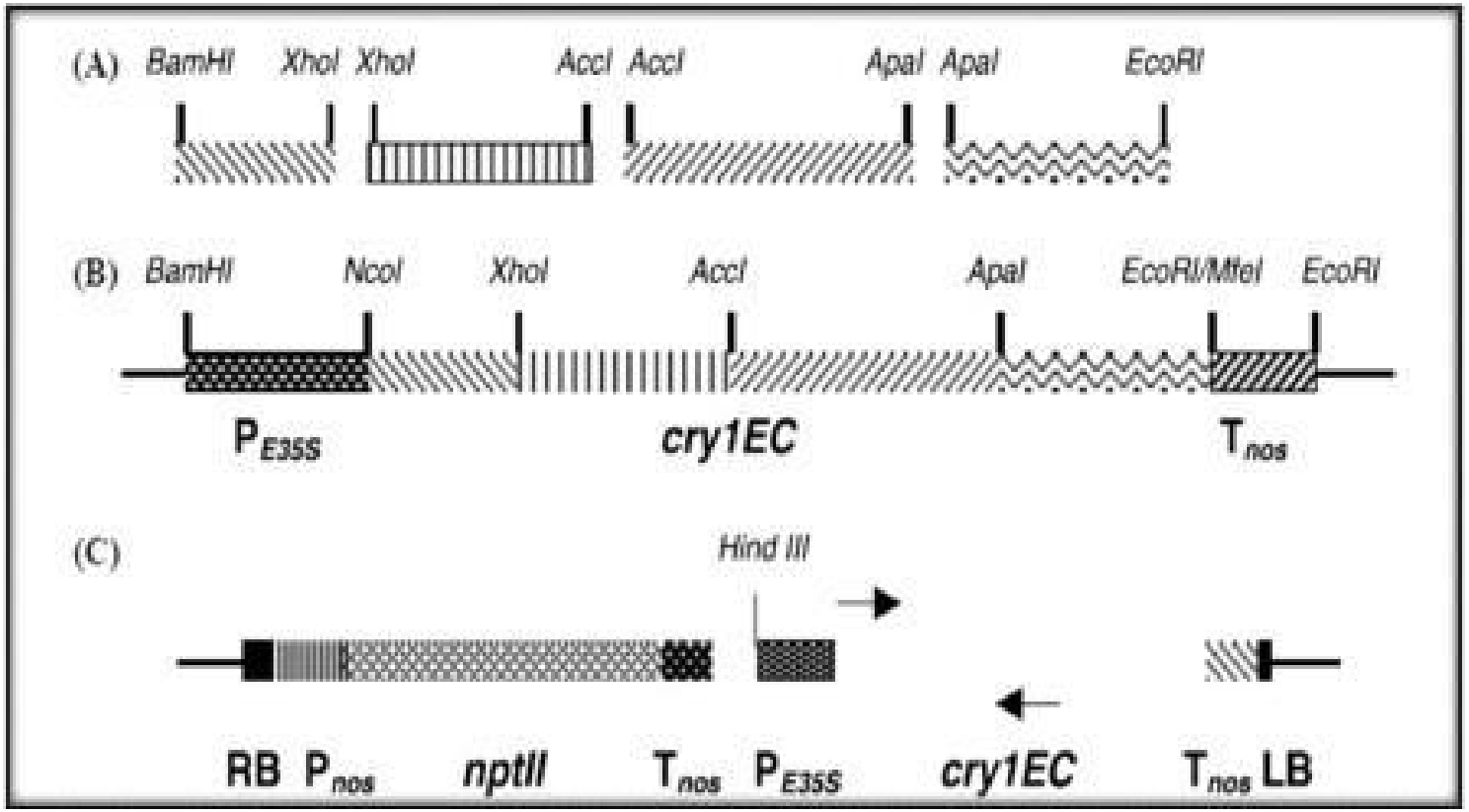


Fig 13 : Construction of *Cry1Ec* for plant transformation

Fig 14 : Gene sequence of M *Cry1Ec (*1915bp)

After the completion of required cycles of amplification, the samples were stored at 4 ^{0}C in a refrigerator until further use. Here, for amplification of plasmid we standardized the protocol by using 6 temperatures (60.6 ^{0}C, 62.3 ^{0}C, 57.2 ^{0}C, 56.5 ^{0}C, 55.0 ^{0}C and 54.1 ^{0}C). The results showed that the plasmid has amplified at four temperatures (57.2 ^{0}C, 56.5 ^{0}C, 55.0 ^{0}C and 54.1 ^{0}C) (Plate 8).

4.6.4 *In planta genetic* transformation

Several methods of injuring the plant target tissue for transformation and regeneration were examined in an effort to improve the efficiency of production of transgenic cotton. *Agrobacterium tumefaciens* strain carrying *Cry1 Ac- Cry1Ec* was used for transformation of RCR4 genotype. The effect of wounding on established seedling, effect of vertical cut on well established seedling and regeneration was studied.

The seedlings in pots were co-cultivated with solid *Agrobacterium* culture after cutting the meristematic tip with sharp knife. The number of seedlings co-cultivated, number of seedlings established and the number of seedlings showing transformed status are presented in Table 27. PCR was performed to confirm the presence of the transgene in the plants that were selected to be advanced further. The results showed that non of plants had trangenes *Cry1Ac- Cry1Ec* as detected through PCR amplification.

In planta genetic transformation was carried out and the plants were tested in T_0 generation by means of PCR amplification for the genes *Cry1Ac- Cry1Ec*. The results obtained were not amplified the *Cry1Ac- Cry1Ec.* Hence the transformation of the genes was not up to mark and the plants of T_1 generation are also not confirmed.

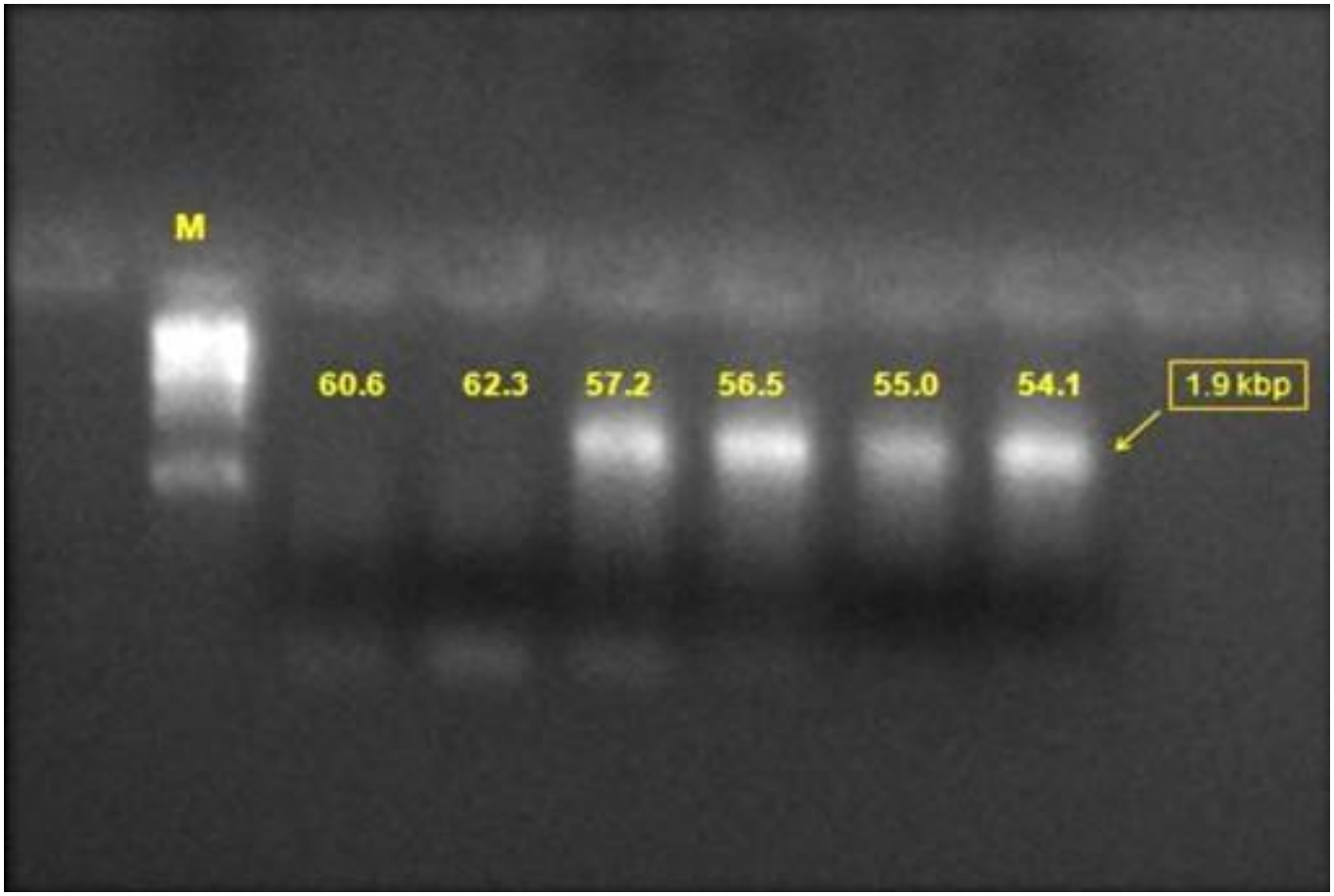


Plate 8 : Plasmid amplification at four temperatures

Table 27. Number of cotton seedlings co-cultivated, established and transformed in *planta* genetic transformation study

Genotype	Group	Total number of seedlings	Number of seedlings co-culivated	Number of plants established	Number of plants transformed
RCR4	Group 1	100	92	81	Nil
	Group 2	111	97	88	Nil
	Group 3	117	87	75	Nil
	Group 4	90	77	62	Nil
Total		**418**	**353**	**306**	**Nil**

DISCUSSION

Cotton is one of the most important commercial crops of India cultivated mainly for its fiber and other by products. Cotton, through cloth, has influenced the culture and civilizations. In the process of forming clothes and garments, it provides livelihood and employment to workers engaged in cloth making, designers, traders and the like. Cotton is one of the few crops which are accessible to development of genotypes as varieties and at the same time amenable for commercial exploitation of heterosis. Development of several hybrids during the last decade has contributed to a quantum jump in cotton productivity. Though cotton production in the country has registered marked improvement in recent years, the yield levels of hybrids appear to have reached stagnation. The important reasons attributed for this is the lack of systematic efforts made to develop hybrid oriented populations, derived lines with improved combining ability and develop new hybrids based on such genetically diverse high combiner lines.

The success of heterosis breeding in any crop depends on the choice of the genetic distance of parents. The concept of combining ability given by Sprague and Tatum (1942) reiterates' the importance of suitable parents to nick well in the expression of heterosis. Thus, evaluation of various lines for their nickwell ability is a pre-requisite for the final selection of parental lines in hybridization programme. Magnitude of heterosis in any cross is determined by genetic diversity and degree of dominance (Falconer, 1981).

In the recent years the concept of developing heterotic populations is put to test in self pollinated crops like cotton, segregating populations based on diverse pairs of genotypes can be the ideal base material required for implementing procedures like reciprocal selection for improving combining ability. In hybrid research study on cotton, a large number of crosses involving varietal lines are used for assessing combining ability status. On constantly observing the most potential crosses attempts are made to infer about the causes of high heterosis.

If more lines are found to be giving superior crosses with a tester then it is possible to initiate multiple crosses among such lines selected for combining ability and this can lead to creation of sub population (broad gene pool) of recombination variability for combining ability as the population developed in this manner will be improved in ability to combine with the tester. This heterotic gene pool can be exploited for developing superior hybrid combinations with the tester concerned (Patil and Patil, 2003).

India's extra long staple (ELS) cotton production has been stagnant over the last few years. There are very few Indian cotton varieties (DCH 32, TCH-213 and Suvin grown mostly in Southern India) that meet international ELS specification. The fiber quality and yields of these varieties have deteriorated in recent years causing marketing problems and lower returns to growers. Therefore, farmers are increasingly shifting to long staple varieties (Bunny, Brahma and other 30-34 mm cotton varieties), which have higher yields and fewer quality problems. Efforts to improve the productivity of ELS parent lines have been met with limited success. Therefore, it is of utmost importance to improve the existing ELS barbadense varieties and hybrids and to develop more productive varieties and hybrids involving barbadense genotypes.

The conventional pedigree method and other breeding procedures have been successfully used for improving the *per se* performance with respect to yield and yield components. These approaches have not been utilized to improve combining ability as a trait in cotton. In the present study, it was hence, decided to create recombinational variability for combining ability and to assess the nature and magnitude of variability for combining ability in F_4 generation. The genotypic differences of parents used in developing populations influences magnitude and nature of recombinational variability released for different traits. There is a need of potential differences between parents to ensure larger and more useful variability released in the populations developed. Keeping this in mind, the base material of the present study was identified from the detailed initial study involving large number of crosses. In this study, two barbadense and four hirsutum lines giving best hybrid (H×B), combinations between them were selected. To create recombinational variability, the two barbadense genotypes were crossed to get F_1 and it was advanced to F_4 generation. In the present phase of this continuing study, the F_4 lines of this population (barbadense x barbadense) is utilized for assessing recombinational variability for combing ability against selected hirsutum testers. Nature and magnitude of variability for combining ability was assessed against hirsutum tester included in the heterotic box.

In the present scenario it is necessary to increase production of ELS (Etra Long Stable) cottons. Present study aimed at developing heterotic groups of hirsutum *vs* barbadense cottons, based on a detailed line x tester (4 barbadense lines x 23 hirsutum testers). DB 533 and DB 534 the selected barbadense elite combiners were utilized to create recombinational variability for combining ability. These two barbadense varietal lines (DB 533 and DB 534) were crossed and advanced to F_4 generation for creating recombinational variability for combining ability against the hirsutum testers (DH 98-27 (T_1), ZCH 8 (T_2), 178-24(T_3) and DH 18-31 (T_4)).

In any hybrid programme, a large number of crosses need to be made, while only few of the hybrids will show good performance over the standard check. This process is extremely labour intensive, time- consuming and tedious. Molecular markers increasingly detect locus differences among genotypes and represent a powerful tool for the assessement of genetic diversity in plant species (Tanksley, 1983).

A number of efforts have been made in various crop plants to investigate the relationship between DNA marker- based genotype variation of the parents to be uased in a hybrid breeding programme and heterosis with varying results. Studies in maize (Lee *et al*., 1989; Goldshalk *et al.,* 1990; Smith *et al*., 1990; Dudley and Saghai, 1991; Stuber *et al.*, 1992; Betran *et al.,* 2003), rice (Xiao *et al*., 1995; Zhang *et al*., 1996; Zho *et al*., 1999) and wheat (Martin *et al.,* 1995) gave different and contradictory results. Correlation of GD with hybrid performance and heterosis in inter specific hybrids were non- significant. Therefore, they were not generally useful for heterosis prediction. However, it was a better predictor for ginning outturn, lint index, seed cotton yield and fiber micronaire value. Bernardo (1992) investigated that inadequate genome coverage, random dispersion of molecular markers and different levels of dominance could be the reasons for low correlation between molecular distances and heterosis and/or F_1 performance. The existence of multiple allelism and epistasis could also cause the low correlation of GD and F_1 performance/ heterosis. Seed cotton yield and its component traits, as quantitative traits, were controlled by complex QTLs which show large variation in different environments. On the other hand, the fibre micronaire value may be controlled by relatively simple QTLs. In this study apparently there was insufficient linkage between markers and QTLs to predict hybrid performance. This may be why correlations of GD with hybrid performance and heterosis were mostly non significant, but were significant for other characters.

The results obtained from the present investigations have been discussed under the following headings.

- Development of heterotic groups (hirsutum *vs* barbadense*)* based on combining ability and hybrid performance
- Evaluation of recombinational variability for combining ability
- Correlation co-efficient analysis
- Path co-efficient analysis
- Molecular marker study in cotton
- *In planta* genetic transformation

5.1 Development of heterotic groups (hirsutum vs barbadense) based on combining ability and hybrid performance

In hybrid research study on cotton, large number of crosses involving varietal lines are used for assessing combining ability status. On constantly observing the most potential crosses attempts are made to infer about the causes of high heterosis. What are the combinations that give potential crosses? What would be the probable cause for high potentiality revealed by the F_1? What is the genetic base or is there any physiological mechanism linked to high productivity of F_1 etc., are the questions which are examined and on the basis of the information available, heterotic groups are developed (Patil *et al*., 2011).

The most potential crosses observed in present study have been examined and based on this the combining ability behavior (Pattern) of the line involved is determined. With the help of this information diverse groups are formed which are capable of giving potential hybrids between them.

A study of set of hybrids involving the line as a common parent gives an idea about the combining ability pattern of the concerned line. The higher or lower performance of the hybrids is itself taken as reflection of genetic distance existing between the parents. It has been possible to identify

heterotic combinations (potential crosses) based on their percent superiority over the commonly used check. When these crosses show up to be consistently potential, they are considered while forming heterotic groups involving parents of such crosses.

The exercise of identifying diverse groups is a continuous process because the new breeding lines developed and stabilized and those lines obtained from other sources are included in developing crosses and these lines could be added in different heterotic groups after studying their combining ability behavior (pattern) by crossing with representative genotypes of different groups. Thus the grouping of genotypes is continuously revised and refined.

In the recent years, the concept of developing heterotic groups is put to test in self pollinated crops like cotton. Segregating populations based on diverse pairs of genotypes can be the ideal base material required for implementing procedures like reciprocal selection for improving combining ability (Patil and Paltil 2003, Patil *et al.,* 2011).

5.1.1 Line x Tester analysis for confirmation of inter specific heterotic groups (YHB)

The research programme on development of hybrids at UAS Dharwad has focused attention on developing heterotic groups, meant for evolving intra hirsutum hybrids and inter specific hybrids. Efforts are made to develop different heterotic groups like Stay green x Compact, Robust x Compact, Robust x Higher RGR and Stay green x higher RGR *i.e.* (Patil and Patil, 2003). These studies have also shown ways of exploiting heterotic groups by following novel approaches of creating recombinational variability for combining ability and exploiting the same through reciprocal selection for combining ability (Mallikarjun, 2005 and Somashekar, 2006).

The ongoing study at ARS, Dharwad on evaluation of inter specific hybrids led to formation of a heterotic box of two barbadense lines DB 533 and DB 534 and hirsutum lines DH 98-27, ZCH 8, 178-24 and DH 18-31. To create recombinational variability DB 533 and DB 534 crossed was made and material was advanced to F_4 generation with an objective of evaluating recombinational variability for combining ability in F_4 generation. The line x tester study was planned to assess the relative potential of these barbadense and hirsutum lines and confirmed appropriateness of the choice of this heterotic box of two barbadense and four hirsutum lines. The objective of this study was to determine the relative ranking of the selected barbadense and hirsutum lines when compared with the new lines developed during this period.

The preliminary RBD analysis was carried out for eight characters under study for 92 crosses and three commercial checks RAHB 87, MRC 6918 and DCH 32. 'F' test indicated highly significant variation among the crosses for all the eight characters except plant height and number of sympodia per plant. These results are in confirmity with the studies of Vande and Thombre (1983), Vaman *et al.* (1985), Mirkhmedov *et al.* (1987), Mehla *et al.* (1988), Simongulyan and Kim (1990), Munasov *et al.* (1990), Tagiev (1991), Virk *et al.* (1991), Dever and Gannaway (1992) and Akumurdov and Chapau (1992). These authors also observed substantial amount of variability for seed cotton yield among F_2, F_4 and F_5 generations of different cotton crosses. Among the lines (males), the mean sum of squares (MSS) were not significant for all characters except seed cotton yield and mean boll weight. Testers (females) exhibited significant difference for four characters seed index, ginning outturn, lint index and seed cotton yield. Whereas, line x tester interaction were highly significant for all characters except plant height and number of sympodia per plant.

The estimates of variance due to general combining ability (GCA), variance due to specific combining ability (SCA), the magnitude of SCA variance were greater than GCA variance for all 8 characters and the variance ratio was less than half in these traits. Singh *et al*. (1983), Mandloi *et al.* (1998), Neelima (2002), Ahuja and Tuteja (2003), Muthuswamy *et al*. (2003), Saravanan *et al*. (2003), Verma *et al*. (2004), Mohammad *et al*. (2007), Paulo Antonio de Aguiar *et al.* (2007), Ashok Kumar and Ravikesavan (2008), Kalpande *et al*. (2008), Kumboh *et al*. (2008), Cetin Karademir *et al*. (2009) and Deosarkar *et al*. (2009b) also confirmed the above findings for seed cotton yield character.

The line x tester study was planned to assess the relative potential of the barbadense and hirsutum in developing inter specific hybrid combinations. The objective of this part of the study was to determine the relative of 4 barbadense and 23 hirsutum lines. Barbadense were used as lines and hirsutum were used as testers.

Among four barbadense lines positive *gca* effects for seed cotton yield was recorded by DB 533 and DB 534 confiriming the potential of these barbadense lines in developing productive inter specific hybrids. Among 23 hirsutum testers, four testers DH 98-27, ZCH 8, 178-24 and DH 18-

31exhibited good positive values of *gca* effects for seed cotton yield and were located among top ten testers ranks 2, 8, 1 and 7 respectively when compared to other hirsutum testers (Table 6 and Table 28).

Among these different inter specific hybrids, the mean performance of eight crosses [DH 18-31 x DB 533, DH 98-27 x DB 533, 178-24 x DB 533, ZCH 8 x DB 533, DH 18-31 x DB 534, DH 98-27 x DB 534, 178-24 x DB 534 and ZCH 8 x DB 534] associated with this heterotic box was found to be 2336 kg/ha as compared to the overall mean of line x tester crosses which was 2036 kg/ha. This accounted for 15% superiority over the mean of all crosses (Appendix 1).

Pooled score for *gca* effect

Simple pooled *gca* score method

In this approach, significant *gca* effect in desirable direction is given positive weightage (+1) and negative weighatage (-1) is given for *gca* effect in undesirable direction (Arunachalam and Bandopadhyay, 1979). These values are added over different yield influencing characters to arrive at pooled score of *gca* effects. The inherent disadvantage with this system is that all the parents with significant *gca* effects in desirable direction get the same score (positive). Hence, it is not possible to quantify the magnitude of difference existing among the genotypes of this group which get a positive score. Therefore, it is necessary develop a system of working out pooled scores of *gca* by utilizing the actual *gca* values and ensuring quantification of every possible difference existing in *gca* effects between only two parents.

Per cent *gca* method

When the actual *gca* values are added across characters to arrive at pooled score, problem arises because of difference in unit of measurement of each character. Absolute values of *gca* effects may be big (plant height) or small (boll weight) depending on the character and if used, the importance of the character may not be projected correctly. If the raw values of *gca* effects are added across the characters, the character with higher *per se* effect influence the pooled scores most as against the character with low *per se gca* values. To overcome this disadvantage, the raw *gca* values have to be converted into per cent *gca* values.

Thus, by working out per cent *gca* values, the minute differences in *gca* values are also focussed and the possible problem arising out of the differences in unit of measurement, high and lower *per se gca* values associated with the type of character concerned are overcome.

Weighted per cent *gca* method

In this method further improvement is brought about in arriving at the pooled *gca* scores of the parents. In per cent *gca* method, the per cent *gca* values are straight away added across the characters which means each character including yield and yield components are all given equal weightage. The experience of the breeders would suggest sometimes that, in arriving the pooled score, it is desirable to attach differential weightages to each of the characters studied depending upon its economic importance, contribution to yield *etc.* These weightages can be multiplied with per cent *gca* values of corresponding characters and then added to arrive at the pooled *gca* score for each parent. In the present study weightages for different yield related characters were worked out by consulting the senior breeder related to cotton *viz.,* Dr. S. S. Patil, Senior Scientist, Agricultural Research Station, Dharwad and Dr. B. C. Patil, principal scientist (Plant physiology), ARS, Dharwad Farm.

Based on simple pooled *gca* score method (Table 29), the hirsutum testers DH 13-7 and DH 98-27 (Decreasing order) are recognized as the most potential parents. Among the barbadense lines, the lines DB 534 and DB 533 based on simple pooled *gca* score method showed the most general combiner parents. Based on per cent *gca* method, the hirsutum testers DH 13-7, DH 98-27 and DH 45-23 (Decreasing order) were the most potential combiners (Table 30). Among the barbadense lines, the lines DB 5343 and DB 533 based on per cent *gca* score method showed the most potential parents. Similarly, based on weighted *gca* method the most potential combiners were found to be the hirsutum testers DH 13-7, DH 98-27 and DH 18-31. Among the barbadense lines, the lines DB 534 and DB 533 based on weighted *gca* method is the most potential parents (Table 31).

Table 28. Combining ability status of most potential line x tester inter specific crosses (YHB) with respect to yield

Sl. No.	Potential crosses	Seed cotton yield (kg/ha)				Fiber strength (g/tex)	Rank	BMC
		per se	*gca* effect		*sca* effect			
			gca of line	*gca* of tester				
1	DH 18-31 x DB 533	3128.72	242.92**	329.65**	528.15**	24.83	1	**BMC**
2	DH 13-7 x DB 533	3047.62	242.92**	271.47**	505.24**	23.57	2	
3	ZCH 8 x DB 533	2868.23	242.92**	216.37**	380.94*	23.91	3	**BMC**
4	DH 46-1 x DB 533	2808.03	242.92**	192.11*	345*	25.80	4	
5	DH 23-4 x DB 534	2753.58	75.54*	269.95**	562.18**	25.80	5	
6	DH 98-27 x DB 532	2709.09	-4.92	333.42**	352.59*	23.29	6	
7	DH 37-4 x DB 533	2641.42	242.92**	144.46	226.05	25.99	7	
8	DH 11-8 x DB 534	2635.81	75.54*	149.00	565.35**	25.23	8	
9	DH 49-1 x DB 533	2615.40	242.92**	164.65*	179.83	25.83	9	
10	ZCH 8 x DB 532	2550.55	-4.92	216.37**	311.09*	26.17	10	
11	DH 98-27 x DB 533	2525.42	242.92**	333.42**	-78.91	23.45	11	**BMC**
12	DH 35-17 x DB 531	2524.83	-313.54**	307.44**	320.86*	24.48	12	
13	178-24 x DB 533	2487.64	242.92**	236.63**	-19.9	23.88	13	**BMC**
	MRC 6918 *Bt* check	**2358.05**						
	Mean of lxt crosses	**2036.47**						
	Mean of bench mark crosses	**2335.88**						

* Significant at P = 0.05 ** Significant at P = 0.01 BMC: Bench Mark Crosses

Table 29. Pooled scores of hirsutum testers and barbadense lines based on Simple pooled *gca* score

Sl. No	Parents	Seed cotton yield (kg/ha)	Plant height (cm)	No. of sympodia	No. of bolls	Mean boll weight (g)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Pooled gca
		1	2	3	4	5	6	7	8	
	Hirsutum Testers									
1	**DH 98-27**	1	0	0	0	0	0	1	1	3
2	**DH 18-31**	1	0	0	-1	1	0	0	0	1
3	DH 35-17	1	0	0	1	-1	-1	0	0	0
4	DH 13-7	1	0	0	1	0	1	1	1	5
5	DH 23-4	1	0	0	-1	-1	1	0	0	0
6	DH 24-4	1	0	0	-1	0	0	0	0	0
7	**178-24**	1	0	0	-1	0	0	0	0	0
8	**ZCH 8**	1	0	0	1	-1	-1	0	0	0
9	DH46-1	1	0	0	0	0	0	-1	-1	-1
10	DH 49-1	1	0	0	0	1	0	-1	-1	0
11	DH 11-8	0	0	0	-1	0	1	0	1	1
12	DH 37-4	0	0	0	1	0	-1	0	0	0
13	DH 82-3	0	0	0	0	-1	0	0	0	-1
14	DH 91-1	0	0	0	-1	-1	0	0	0	-2
15	DH 53-2	0	0	0	0	1	-1	0	0	0
16	DH 23-1	0	0	0	0	0	0	0	0	0
17	DH 45-23	0	0	0	-1	1	1	0	0	1
18	DH 23-21	-1	0	0	1	-1	0	1	1	1
19	DH 31-2	-1	0	0	0	1	0	0	0	0
20	DH 14-2	-1	0	0	0	0	0	0	0	-1
21	DH 75- 23	-1	-1	0	-1	1	-1	0	0	-3
22	DH 29-1	-1	0	0	1	0	0	-1	-1	-2
23	DH 8-7	-1	0	0	1	0	0	0	0	0
	Barbadense Lines									
1	**DB 533**	1	0	0	-1	0	0	0	0	0
2	**DB 534**	1	0	0	1	1	1	0	0	4
3	DB 532	0	0	0	1	-1	0	-1	0	-1
4	DB 531	-1	0	0	0	-1	0	0	0	-2

Table 30. Pooled scores of hirsutum testers and barbadense lines based on per cent pooled *gca* score

Sl. No	Parents	Seed cotton yield (kg/ha)	Plant height (cm)	No. of sympodia	No. of bolls	Mean boll weight (g)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Pooled gca
		1	2	3	4	5	6	7	8	
	Hirsutum Testers									
1	**DH 98-27**	16.37	-2.87	5.51	0.43	-1.35	1.62	10.32	16.11	46.14
2	**DH 18-31**	16.19	1.61	-5.76	-9.95	6.76	8.18	-3.34	2.72	16.40
3	DH 35-17	15.10	3.74	5.37	16.20	-10.54	-6.48	0.11	-6.69	16.81
4	DH 13-7	13.33	-2.02	-1.37	4.56	1.89	9.56	5.32	17.57	48.85
5	DH 23-4	13.26	1.02	-1.37	-9.77	-4.05	5.30	-1.62	3.35	6.11
6	DH 24-4	12.65	-0.55	-4.88	-7.29	-0.27	-3.89	-1.76	-6.49	-12.48
7	**178-24**	11.62	1.53	-0.77	-10.23	3.24	-1.05	-1.08	-0.63	2.63
8	**ZCH 8**	10.62	2.76	1.86	6.19	-4.59	-11.35	4.67	-6.28	3.89
9	DH46-1	9.43	-2.58	-4.88	-1.23	0.00	2.84	-14.34	-16.95	-27.70
10	DH 49-1	8.09	-1.58	0.84	2.79	9.19	-0.57	-7.76	-11.09	-0.10
11	DH 11-8	7.32	-7.83	-5.76	-3.15	-1.89	5.45	3.56	9.83	7.51
12	DH 37-4	7.09	2.49	-6.78	4.96	-2.70	-7.78	3.09	-3.97	-3.60
13	DH 82-3	6.98	-1.14	-1.23	-0.15	-7.57	-2.59	4.42	2.93	1.65
14	DH 91-1	3.30	2.88	5.23	-7.29	-4.05	-1.54	-3.38	-6.28	-11.12
15	DH 53-2	2.81	-1.04	-0.77	-1.68	4.59	-5.59	2.98	-1.88	-0.59
16	DH 23-1	1.60	-1.09	4.36	1.44	1.08	0.57	0.11	0.21	8.27
17	DH 45-23	1.26	3.89	7.27	-3.77	4.05	9.48	-1.11	8.37	29.44
18	DH 23-21	-22.49	0.67	3.62	15.87	-8.11	4.13	5.20	11.44	10.33
19	DH 31-2	-23.90	3.78	0.98	-2.51	4.59	-0.16	1.87	2.51	-12.84
20	DH 14-2	-26.44	1.93	2.14	2.85	-2.43	0.16	0.50	1.46	-19.82
21	DH 75- 23	-27.35	-8.66	-5.48	-8.06	4.59	-8.48	3.13	-4.39	-54.71
22	DH 29-1	-28.37	0.36	1.55	4.07	3.78	1.78	-13.08	-15.27	-45.18
23	DH 8-7	-28.46	2.69	0.39	5.67	3.78	0.41	2.26	3.97	-9.28
	Barbadense Lines									
1	**DB 533**	11.93	0.71	-0.41	-4.62	0.00	-1.91	0.86	-0.56	5.98
2	**DB 534**	3.71	-2.34	-0.39	3.25	4.32	2.15	0.83	2.97	14.49
3	DB 532	-0.24	0.46	0.68	1.59	-2.16	-0.11	-2.20	-2.93	-4.91
4	DB 531	-15.40	1.17	0.12	-0.21	-2.43	-0.12	0.54	0.52	-15.82

Table 31. Pooled scores of hirsutum testers and barbadense lines based on weighted per cent pooled *gca* score

Sl. No	Parents	Seed cotton yield (kg/ha)	Plant height (cm)	No. of sympodia	No. of bolls	Mean boll weight (g)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Pooled gca
		1	2	3	4	5	6	7	8	
	Hirsutum Testers									
1	**DH 98-27**	163.72	-5.73	16.54	2.36	-9.46	6.48	56.74	104.71	335.36
2	**DH 18-31**	161.87	3.23	-17.28	-54.75	47.30	32.74	-18.39	17.68	172.40
3	DH 35-17	150.97	7.49	16.12	89.11	-73.78	-25.93	0.59	-43.51	121.05
4	DH 13-7	133.30	-4.04	-4.11	25.10	13.24	38.25	29.26	114.23	345.23
5	DH 23-4	132.56	2.04	-4.11	-53.74	-28.38	21.20	-8.90	21.76	82.44
6	DH 24-4	126.47	-1.10	-14.65	-40.09	-1.89	-15.56	-9.69	-42.15	1.33
7	**178-24**	116.20	3.06	-2.32	-56.26	22.70	-4.21	-5.93	-4.08	69.15
8	**ZCH 8**	106.25	5.52	5.58	34.03	-32.16	-45.38	25.70	-40.79	58.75
9	DH46-1	94.33	-5.16	-14.65	-6.74	0.00	11.35	-78.88	-110.15	-109.89
10	DH 49-1	80.85	-3.16	2.53	15.33	64.32	-2.27	-42.70	-72.07	42.83
11	DH 11-8	73.17	-15.67	-17.28	-17.35	-13.24	21.78	19.57	63.91	114.89
12	DH 37-4	70.94	4.98	-20.34	27.29	-18.92	-31.12	17.00	-25.84	24.00
13	DH 82-3	69.83	-2.28	-3.69	-0.84	-52.97	-10.37	24.32	19.04	43.03
14	DH 91-1	33.03	5.76	15.70	-40.09	-28.38	-6.16	-18.58	-40.79	-79.52
15	DH 53-2	28.06	-2.08	-2.32	-9.26	32.16	-22.37	16.41	-12.24	28.36
16	DH 23-1	16.01	-2.18	13.07	7.92	7.57	2.27	0.59	1.36	46.60
17	DH 45-23	12.59	7.79	21.81	-20.72	28.38	37.93	-6.13	54.39	136.04
18	DH 23-21	-224.92	1.33	10.85	87.26	-56.76	16.53	28.61	74.38	-62.72
19	DH 31-2	-239.01	7.55	2.95	-13.81	32.16	-0.65	10.28	16.32	-184.21
20	DH 14-2	-264.42	3.87	6.43	15.67	-17.03	0.65	2.77	9.52	-242.55
21	DH 75- 23	-273.54	-17.32	-16.44	-44.30	32.16	-33.94	17.20	-28.56	-364.73
22	DH 29-1	-283.67	0.72	4.64	22.40	26.49	7.13	-71.96	-99.27	-393.52
23	DH 8-7	-284.58	5.39	1.16	31.16	26.49	1.62	12.46	25.84	-180.47
	Barbadense Lines									
1	**DB 533**	119.28	1.42	-1.24	-25.44	0.00	-7.65	4.74	-3.67	87.45
2	**DB 534**	37.09	-4.68	-1.17	17.86	30.27	8.59	4.55	19.31	111.81
3	DB 532	-2.42	0.93	2.04	8.76	-15.14	-0.45	-12.12	-19.04	-37.43
4	DB 531	-153.96	2.33	0.36	-1.18	-17.03	-0.49	2.97	3.40	-163.60
	Weightage	**10**	**2**	**3**	**5.5**	**7**	**4**	**5.5**	**6.5**	

5.1.2 Comparison of hybrids based on heterotic box with checks (Best HB)

The efforts on creating recombinational variability have begun with two barbadense and four hirsutum lines. However, to compare the potentiality of these hybrids with other potential hybrids developed over years at Dharwad centre and best commercial hybrids (*Bt* and non *Bt*). A separate evaluation of these hybrids was taken up.

Study on this set of crosses was denoted as best HB trial. The data generated on 49 best HB crosses of this study is utilized to confirm the performance of eight crosses of the heterotic box. The potential of 8 bench mark crosses of heterotic box [ZCH 8 x DB 533, DH 98-27 x DB 534, DH 18-31 x DB 533, ZCH 8 x DB 534, 178-24 x DB 533, DH 98-27 x DB 533, DH 18-31 x DB 534 and 178-24 x DB 534] recorded higher *per se* performance for seed cotton yield ranking 1, 2, 4, 6, 8, 10, 11 and 14 out of 49 crosses (Table 32). These crosses also recorded superior value for yield attributing characters like number of bolls and mean boll weight. The mean performance of these crosses associated with this heterotic box was found to be 2174 kg/ha as compared to the overall mean of best HB inter specific hybrids which was 1921kg/ha (Appendix 2).

The crosses namely ZCH 8 x DB 533, DH 98-27 x DB 534, DH 18-31 x DB 533, ZCH 8 x DB 534 and 178-24 x DB 533 recorded highest yield combining good fibre micronaire and fibre length. These crosses are examples for blending of both quality and yield (Table 32).

5.1.3 Evaluation of 53 F_5 barbadense lines

There is a steep rise in production of long staple cotton, while production of extra long staple, short staple and even medium staple cotton has come down drastically. Because of this, India is importing extra long staple cotton by causing heavy birth on exchequer and there is a need of improving performance of inter specific hybrids. This is possible through genetic improvement of barbadense lines. So that both productivity and fiber quality of barbadense improved. An improved barbadense varietal base is essential for improving performance of inter specific hybrids.

The elite barbadense combiners namely DB 533 and DB 534 were indentified for creation and exploitation of recombinational variability for combining ability. In 2007- 2008 this cross was made and early segregating generations were raised during 2008- 2009 / 2009-2010, out of 171 F_3 lines 53 were identified based on productivity and fiber quality and advanced to succeeding generations. In F_4 generation 28 barbadense lines were utilized to assess recombinational variability for combining ability. These selected F_4 lines were crossed with 4 hirsutum testers figuring in the heterotic box identified in this study. This became the base material (28 barbadense lines x 4 hirsutum testers) for evaluating of recombinational variability for combining ability.

This study also focused attention on determining whether these barbadense lines can straight away be utilized as varieties for producing ELS cottons. Hence, 53 F_5 barbadense lines were evaluated for productivity traits and fiber quality traits and compared with Suvin known to be standard barbadense variety in international market.

Among 53 barbadense lines (included Suvin variety as check), thirteen lines recorded higher *per se* performance for seed cotton yield than Suvin (Table 33). These lines also recorded high values for other characters like number of bolls per plant, mean boll weight, seed index, ginning outturn, lint index, photosynthetic rate and stomatal conductance. These parents exhibited good fiber quality traits like, 2.5% S/L, fiber micronaire value, fiber tenacity and S/L ratio. The *per se* performance of these potential barbadense lines showed higher values than suvin for seed cotton yield and fiber strength.

The potential barbadense line DB 533 x DB 534 F5 IPS 18 (Plate 9) showed superiority over Suvin line for seed cotton yield, mean boll weight, seed index, ginning outturn, lint index, fiber micronaire value, fiber strength and S/L ratio and can be used for developing separate trait based populations with other barbadense lines for yield components and fibre quality. Confirmation of their superiority will enable release of these new lines as an alternative for Suvin variety of barbadense.

5.2 Evaluation of recombinational variability for combining ability

Different schemes of improving combining ability are regularly practiced in maize and use of such schemes has led to development of improved hybrids in maize. These procedures are extended to other cross pollinated crops as well. The recurrent selection procedures are also suggested for often cross pollinated crops by considering sorghum as an example (Doggett and Eberhart, 1968) utilizing male sterility system. The system of mating in cotton differs to the extent that unlike in maize,

Table 32. Top desirable best HB hybrids with *per se* performance for 5 quantitative characters

Sl. No.	Crosses	Seed Cotton yield (kg/ha)	No. of bolls	Mean boll weight (g)	Micronaire value (µg/inch)	2.5% SL (mm)	Rank	BMC
1	ZCH 8 x DB 533	2277.81	30.00	4.70	3.20	35.60	1	BMC
2	DH 98-27 x DB 534	2239.26	21.67	5.10	3.00	35.40	2	BMC
3	177-24 x DB 531	2223.63	28.00	3.50	2.60	40.40	3	
4	DH 18-31 x DB 533	2216.33	31.67	3.60	3.10	33.90	4	BMC
5	DH 84-7 x DB 533	2211.12	39.00	5.20	2.90	38.00	5	
6	ZCH 8 x DB 534	2182.99	34.00	3.70	3.00	39.70	6	BMC
7	DH 10-2 x DB 531	2153.81	28.33	5.00	3.30	38.80	7	
8	178-24 x DB 533	2151.73	34.00	4.30	3.00	36.40	8	BMC
9	DH 11-10 x DB 534	2136.10	31.67	4.70	3.30	37.30	9	
10	DH 98-27 x DB 533	2130.89	31.00	4.60	3.30	35.30	10	BMC
11	DH 18-31 x DB 534	2101.71	32.67	4.90	3.20	37.50	11	BMC
12	DH 25-3 x DB 533	2098.59	44.33	3.60	3.10	35.40	12	
13	DH 44-14 x DB 534	2093.38	32.33	4.70	3.00	37.60	13	
14	178-24 x DB 534	2092.34	35.33	4.10	3.20	36.20	14	BMC
	MRC6918 *Bt* check	**2070.00**						
	Mean of HB crosses	**1921.38**						
	Mean of bench mark crosses	**2174.13**						

BMC: Bench Mark Crosses

Table 33. Top desirable barbadense lines with *per se* performance for 12 quantitative characters

Sl. No.	Parents	Seed cotton yield (kg/ha)	No. of bolls	Mean boll weight (g)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Photosynthetic rate (µmol CO_2 m^{-2} s^{-1})	Stomatal conductance ((µmol m^{-2} s^{-1})	2.5% SL (mm)	Micronaire value (µg/inch)	Tenacity (g/tex)	S/L ratio
		1	2	3	4	5	6	7	8	9	10	11	12
1	DB 533 x DB 534 F5 IPS 132	2175.70	29.67	3.17	11.00	31.09	4.96	9.52	0.30	35.58	3.72	28.63	0.80
2	DB 533 x DB 534 F5 IPS 18	2151.21	27.67	2.93	10.00	35.13	5.41	19.10	0.61	32.12	4.14	29.15	0.91
3	DB 533 x DB 534 F5 IPS 80	1994.39	34.17	2.30	10.00	29.94	4.27	13.08	0.42	37.42	3.46	30.23	0.81
4	DB 533 x DB 534 F5 IPS 109	1934.47	31.67	2.42	9.00	32.65	4.36	11.96	0.45	33.32	3.92	30.05	0.90
5	DB 533 x DB 534 F5 IPS 21	1855.80	32.33	2.87	10.00	29.24	4.13	23.62	0.79	37.42	3.38	29.05	0.78
6	DB 533 x DB 534 F5 IPS 11	1791.72	30.00	2.50	9.00	30.05	3.87	19.64	0.64	31.98	3.65	28.78	0.90
7	DB 533 x DB 534 F5 IPS 37	1728.68	33.17	2.93	10.00	30.97	4.49	20.60	0.74	35.75	3.72	29.17	0.82
8	DB 533 x DB 534 F5 IPS 39	1727.64	29.67	2.57	9.00	33.53	4.54	15.66	0.63	33.25	4.12	29.35	0.88
9	DB 533 x DB 534 F5 IPS 88	1566.65	35.33	2.50	8.00	30.50	3.51	17.02	0.52	33.15	3.52	31.67	0.96
10	DB 533 x DB 534 F5 IPS 57	1564.56	26.67	2.87	8.00	35.23	4.35	21.73	0.70	32.65	4.03	30.80	0.94
11	DB 533 x DB 534 F5 IPS 79	1559.35	28.17	2.63	8.00	33.61	4.05	14.52	0.70	32.42	3.87	30.64	0.95
12	DB 533 x DB 534 F5 IPS 65	1541.12	31.50	2.80	9.00	34.76	4.79	22.29	0.85	33.08	4.02	30.39	0.92
13	DB 533 x DB 534 F5 IPS 10	1454.11	31.33	2.33	9.00	34.64	4.77	20.16	2.03	33.08	4.07	30.75	0.93
14	**Suvin**	1421.81	31.17	2.57	9.00	31.94	4.22	25.88	0.90	33.58	3.77	29.02	0.86

DB 533 X DB 534 F5 IPS 18

Plate 9 : Most productive barbadense line showed superior than Suvin line

here it is difficult to create random mating populations, which is an integral step in every cycle of population improvement programme. Moreover Pederson (1974) and Bos (1977) have argued against the worth of continuous intermating in autogamous crops. In several studies conducted on improving combining ability in often cross pollinated crops like red gram (Patil, 1997), sorghum (Patil and Pandit, 1991 and Madhusudhana, 1993) and cotton (Patil and Patil, 2003, Mallikarjun, 2005 and Somashekar, 2006), attempts were made to exploit the potentiality of the simple traditional method of practicing selection in segregating generations (obtained though hybridization) and utilizing the recombinational variability for improving combining ability as a trait. These studies have clearly indicated that combining ability of lines could be improved by following selection for combining ability (as a trait) in segregating generations.

However, such recurrent selection procedures are not reported to have been practiced in cotton. Though, all the recurrent selection procedures involve recombination to increase the frequency of favourable alleles, Pederson (1974) and Bos (1977) clearly demonstrated that such deliberate recombinations are not highly advantageous over selfing in autogamous species. Further, they pointed out that recombination may at the most aid in breaking some tight linkage. These observations point to the fact that, in self or predominantly self pollinated crops one time crossing of selected diverse parents and practicing selection in segregating generations may be ideal in improving trait under consideration. In routine procedures of pedigree, bulk or single seed descent methods variability is created by crossing parental varieties which are genetically diverse for *per se* performance and selection is practiced in segregating generations. If combining ability is handled as a trait, the above procedure can also be followed and selection can be practiced for improving combining ability in segregating generation leading to improvement in combining ability among the new segregating lines derived from the cross.

There are several advantages of evaluating combining ability of lines in early segregating generations. Identification of superior combining lines in early segregating generations would at least avoid undue multiplication and advancing of material of little genetic worth *i.e.,* with low combining ability. Jenkin's (1935) study revealed that combining ability of a line is heritable and thereby he indicated that potential parents of hybrids can be selected in an early generation of inbreeding. It is well known that plants in early segregating generation have a higher level of heterozygosity, while, the segregating lines in later generations *viz.,* F_5, F_6 and F_7 would be nearly homozygous. Hence, evaluating for combining ability in later generation perhaps would be automatically more reliable. Despite this, it is felt that selection needs to be initiated as early as possible in a generation where the constitution would have reached a satisfactory level of uniformity (homozygosity). In fact, F_4 is a generation in which for the first time even in conventional pedigree method emphasis for the selection (for performance) is laid exclusively on the line mean. It means that F_4 onwards one need not distinguish individual plants performance in a line (Allard, 1960).

This study was aimed at evaluating recombinational variability for combining ability in F_4 generation. To assess variability for combining ability, twenty eight F_4 (*Gossypium barbadense L.*) lines were crossed with four common diverse testers (*Gossypium hirsutum L.*) *viz.,* DH 98-27 (T_1), ZCH8 (T_2), 178-24 (T_3) and DH 18-31 (T_4) for use in assessing the variability for combining ability.

In this study an improvement in combining ability is defined (described) as improvement in performance of derived F_1s over respective other crosses involving the tester concerned. When we refer to "performance of derived F_1" we primarily look at on the performance of seed cotton yield as a measure of combining ability. Seed cotton yield is the most important character directly reflecting the economic worth of the crop. Hence, it is more meaningful to assess the combining ability of a line in terms of the seed cotton yield of the F_1s derived from it. The combining ability of each line with four testers was assessed for comparing the derived F_1s with the other crosses and commercial checks.

5.2.1 Mean performance, heterosis and combining ability effects

In this context, line x tester mating design proposed by Kempthorne (1957) helps the breeders which provide information on the combining ability status of genotypes used and also on the nature of gene action involved. Estimates of combining ability parameters places heterosis breeding methodology on a further scientific footing. The estimates of combining ability effects (*gca* and *sca*) and variance (GCA and SCA) for all characters of the population are discussed here.

Heterosis is the superiority of F_1 over the mean of the parents or over the better parent or over the standard check (Hays *et al.*, 1956), with respect to agriculturally useful traits. The primary objective of heterosis breeding is to achieve a quantum jump in yield and quality of crop plants.

Table 34. Range of heterosis over mid parent, standard checks for different quantitative characters recorded in derived F_1 crosses

Character	Heterosis range in per cent over								
	Mid parent			MRC6918			DCH32		
	Min	Max	Width	Min	Max	Width	Min	Max	Width
1- Seed cotton yield (kg/ha)	-38.94	108.16	147.10	-44.37	39.97	84.34	-42.65	44.31	86.96
2- Plant height (cm)	-6.96	68.57	75.53	-21.24	33.80	55.04	-27.33	23.46	50.79
3- Number of monopodia	-41.58	446.82	488.40	-44.50	22.00	66.50	-33.33	46.55	79.88
4- Number of sympodia	-17.95	52.83	70.78	-17.95	29.08	47.03	-25.58	17.07	42.65
5- Number of bolls	-5.27	135.61	140.88	-26.60	40.78	67.38	-16.86	59.45	76.31
6- Mean boll weight (g)	-34.94	32.28	67.22	-35.62	15.07	50.69	-28.79	27.27	56.06
7- Reproductive points on sympodia	-57.53	59.75	117.28	-34.31	81.30	115.61	-45.29	51.00	96.29
8- Length of sympodia at 50% height (cm)	-32.74	84.71	117.45	-22.08	75.25	97.33	-39.34	36.43	75.77
9-Seed index (g)	-29.96	80.45	110.41	-26.43	83.87	110.30	-26.32	84.16	110.48
10-Ginning outturn (%)	-58.48	11.31	69.79	-51.63	25.65	77.28	-58.91	6.74	65.65
11- Lint index (g)	-44.65	53.71	98.36	-33.29	82.61	115.90	-46.91	45.34	92.25
12- Photosynthetic rate ($\mu molCO_2m^{-2}s^{-1}$)	-84.91	74.56	159.47	-89.07	18.97	108.04	-86.97	41.83	128.80
13- Stomatal conductance ($\mu molm^{-2}s^{-1}$)	-90.67	75.94	166.61	-88.16	53.95	142.11	-74.29	234.29	308.58
14- Transpiration rate (mmol $H_2Om^{-2}s^{-1}$)	-79.10	-5.85	73.25	-67.93	55.26	123.19	-59.94	93.92	153.86

Table 35. *Per se* performance and heterosis of top three potential derived F_1 crosses for different quantitative characters

Sl. No	Characters	Desirable crosses	*Per se* performance			Heterosis		
			Female	Male	F_1	MP	MRC6918 Check	DCH32 Check
1	Seed cotton yield (kg/ha)	[DH 98-27 x (DB 533 x DB 534 F4 IPS 49)]	2503.93	1368.15	2884.26	108.16	39.97	44.31
		[DH 98-27 x (DB 534 x DB 533 F4 IPS 22)	2503.93	1250.40	2800.90	77.72	35.93	40.14
		[DH 98-27 x (DB 533 x DB 534 F4 IPS 52)]	2503.93	1092.54	2636.78	85.62	27.96	31.93
2	Plant height (cm)	[DH 98-27 x (DB 533 x DB 534 F4 IPS 24)]	94.00	74.67	143.83	31.97	10.07	1.57
		[DH 98-27 x (DB 533 x DB 534 F4 IPS 62)]	94.00	100.33	141.33	27.26	14.73	5.87
		[DH 98-27 x (DB 533 x DB 534 F4 IPS 52)]	94.00	72.67	137.50	-2.38	-17.06	-23.46
3	Number of monopodia	[178-24 x (DB 533 x DB 534 F4 IPS 71)]	1.00	1.51	2.44	55.22	-10.75	7.21
		[ZCH 8 x (DB 533 x DB 534 F4 IPS 55)]	1.90	0.42	2.37	23.79	-16.75	0.00
		DH 98-27 x [(DB 533 x DB 534 F4 IPS 26)]	1.42	0.67	2.33	74.11	4.25	25.23
4	Number of sympodia	[178-24 x (DB 533 x DB 534 F4 IPS 14)]	18.33	16.00	25.17	16.50	2.56	-6.98
		[DH 18-31 x (DB 533 x DB 534 F4 IPS 13)]	22.83	19.33	25.17	-4.48	0.00	-9.30
		[DH 98-27 x (DB 533 x DB 534 F4 IPS 16)]	20.67	15.33	24.83	14.14	0.00	-9.30
5	Number of bolls	[DH 98-27 x (DB 533 x DB 534 F4 IPS 36)]	34.67	29.50	66.17	28.72	-14.19	-2.81
		[DH 18-31 x (DB 533 x DB 534 F4 IPS 32)]	25.67	27.83	59.50	66.85	-3.55	9.24
		[DH 98-27 x (DB 533 x DB 534 F4 IPS 14)]	34.67	28.50	58.50	99.38	12.06	26.93
6	Mean boll weight (g)	[DH 98-27 x (DB 533 x DB 534 F4 IPS 33)]	4.30	1.67	4.20	-15.98	-23.29	-15.15
		[DH 18-31 x (DB 533 x DB 534 F4 IPS 12)]	4.45	2.17	3.90	9.74	-2.74	7.58
		[DH 98-27 x (DB 533 x DB 534 F4 IPS 23)]	4.30	1.90	3.85	-10.77	-20.55	-12.12
7	Reproductive points on sympodia	[DH 98-27 x (DB 533 x DB 534 F4 IPS 25)]	3.12	4.08	5.28	-12.06	25.73	4.71
		[ZCH 8 x (DB 533 x DB 534 F4 IPS 105)]	3.50	4.47	5.08	11.03	28.64	7.14
		[DH 98-27 x (DB 533 x DB 534 F4 IPS 23)]	3.12	4.00	4.92	-16.55	8.58	-9.57

Contd....

Sl. No	Characters	Desirable crosses	*Per se* performance			Heterosis		
			Female	Male	F_1	MP	Check 1	Check 2
8	Length of sympodia at 50% height (cm)	[DH 98-27 x (DB533 x DB 534 F4 IPS 44)]	28.50	34.33	54.92	57.83	58.24	23.19
		[DH 98-27 x (DB 533 x DB 534 F4 IPS 62)]	28.50	39.75	53.33	2.04	13.02	-12.01
		[DH 98-27 x (DB 533 x DB 534 F4 IPS 105)]	28.50	35.83	49.58	8.26	11.42	-13.25
9	Seed index (g)	[DH 98-27 x (DB 533 x DB 534 F4 IPS 32)]	9.72	7.62	17.50	80.45	83.87	84.16
		[DH 98-27 x (DB 533 x DB 534 F4 IPS 52)]	9.72	10.06	12.89	40.40	35.42	35.63
		[DH 98-27 x (DB 533 x DB 534 F4 IPS 25)]	9.72	9.55	12.83	41.96	34.84	35.05
10	Ginning outturn (%)	[178-24 x (DB 533 x DB 534 F4 IPS 44)]	34.25	29.58	35.31	4.44	23.63	5.03
		[DH 98-27 x (DB 533 x DB 534 F4 IPS 26)]	35.20	29.19	34.25	-0.31	19.92	1.87
		[DH 18-31 x (DB 533 x DB 534 F4 IPS 17)]	39.14	30.23	33.83	-10.96	3.57	-12.02
11	Lint index (g)	[DH 98-27 x (DB 533 x DB 534 F4 IPS 32)]	6.14	2.95	7.40	53.71	82.61	45.34
		[DH 18-31 x (DB 533 x DB 534 F4 IPS 62)]	6.56	2.03	6.57	23.46	61.90	28.85
		[DH 18-31 x (DB 533 x DB 534 F4 IPS 105)]	6.56	4.43	6.57	12.31	50.18	19.53
12	Photosynthetic rate ($\mu molCO_2 m^{-2} s^{-1}$)	[ZCH 8 x (DB 533 x DB 534 F4 IPS 52)]	22.35	25.84	34.25	74.56	18.97	41.83
		[ZCH 8 x (DB 533 x DB 534 F4 IPS 13)]	22.35	27.15	32.85	45.72	14.10	36.03
		[DH 98-27 x (DB 533 x DB 534 F4 IPS 16)]	23.64	26.69	32.53	20.34	13.01	34.73
13	Stomatal conductance ($\mu molm^{-2} s^{-1}$)	[ZCH 8 x (DB 533 x DB 534 F4 IPS 52)]	0.81	0.82	1.17	75.94	53.95	234.29
		[ZCH 8 x (DB 533 x DB 534 F4 IPS 13)]	0.81	1.00	1.16	47.60	51.97	230
		[ZCH 8 x (DB 533 x DB 534 F4 IPS 32)]	0.81	0.74	1.07	1.19	40.13	204.29
14	Transpiration rate ($mmol\ H_2Om^{-2} s^{-1}$)	[DH 98-27 x (DB 533 x DB 534 F4 IPS 1)]	10.09	8.87	10.04	-26.15	55.26	93.92
		[178-24 x (DB 533 x DB 534 F4 IPS 38)]	11.77	8.93	8.78	-5.85	35.63	69.4
		178-24 x [DB 533 x DB 534 F4 IPS 48]	11.77	9.85	8.77	-6.25	35.55	69.31

Table 36. *Per se* performance of top three potential derived F_1 crosses, population mean and commercial checks mean for different quantitative characters

Characters	[DH 98-27 x (DB 533 x DB 534 F4 IPS 49)]	[DH 98-27 x (DB 534 x DB 533 F4 IPS 22)	[DH 98-27 x (DB 533 x DB 534 F4 IPS 52)]	Population mean	Commercial Checks Mean	
					MRC 6918	DCH 32
1- Seed cotton yield (kg/ha)	2884.26	2800.90	2636.78	1957.45	2060.56	1998.67
2- Plant height (cm)	119.50	102.67	137.50	111.69	107.50	116.50
3- Number of monopodia	1.33	2.22	2.00	1.77	2.00	1.67
4- Number of sympodia	22.83	23.67	24.50	21.33	19.50	21.50
5- Number of bolls	49.17	52.67	43.67	46.21	47.00	41.50
6- Mean boll Weight (g)	3.45	2.55	3.05	3.10	3.65	3.30
7- Reproductive points on sympodia	4.11	3.67	4.50	3.51	2.92	3.50
8- Length of sympodia at 50% height (cm)	42.58	39.33	39.75	34.26	31.33	40.25
9- Inter branch distance (cm)	6.50	7.67	7.00	7.10	6.50	7.33
10-Seed index (g)	10.22	9.95	12.89	10.06	9.52	9.50
11-Ginning outturn (%)	27.59	30.20	33.36	29.87	28.56	33.62
12- Lint index (g)	5.44	4.69	6.17	4.70	4.05	5.10
13- Photosynthetic rate ($\mu molCO_2m^{-2}s^{-1}$)	30.37	6.40	31.27	24.47	28.78	24.15
14- Stomatal conductance ($\mu molm^{-2}s^{-1}$)	0.80	0.25	0.82	0.62	0.76	0.35
15- Transpiration rate ($mmol\ H_2Om^{-2}s^{-1}$)	6.27	5.57	5.79	6.14	6.47	5.18
16- 2.5% SL (mm)	34.86	36.66	34.89	34.04	34.16	32.07
17- UR %	44.45	43.97	44.31	44.59	45.13	44.37
18-Micronaire value (µg/inch)	3.16	3.12	3.47	2.85	2.82	2.83
19- Maturity ratio (%)	0.61	0.61	0.61	0.59	0.67	0.54
20- Tenacity (g/t)	28.29	26.42	27.99	27.52	29.22	27.96
21- Elongation %	6.46	6.42	6.47	6.53	6.67	6.45

Cotton improvement programmes primarily lay emphasis on development of hybrids, which have contributed in improving the productivity of cotton. Hybridization is the most potent technique for breaking yield barriers. Selection of parents on the basis of phenotypic performance alone is not a sound procedure, since phenotypically superior lines may yield poor combinations. It is therefore essential that parents should be chosen on the basis of their combining ability. Combining ability analysis is the most widely used biometrical tool for identifying prospective parents and for formulating breeding procedures most likely to succeed.

In the present study, diverse lines formed the base material and in the following paragraphs, heterotic behavior of hybrids for various traits is presented. The range of heterosis over mid parent and standard checks, top three hybrids in respect of each of the character studied and relative performance of top three hybrids in respect of each of the character studied and relative performance of top three hybrids is presented in Table 34, 35 and 36 respectively.

5.2.1.1 Seed cotton yield (kg/ha)

The difference between seed cotton yield of parents and hybrids were significant as evidenced by significant variance due to parents v/s hybrids. Among the lines, DB 533 x DB 534 F_4 IPS 49, DB 534 x DB 533 F_4 IPS 22 and DB 533 x DB 534 F_4 IPS 52 are high yielder. The higher yielding crosses are DH 98-27 X (DB 533 x DB 534 F_4 IPS 49), DH 98-27 X (DB 534 x DB 533 F_4 IPS 22) and DH 98-27 X (DB 533 x DB 534 F_4 IPS 52). All these crosses involved one parent with high seed cotton yield, number of bolls per plant and boll weight. The majority of crosses showing significant positive heterosis over mid parent for seed cotton yield also showed significant positive heterosis over mid parent for number of bolls per plant, while highest yielding cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 49) exhibited significant positive heterosis over mid parent for number of bolls per plant, seed cotton yield, number of monopodia per plant, seed index and photosynthetic rate.

For seed cotton yield, SCA variance was higher than GCA variance. The component of variance due to SCA was higher than the GCA for this trait. The ratio of general combining ability of variance to specific combining ability of variance was low indicating the role of non-additive gene action in governing the inheritance of this trait. Singh *et al*. (1983), Mandloi *et al.* (1998), Neelima (2002), Ahuja and Tuteja (2003), Muthuswamy *et al*. (2003), Saravanan *et al*. (2003), Verma *et al*. (2004), Mohammad *et al*. (2007), Paulo Antonio de Aguiar *et al.* (2007), Ashok Kumar and Ravikesavan (2008), Kalpande *et al*. (2008), Kumboh *et al*. (2008), Cetin Karademir *et al*. (2009) and Deosarkar *et al*. (2009b) also confirmed the above findings.

The parents DB 533 x DB 534 F_4 IPS 17, DB 533 x DB 534 F_4 IPS 32, DB 533 x DB 534 F_4 IPS 13, DB 533 x DB 534 F_4 IPS 6, DB 533 x DB 534 F_4 IPS 8 and DH 98-27 recorded significant positive *gca* effects for seed cotton yield and these parents are the good general combiners in desirable directions. One of the parents are involved in the high yielding crosses like DH 98-27 X (DB 533 x DB 534 F_4 IPS 49), DH 98-27 X (DB 534 x DB 533 F_4 IPS 22) and DH 98-27 X (DB 533 x DB 534 F_4 IPS 52). The top three performing crosses are involving the parents with low x high, high x low and high x high *gca* effects. Majority of workers *viz.,* Tuteja *et al*. (1996), Doss and Kadambavanasundaram (1997), Siruguppa and Parameswarappa (1998), Neelima (2002) and Potdukhe (2002) also reported heterosis over mid parent.

5.2.1.2 Plant height (cm)

Plant height is one of the important character of growth and development of the cotton canopy. There was increase in number of sympodia per plant and number of bolls per plant with increase in plant height. Among the parents, the tester DH18-31 was the tallest plant followed by DB 533 x DB 534 F_5 IPS 62, DB 533 x DB 534 F_5 IPS 105 and ZCH 8 and these were also high yielding genotypes indicating the importance of height to productivity. The tallest among the hybrids was DH 98-27 X (DB 533 X DB 534 F_4 IPS 24) and the shortest was DH 18-31 X (DB 533 X DB 534 F_4 IPS 24). Most of the hybrids showed significant and positive heterosis for plant height. Significant and positive heterosis for plant height was earlier reported by Singh and Narayanan (1993), Bhatade and Rajeshwar (1994), Sambamurthy *et al*. (1995) and Rajput *et al*. (1997). Three parents namely DB 533 x DB 534 F_4 IPS 30, DB 533 x DB 534 F_4 IPS 36 and DB 533 x DB 534 F_4 IPS 1 exhibited significant positive *gca* effects and where found to be good general combiner. These parents are likely to generate more desirable transgressive segregants in breeding programmes. The component of variance due to SCA was higher than the GCA for this trait. The ratio of GCA to SCA component of variance was low indicating the preponderance of non-additive gene action. Bhatade *et al*. (1980), Singh and Singh (1980), Kalsy *et al.* (1981), Virk and Kalsy (1982), Gill and Singh (1982), Shanti and Selvaraj (1995), Saravanan *et al.* (2003), Verma *et al*. (2004), Patel *et al*. (2005), Subramanian *et al.*

(2005), Mohammad Ilyas *et al*. (2007), Kumboh *et al*. (2008), Deosarkar *et al.* (2009b) and Mohammad Reza *et al*. (2010) also confirmed the above findings through their studies.

5.2.1.3 Number of monopodia per plant

The monopodial branches utilize more energy and delay the reproductive parts. More vegetative branches are undesirable and any genetic parameter in negative direction is desirable. Such a passion for negative with respect to *gca* was found in lines viz., DB 533 x DB 534 F_4 IPS 25, DB 533 x DB 534 F_4 IPS 49, DB 533 X DB 534 F_4 IPS 24, DB 533 x DB 534 F_4 IPS 32 and DB 533 x DB 534 F_4 IPS 6. Among the testers, DH 98-27 and ZCH8 showed negative *gca* effects. Effect of negative *gca* has been noticed in mean performance of hybrids involving above parents. The lower mean performance of hybrids for number of monopodia per plant has been further reflected on heterosis.

The variance due to specific combining ability was greater than the general combining ability for this trait. The ratio of GCA components of variance to the SCA component of variance was found to be low indicating the influence of non-additive gene action. Similar results were earlier reported by Hapase *et al*. (1987), Shanti and Selvaraj (1995), Murthy and Ranganadhacharyulu (1998), Neelima *et al*. (2002), Narisireddy and Satyanarayana (2004), Patel *et al*. (2005) and Deosarkar *et al.* (2009b).

In many crosses, heterosis over mid parent has been observed as significant positive heterosis. Similar reports were made by Reddy (2001), Neelima (2002) and Potdukhe (2002).

5.2.1.4 Number of sympodia per plant

The range of variation, both among lines and testers, was less. The *per se* performance of testers was greater than the average of lines. Some of the hybrids exhibited significant positive heterosis over mid parent. Significant heterosis over mid parent for this character was observed by Reddy (2001), Neelima (2002) and Potdukhe (2002).

The estimate of SCA variance was higher than GCA variance for number of sympodia per plant. The ratio of general combining ability component of variance to specific combining ability component of variance was low indicating the predominance of non-additive gene action. These results are in confirmity with the findings of Singh and Gupta (1970), Kalsy and Garg (1980), Singh and Raut (1983), Valarmathi and Jehangir (1998b), Reddy (2001), Laxman and Ganesh (2003), Deshpande and Baig (2003), Narisireddy and Satyanarayana (2004), Sivaprasad *et al.* (2004a), Subramanian *et al.* (2005), Wankhade *et al*. (2008), Kumboh *et al*. (2008), Deosarkar *et al.* (2009b), Patel *et al.* (2009) and Mohammad Reza *et al*. (2010).

The parents *viz.,* DB 533 x DB 534 F_4 IPS 52, DB 533 X DB 534 F_4 IPS 24, DB 533 x DB 534 F_4 IPS 14, DB 533 x DB 534 F_4 IPS 25, DB 533 x DB 534 F_4 IPS 49 and DB 533 x DB 534 F_4 IPS 48 among lines recorded highest positive *gca* effects and DH 18-31 and DH 98-27 exhibited positive *gca* in testers indicating that they are good general combiners. These parents may be utilized in hybrid breeding programmes for improving this trait because they have got favorable alleles. The crosses DH 98-27 X (DB 533 x DB 534 F_4 IPS 71) and 178-24 X (DB 533 x DB 534 F_4 IPS 48) showed significant *sca* effects and this coincided with high performance of the hybrid.

5.2.1.5 Number of bolls per plant

The mean number of bolls per plant was higher in lines than testers. The mean of hybrids exceeded the performance of both the parents. Majority of the crosses exhibited significant positive heterosis over mid parent. Siruguppa and Parameswarappa (1998), Reddy (2001), Neelima (2002) and Potdukhe (2002) also revealed the heterosis over mid parent for this trait.

The line DB 533 X DB 534 F_4 IPS 24 revealed the highest significant positive *gca* effect. Among the tester, DH 98-27 showed the highest significant positive *gca* effect. The crosses *viz.,* ZCH 8 X (DB 533 x DB 534 F_4 IPS 30) and 178-24 X (DB 533 x DB 534 F_4 IPS 17) recorded significant positive *sca* effects. These crosses also yielded high seed cotton and thus revealing the importance of total bolls as one of the most important contributing factor to higher yields. General predictability ratio indicate the importance of non additive variance rather than additive variance. Hapase *et al*. (1987), Raut *et al*. (1989), Singh and singh (1980), Patil (1989), Shanti and Selvaraj (1995), Neelima (2002), Subramanian *et al.* (2005), Mohammad Ilyas *et al*. (2007), Wankhade *et al*. (2008), Kumboh *et al*. (2008), Deosarkar *et al.* (2009b), Naqib Ullah *et al*. (2009) and Mohammad Reza *et al*. (2010) reported the importance of SCA variance in the inheritance of this trait.

5.2.1.6 Mean boll weight (g)

In cotton, boll weight and boll number in inter specific and intra specific hybrids are reported as major components of heterosis in yield (Pavasia *et al*., 1999b).

The heaviest bolls are observed in the parents 178-24 and DH18-31. Among the crosses, the heaviest bolls were observed in the order of DH 98-27 X (DB 533 x DB 534 F_4 IPS 33), DH 18-31 X (DB 533 x DB 534 F_4 IPS 12), DH 98-27 X (DB 533 x DB 534 F_4 IPS 23) and DH 98-27 X (DB 533 x DB 534 F_4 IPS 8). Analysis of variance reveals the involvement of non additive variance. Similar reports were made by Bhandari (1980), Jagtap (1986), Shanti and Selvaraj (1995), Panchal *et al*. (1995), Tuteja *et al*. (1996), Neelima (2002), Subramanian *et al.* (2005), Mohammad Ilyas *et al*. (2007), Wankhade *et al*. (2008), Kumboh *et al*. (2008), Deosarkar *et al.* (2009b), Naqib Ullah *et al*. (2009) and Mohammad Reza *et al*. (2010).

5.2.1.7 Reproductive points on sympodia

The parents *viz.,* DB 533 x DB 534 F_5 IPS 62, DB 533 x DB 534 F_5 IPS 48 and DB 534 x DB 533 F_5 IPS 22 exhibited higher *per se* performance for this trait. The cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 25) showed the higher *per se* performance.

The lines DB 533 x DB 534 F_4 IPS 15 and DB 533 x DB 534 F_4 IPS 33 recorded highest significant positive *gca* effects, while the tester ZCH 8 exhibited significant negative *gca* effect. Analysis of variance has shown the importance of non additive gene action. Significant positive heterosis over mid parent and commercial check was reported by Mallikarjun (2005), Somashekhar (2006) and Deepakbabu (2007).

5.2.1.8 Length of sympodia at 50% height (cm)

Most of the crosses recorded significant positive heterosis over mid parent and over the check MRC 6918, while showed significant negative heterosis over DCH 32 check. Significant positive heterosis over mid parent and commercial check was reported by Mallikarjun (2005), Somashekar (2006).

The parents *viz.,* DB 533 x DB 534 F_5 IPS 62, DH 18-31 and DB 533 x DB 534 F_5 IPS 71 reported the higher *per se* performance for this trait. The cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 44) registered the highest *per se* performance. Majority of crosses that has shown significant heterosis for this trait also exhibited high values of seed cotton yield.The parents DB 533 x DB 534 F_4 IPS 30 and DB 533 x DB 534 F_4 IPS 36 exhibited significant positive *gca* effects. The crosses which have shown significant *sca* effects for this trait also exhibited high *per se* performance for seed cotton yield. Analysis of variance revealed the importance on non additive gene action.

5.2.1.9 Inter branch distance (cm)

The crosses 178-24 X (DB 533 x DB 534 F_4 IPS 13) and ZCH 8 X (DB 533 x DB 534 F_4 IPS 26) exhibited higher performance for this trait, while the parents DB 533 x DB 534 F_5 IPS 6, 178-24 and DH 18-31 showed higher performance for inter branch distance. There is importance of reduction in inter boll distance for increasing the seed cotton yield per plant. But, in case of low yielders, even though there is decrease in inter boll distance, they did not exhibit higher performance indicating that reduction in inter boll distance alone cannot influence the yield. Similar reports were made by Anuradha (1998).

5.2.1.10 Seed index (g)

Mean of lines was lesser than testers. Among the parents, DB 533 x DB 534 F4 IPS 30 was having the highest *gca* effect (1.30). Most of the crosses involving this as parent showed significant positive heterosis over mid parent. Heterosis over mid parent was reported by Reddy (2001), Neelima (2002) and Potdukhe (2002), Karande *et al.* (2004) and Maisuria *et al.* (2006). The crosses *viz.,* DH 98-27 X (DB 533 x DB 534 F_4 IPS 32) and DH 98-27 X (DB 533 x DB 534 F_4 IPS 52) exhibited highest significant positive *sca* effect. As non-additive gene action was predominant, breeding methods involving selection, intermating among selected ones and reselection may help to improve this trait besides exploiting through heterosis breeding. Similar results were reported by Chakresh kumar *et al*. (1984), Hapase *et al*. (1987), Mandloi *et al.* (1998), Gururajan (2000), Reddy (2001), Muthuswamy *et al.* (2003), Laxman and Ganesh (2003), Ahuja and Tuteja (2003), Deshpande and Baig (2003), Manickam and Gururajan (2004), Paulo Antnio de Aguiar *et al*. (2007) and Deosarkar *et al.* (2009b).

5.2.1.11 Ginning outturn (%)

The parent DH 18-31 registered the highest GOT followed by ZCH 8, DB 533 x DB 534 F_5 IPS 57 and DH 98-27. The cross 178-24 X (DB 533 x DB 534 F_4 IPS 44) exhibited higher *per se* performance. The highest mid parental heterosis was noticed in the cross DH 18-31 X (DB 533 x DB 534 F_4 IPS 105). Mid parental heterosis for GOT was reported earlier by Reddy (2001), Neelima (2002), Potdukhe (2002) and Sivaprasad (2003).

The parents *viz.,* DB 533 x DB 534 F_4 IPS 16 and DB 533 x DB 534 F_4 IPS 17 registered the significant positive *gca* effects, whereas, the crosses *viz.,* ZCH 8 X (DB 533 x DB 534 F_4 IPS 26) and ZCH 8 X (DB 533 x DB 534 F_4 IPS 16) exhibited the significant positive *sca* effects. Analysis of variance indicated the involvement of non additive gene action. Deshpande and Bhale (1984), Tuteja *et al*. (1996) and Valarmathi and Jehangir (1998), Gururajan (2000), Deshpande and Baig (2003), Ahuja and Tuteja (2003), Muthuswamy *et al.* (2003), Manickam and Gururajan (2004), Subramanian *et al.* (2005), Preetha and Raveendran (2008), Kumboh *et al*. (2008), Cetin Karademir *et al*. (2009) and Deosarkar *et al*. (2009b) also reported the similar results.

5.2.1.12 Lint index (g)

The female parents *viz.,* DH 18-31 and 178-24 possessed the highest lint index, among the crosses [DH 98-27 X (DB 533 x DB 534 F_4 IPS 32)] registered the highest lint index. Heterosis over mid parent was reported by Doss and Kadambavanasundaram (1997), Reddy (2001), Neelima (2002) and Potdukhe (2002). Parents *viz.* (DB 533 x DB 534 F_4 IPS 17) (DB 533 x DB 534 F_4 IPS 32) and (DB 533 x DB 534 F_4 IPS 48) recorded positive *gca* effects for lint index. The crosses developed involving these parents expressed higher *per se* for lint index. Hence, it is possible to exploit this non additive genetic action by heterosis breeding. Grakh and Choudhary (1983), Mandloi *et al*. (1998) and Murthy and Ranganadhacharyulu (1998), Jagtap and Mehetre (1998), Muthuswamy *et al*. (2003), Manickam and Gururajan (2004), Sivaprasad *et al.* (2004a), Subramanian *et al.* (2005), Preetha and Raveendran (2008) and Basal *et al*. (2009) have also reported the non additive gene action for lint index.

5.2.1.13 Photosynthetic rate ($\mu molCO_2m^{-2}s^{-1}$)

The photosynthetic rates of cotton leaves under a given environmental conditions is a function of the various biophysical and biochemical processes involved during the diffusion of CO_2 from atmosphere to chloroplast and the subsequent enzymatic reactions. The parents *viz.,* 178-24, DB 533 x DB 534 F_5 IPS 13 and DB 533 x DB 534 F_5 IPS 49) possessed the highest photosynthetic rate, among the crosses ZCH 8 X (DB 533 x DB 534 F_4 IPS 52) registered the highest photosynthetic rate. The parents DB 533 x DB 534 F_4 IPS 26 and DB 533 x DB 534 F_4 IPS 17 recorded higher significant positive *gca* effects. The cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 25) exhibited higher value of significant positive *sca* effect.

The majority of crosses showing significant positive heterosis over mid parent for photosynthetic rate. For photosynthetic rate, SCA variance was higher than GCA variance. The component of variance due to SCA was higher than the GCA for this trait. The ratio of general combining ability of variance to specific combining ability of variance was low indicating the role of non-additive gene action in governing the inheritance of this trait.

5.2.1.14 Stomatal conductance ($\mu molm^{-2}s^{-1}$)

The rate of stomatal conductance, or its inverse, stomatal resistance, is directly related to the boundary layer resistance of the leaf and the absolute concentration gradient of water vapor from the leaf to the atmosphere. Stomatal conductance showed significant differences among genotypes and the parents *viz.,* DB 533 x DB 534 F_5 IPS 55, DB 533 x DB 534 F_5 IPS 16 and 178-24 possessed the highest stomatal conductance, among the crosses DH 98-27 X (DB 533 x DB 534 F_4 IPS 105) registered the highest stomatal conductance. The parents DB 533 x DB 534 F_4 IPS 26, DB 533 x DB 534 F_4 IPS 25 and DB 533 x DB 534 F_4 IPS 8 recorded higher values of significant positive *gca* effects. The cross ZCH 8 X (DB 533 x DB 534 F_4 IPS 52) exhibited the highest significant positive *sca* effect.

The majority of crosses showing significant negative heterosis over mid parent and MRC 6918 for stomatal conductance, while showed significant positive heterosis over DCH 32 check. Gopinath and Madalageri (1985) reported heterosis for stomatal conductance over mid-parent values. Majority of hybrids possessed higher stomatal conductance as compared to parents. This may be attributed to higher stomatal frequency, length and breadth of stomata observed in hybrids. Austin

(1977) and Jing and Ma (1990) reported that reduced stomatal frequency would reduce stomatal conductance and increase the yield due to increased water use efficiency under water limiting conditions. For stomatal conductance, SCA variance was higher than GCA variance. The component of variance due to SCA was higher than the GCA for this trait. Analysis of variance indicated the involvement of non additive gene action.

5.2.1.15 Transpiration rate (mmol $H_2Om^{-2}s^{-1}$)

The leaf transpiration and stomatal resistance are directly related to number of stomatal present per unit leaf area (Vande Roovart and Fuller, 1935). The parents *viz.,* DB 533 x DB 534 F_5 IPS 105, 178-24, ZCH 8 and DH18-31 possessed the highest transpiration rate, among the crosses DH 98-27 X (DB 533 x DB 534 F_4 IPS 1) registered the highest transpiration rate. The parents DB 533 x DB 534 F_4 IPS 55, DB 533 x DB 534 F_4 IPS 52, DB 533 x DB 534 F_4 IPS 14 and DH 18-31 recorded significant positive *gca* effects. The cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 1) exhibited the highest significant positive *sca* effect.

The majority of crosses showing significant negative heterosis over mid parent and MRC 6918 for transpiration rate, while showed significant positive heterosis over DCH 32 check. For transpiration rate, analysis of variance indicated the involvement of non additive gene action.

5.2.1.16 2.5% span length (mm)

The mean *per se* performance of lines (33.99) and the testers (29.53). The mean of the hybrids was nearer to the parental means. The line DB 533 x DB 534 F5 IPS 34 has shown highest performance for this trait among lines and testers. The cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 16) had highest value of 2.5 % S/L.

5.2.1.17 Fiber uniformity ratio (%)

Among lines, DB 533 x DB 534 F_5 IPS 62 and DB 533 x DB 534 F_5 IPS 25 and in the testers, DH 98-27 and ZCH 8 exhibited highest performance for fiber uniformity ratio. Out of 112 crosses, the crosses *viz*., DH 18-31 X (DB 533 x DB 534 F_4 IPS 8) and 178-24 X (DB 534 x DB 533 F_4 IPS 22) recorded highest value for this trait.

5.2.1.18 Fiber micronaire value (g/inch)

The results revealed that, among lines, DB 533 x DB 534 F_5 IPS 25, DB 534 x DB 533 F_5 IPS 22, DB 533 x DB 534 F_5 IPS 1 and DB 533 x DB 534 F_5 IPS 14 and in the testers DH 18-31 and ZCH 8 were found to be highest performance for fiber micronaire value. Based on *per se* performance, the crosses DH 98-27 X (DB 533 x DB 534 F_4 IPS 105), DH 98-27 X (DB 533 x DB 534 F_4 IPS 71) and DH 98-27 X (DB 533 x DB 534 F_4 IPS 52) was found to be highest crosses for this character.

5.2.1.19 Fiber maturity ratio (%)

Among lines, DB 533 x DB 534 F_5 IPS 25, DB 533 x DB 534 F_5 IPS 71 and DB 533 x DB 534 F_5 IPS 1 and among testers, DH 18-31, DH 98-27 and ZCH 8 are best parents based on performance for this trait. Out of 112 crosses, the crosses *viz*., DH 98-27 X (DB 533 x DB 534 F_4 IPS 71), DH 98-27 X (DB 533 x DB 534 F_4 IPS 105), ZCH 8 X (DB 533 x DB 534 F_4 IPS 44), [DH 98-27 X (DB 533 x DB 534 F_4 IPS 30) and DH 18-31 X (DB 533 x DB 534 F_4 IPS 23) are identified as best crosses combinations based on *per se* performance.

5.2.1.20 Fiber tenacity value (g/tex)

The perusal of results revealed that, among lines, DB 533 x DB 534 F_5 IPS 44, DB 533 x DB 534 F_5 IPS 62, DB 533 x DB 534 F_5 IPS 105 and DB 533 x DB 534 F_5 IPS 38 were found to be good general combiners and among testers, DH 98-27 and 178-24 recorded highest value for fiber tenacity value. Based on *per se* performance, the crosses ZCH 8 X (DB 533 x DB 534 F_4 IPS 30), ZCH 8 X (DB 533 x DB 534 F_4 IPS 25) and DH 18-31 X (DB 533 x DB 534 F_4 IPS 8) were found to be better.

5.2.1.21 Fibre elongation (%)

Among lines, DB 533 x DB 534 F_5 IPS 105, DB 533 x DB 534 F_5 IPS 30 and DB 533 x DB 534 F_5 IPS 25 and among testers, ZCH 8 and DH 98-27 are good combiners based on *per se* performance. Out of 112 crosses, the crosses *viz*., 178-24 X (DB 533 x DB 534 F_4 IPS 49), ZCH 8 X (DB 533 x DB 534 F_4 IPS 12) and ZCH 8 X (DB 533 x DB 534 F_4 IPS 71) are identified as good cross combinations based on *per se* performance.

5.2.2 Pooled score for *gca* effect

5.2.2.1 Simple pooled *gca* score method

In this approach, significant *gca* effect in desirable direction is given positive weightage (+1) and negative weighatage (-1) is given for *gca* effect in undesirable direction (Arunachalam and Bandopadhyay, 1979). These values are added over different yield influencing characters to arrive at pooled score of *gca* effects. The inherent disadvantage with this system is that all the parents with significant *gca* effects in desirable direction get the same score (positive). Hence, it is not possible to quantify the magnitude of difference existing among the genotypes of this group which get a positive score. Therefore, it is necessary to develop a system of working out pooled scores of *gca* by utilizing the actual *gca* values and ensuring quantification of every possible difference existing in *gca* effects between only two parents.

5.2.2.2 Per cent *gca* method

When the actual *gca* values are added across characters to arrive at pooled score, problem arises because of difference in unit of measurement of each character. Absolute values of *gca* effects may be big (plant height) or small (boll weight) depending on the character and if used, the importance of the character may not be projected correctly. If the raw values of *gca* effects are added across the characters, the character with higher *per se* effect influence the pooled scores most as against the character with low *per se gca* values. To overcome this disadvantage, the raw *gca* values have to be converted into per cent *gca* values.

Thus, by working out per cent *gca* values, the minute differences in *gca* values are also focussed and the possible problem arising out of the differences in unit of measurement, high and lower *per se gca* values associated with the type of character concerned are overcome.

5.2.2.3 Weighted per cent *gca* method

In this method further improvement is brought about in arriving at the pooled *gca* scores of the parents. In per cent *gca* method, the per cent *gca* values are straight away added across the characters which means each character including yield and yield components are all given equal weightage. The experience of the breeders would suggest sometimes that, in arriving the pooled score, it is desirable to attach differential weightages to each of the characters studied depending upon its economic importance, contribution to yield *etc.* These weightages can be multiplied with per cent *gca* values of corresponding characters and then added to arrive at the pooled *gca* score for each parent. In the present study weightages for different yield related characters were worked out by consulting the senior breeder related to cotton *viz.,* Dr. S. S. Patil, Senior Scientist, Agricultural Research Station, Dharwad and Dr. B. C. Patil, principal scientist (Plant physiology), ARS, Dharwad Farm.

The overall combining ability status of F_4 barbadense lines was determined by working out pooled *gca* score. Three methods namely simple *gca* score, per cent *gca* and weighted *gca* method were used in arriving at the best general combiner lines. The overall ranking from these approaches differed and the weighted *gca* approach helped in preciese identification of potential combiners. Based on weighted *gca* method, the most potential combiners were found to be the lines DB 533 x DB 534 F_4 IPS 26, DB 533 x DB 534 F_4 IPS 17, DB 533 x DB 534 F_4 IPS 8 and DB 533 x DB 534 F_4 IPS 32 . Among the testers, the tester DH 18-31 based on weighted *gca* method is the most potential parent.

5.2.3 Efficiency of tester (S)

Choice of tester in assessing the combining ability of segregating lines is one of the important aspects in hybrid breeding programme. Though this aspect should assume equal importance in all the crops where hybrid improvement is practiced, the studies on choice of testers, description of ideal tester *etc.* are limited to maize. In maize different authors have expressed different views on efficiency of tester in assessing combining ability.

Hull (1945) visualized a model of over dominance responsible for heterosis and suggested that, tester with homozygous recessive alleles at all loci would be most effective. He used variance among derived F_1 crosses as an index of measuring efficiency of a tester. Rawlings and Thompson (1962) extended this idea and suggested that, testers with low *per se* performance would be most effective because of accumulated recessive alleles (homozygocity) at most loci. Rawlings and Thompson (1962) and Allison and Curnow (1966) suggested even for a repeated selection for low

yield within a population to develop good testers. However, this concept was counter argued as not effective by different maize workers (Hallauer and Miranda, 1981). This group of workers argued that, testers with poor performance would have lot of disadvantages in applied breeding programmes and as an alternative they suggested an unrelated elite tester may be more effective in evaluating lines. An elite unrelated tester has an advantage of identifying the lines with good combining ability and the lines identified in this manner can be directly used in breeding programmes.

Several studies have been conducted to compare the testers with broad and narrow genetic base (Horner *et al.*, 1973; Russell *et al.*, 1973 and Walejko and Russell, 1977). Russell and Eberhart (1975) proposed that, in receprocal recurrent selection an inbred line derived from opposite population would be ideal choice as a tester, while Comstock (1979) suggested that the opposite population would be efficient tester.

Ultimately all these studies indicated that, the lines or populations which are genetically diverse can act as efficient testers. The effective way of identifying genetically diverse tester should again be based on *per se* performance of derived F_1 crossess (test cross F_1s). Patil (1995) used two parameters *i.e.,* mean of derived F_1 (test cross F_1s) and variance of these group of F_1 crosses in qualifying the efficiency of testers.

Applying this approach in present study, twenty eight F_4 lines were selected and they were crossed to four testers to obtain 112 derived F_1 crosses. Based on mean and its variability parameters comparison was made (Table 37) among the testers to assess efficiency of testers in distinguishing combining ability of F_4 lines.

The set of 28 lines distinguished for the ability to combine with each tester. The efficiency of tester in distinguishing of these F_4 lines was determined based on mean seed cotton yield of 28 crosses and co-efficient of variability. In derived F_1 crosses, tester DH 98-27 (T_1) revealed high mean and also higher co-efficient of variance as compared to the other three testers for seed cotton yield. Both DH 98-27 and DH 18-31 (Plate 10) were found to be efficient testers on the basis of high mean and high co-efficient variance. Considering mean and co-efficient variance as parameters T_1 was found to be more efficient in distinguishing the barbadense F_4 lines for their combining ability for utilized to distinguish lines.

5.2.4 Sub-grouping and characterization of lines for combining ability

Based on the mean (of all the crosses), the group of crosses were classified into four classes and given the ranking 1 (>mean + SD), 2 (mean to mean + SD), 3 (mean to mean – SD) and 4 (<mean – SD) as suggested by Patil (1995). Each line was characterized with respect to its combining ability status (pattern) considering the four testers, with the help of this information, the nature and magnitude of variability for combining ability was assessed. The information obtained on the four testers DH 98-27 (A), ZCH8 (B), 178- 24 (C) and DH 18-31 (D) are presented separately.

A method of sub grouping the F_4 lines against each tester was done. Based on this elite combiner F_4 lines were identified against each tester. This approach helped in sub grouping the F_4 lines against a pair of hirsutum testers and identifying lines for deriving sub populations against hirsutum testers. By following the method of determining the combining ability pattern given above each line of F_4 barbadense lines was categorized and compared with the other lines.

Based on the graphical presentation given for tester DH 98-27 (T_1)/A (Fig. 15), it is evident that entire group of lines revealed large variability for ability to combine with this tester. The F_4 lines combine better with the tester DH 98-27 as evidenced by the higher frequency of crosses falling under the category A_1 [DB 533 x DB 534 F_4 IPS 49, DB 534 x DB 533 F_4 IPS 22, DB 533 x DB 534 F_4 IPS 52, DB 533 x DB 534 F_4 IPS 105, DB 533 x DB 534 F_4 IPS 17, DB 533 x DB 534 F_4 IPS 16 and DB 533 x DB 534 F_4 IPS 48]. Whereas, DB 533 x DB 534 F_4 IPS 49 alone line was belonging to this higher combiner category against this common tester DH 98-27 (T_1)/A.

The F_4 barbadense lines reveal better variability in their combinations with the tester ZCH 8 (T_2)/B, as evidenced by higher frequency of crosses falling under this sub-group B_1 [DB 533 x DB 534 F_4 IPS 49, DB 534 x DB 533 F_4 IPS 22, DB 533 x DB 534 F_4 IPS 52, DB 533 x DB 534 F_4 IPS 105, DB 533 x DB 534 F_4 IPS 17 and DB 533 x DB 534 F_4 IPS 16] also belonging to this higher combining category against the tester ZCH8 (T_2)/B.

With respect to tester 178-24 (T_3)/C, it is observed that entire group of lines revealed better variability for ability to combine with this tester. Among the groups of lines tested, the F_4 lines combine better with the 178-27 (T_3)/C as evidenced by the higher frequency of crosses falling under the category C_1 [DB 533 x DB 534 F_4 IPS 49 and DB 534 x DB 533 F_4 IPS 22]. Whereas, DB 533 x DB 534 F_4 IPS 49 were belonging to this higher combiner category against this common tester 178-24 (T_3)/C.

Table 37. Efficiency of testers against the F4 barbadense lines in terms of seed cotton yield (kg/ha)

Parameters	Derived F_1s			
	DH 98-27 (T_1)	ZCH 8 (T_2)	178-24 (T_3)	DH 18-31 (T_4)
Mean	2075.10	1751.43	1762.75	2235.33
Variance	112783.21	43721.24	65114.72	33131.39
Co-efficient of variance (%)	16.18	11.94	14.48	8.14

DH 98-27 (T1)

Plate 10 : Most productive hirsutum testers included in recombinational variability study

With respect to tester DH 18-31 (T_4)/D, it is observed that entire group of lines revealed large variability for ability to combine with this tester. Among the groups of lines tested, the F_4 lines combine better with the DH 18-31 (T_4)/D as evidenced by the higher frequency of crosses falling under the category D_1 [DB 533 x DB 534 F_4 IPS 49, DB 534 x DB 533 F_4 IPS 22, DB 533 x DB 534 F_4 IPS 52 and DB 533 x DB 534 F_4 IPS 17]. Whereas, DB 533 x DB 534 F_4 IPS 49 were belonging to this higher combiner category against this common tester DH 18-31 (T_4)/D.

Based on the graphical presentation given for tester DH 98-27 (T_1)/A and ZCH8 (T_2)/ B (Fig. 16), it is evident that lines *viz*., DB 533 x DB 534 F_4 IPS 49, DB 534 x DB 533 F_4 IPS 22, DB 533 x DB 534 F_4 IPS 52 and DB 533 x DB 534 F_4 IPS 105 revealed large variability for ability to combine with these two testers. The lines DB 533 x DB 534 F_4 IPS 49 and DB 534 x DB 533 F_4 IPS 22 exhibited large variability for ability to combine with two hirsutum testers DH 98-27 (T_1)/A and 178-24 (T_3)/C, ZCH8 (T_2)/B and 178-24 (T_3)/C, ZCH8 (T_2)/B and DH 18-31 (T4)/D and 178-24 (T_3)/C and DH 18-31 (T4)/D. While, the barbadense lines DB 533 x DB 534 F_4 IPS 49, DB 534 x DB 533 F_4 IPS 22 and DB 533 x DB 534 F_4 IPS 52 recorded large variability for ability to combine with two hirsutum testers DH98-27 (T_1)/A and DH 18-31 (T4)/D. Both the lines DB 533 x DB 534 F_4 IPS 49 and DB 534 x DB 533 F_4 IPS 22 have combined very well with four hirsutum testers.This suggest that these two barbadense lines can recombined to initiate second phase of creating recombinational variability for combining ability. The segregating F_4 lines obtained from this cross can be cross to these four hirsutum testers and especially DH 18-31 and DH 98-27 because the mean of crosses with T_1 and T_4 testers is very high.

5.2.5 Transgressive segregation for combining ability

The *per se* performance and per cent superiority of derived F_1 crosses over superior bench mark crosses (SBMC) and per cent inferiority of derived F_1 crosses over inferior bench mark crosses (IBMC) for seed cotton yield were presented in Table 38.

5.2.5.1 With tester T_1 (DH 98-27)

With tester DH 98-27 (T_1) the per cent superiority of derived F_1 crosses over superior straight cross produced as many as 28 positive transgressive segregants. Among these DB 533 x DB 534 F_4 IPS 49 (78.36), DB 534 x DB 533 F_4 IPS 22 (73.20), DB 533 x DB 534 F_4 IPS 52 (63.06) and DB 533 x DB 534 F_4 IPS 105 (61.19) F_4 lines have produced significant transgressive segregants. Whereas, there are no negative transgressive segregants over inferior straight cross for combining ability.

When the performance of derived F_1 crosses was compared with superior bench mark crosses (SBMC) on the basis of per cent superiority (improvement in combining ability), it was evident that the derived F_1 crosses expressed substantially high amount of superiority over superior straight cross.

This indicates that the segregants showed improvement in their ability to combine with tester concerned in desirable direction. It also indicated that the segregants are genetically more diverse from tester T_1. The segregants have genotypic constitution complimentary to that found in the tester T_1. In other words, they accumulate more number of dominant favourable alleles which impart diversity to their genetic constitution as compared to the genetic constitution of the tester T_1 (DH 98-27).

Further, the most practical measure of the potentiality of derived F_1 crosses is obtained by studying the heterosis over commercial check (standard heterosis). The heterosis values of derived F_1 crosses over MRC 6918 and DCH 32, only two of the derived F_1 crosses were significantly superior over the two checks. This indicates that more number of F_1 crosses are inferior over commercial checks.

5.2.5.2 With tester T_2 (ZCH 8)

Along with tester ZCH 8 (T_2), the per cent superiority of derived F_1 crosses over superior straight cross had produced fifteen positive transgressive segregants. Among these, DB 533 x DB 534 F_4 IPS 49 (31.62), DB 534 x DB 533 F_4 IPS 22 (23.51) and DB 533 x DB 534 F_4 IPS 52 (19.34) F_4 lines have produced highest positive transgressive segregants. Whereas, per cent inferiority of derived F_1 crosses over inferior straight cross had produced 5 negative transgressive segregants.

Comparing the mean yields of derived F_1 crosses and superior straight cross, it was evident that the derived F_1 crosses expressed substantially marginal amount of superiority over superior

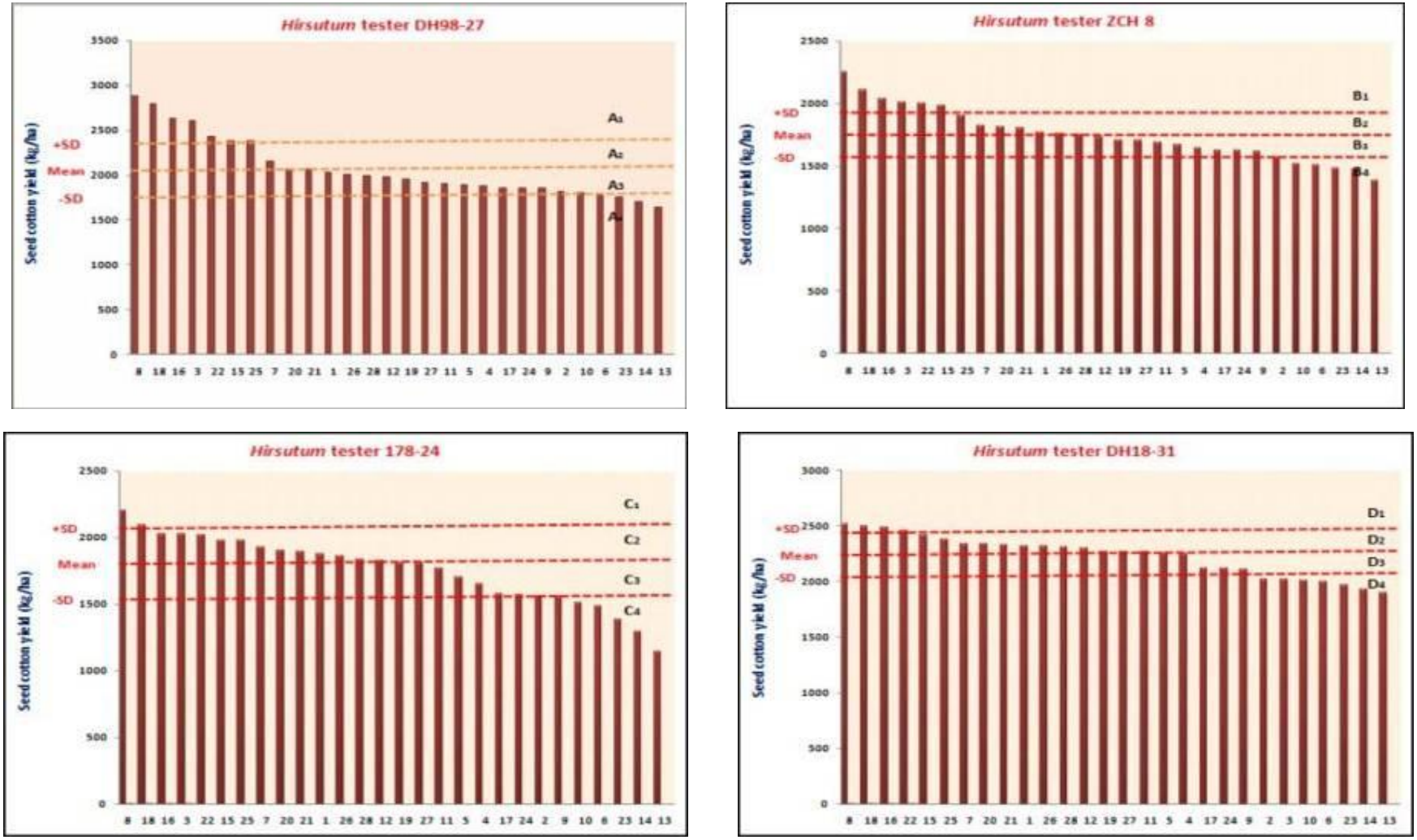
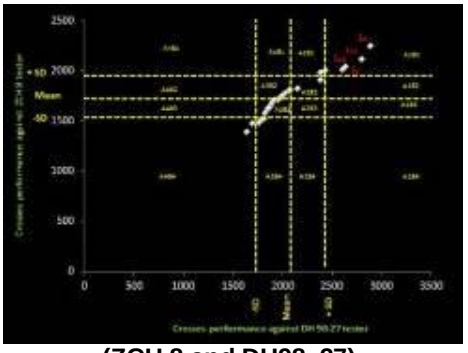
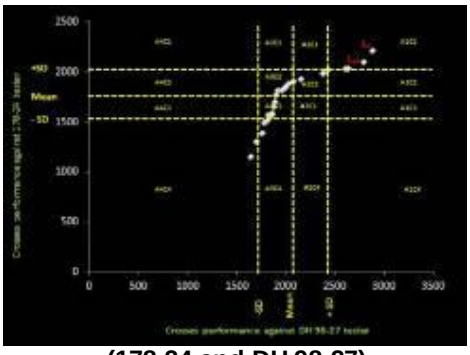


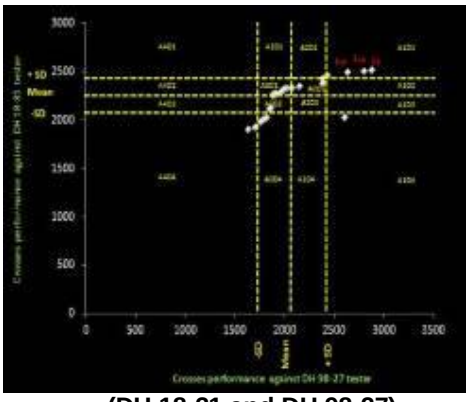
Fig 15 : Sub-grouping of recominant population based on cross performance with hirsutum testers DH 98-27, ZCH 8, 178-24 and DH 18-31



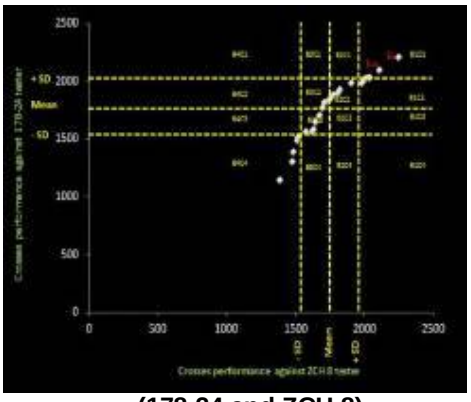
(ZCH 8 and DH98–27)



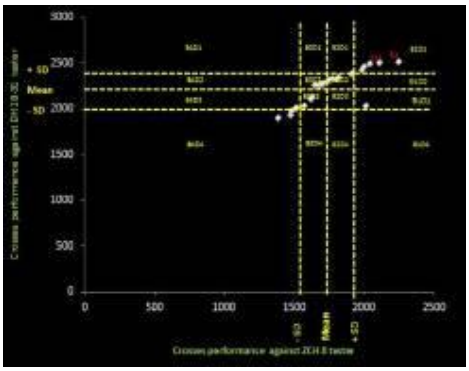
(178-24 and DH 98-27)



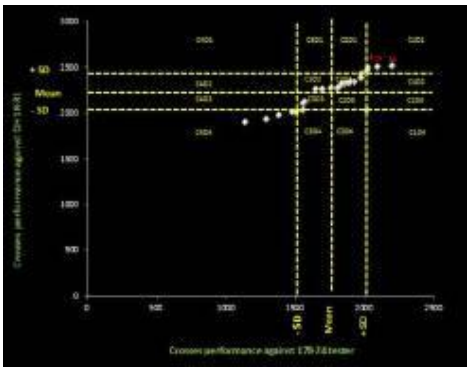
(DH 18-31 and DH 98-27)



(178-24 and ZCH 8)



(DH 18-31 and ZCH)



(DH 18-31 and 178-24)

Fig 16 : Sub-grouping of recombinant population based on cross performance against two hirsutum testers ZCH 8 and DH98-27, 178-24 and DH 98-27, DH 18-31 and DH 98-27, 178-24 and ZCH 8, DH 18-31 and ZCH 8 and DH 18-31 and 178-24

Table 38. Mean and per cent improvement of derived F_1 crosses involving F_4 lines for seed cotton yield (Transgressive Segregation)

F_4 lines	DH98-27 (T_1)			F_4 lines	ZCH8 (T_2)			F_4 lines	178-24 (T_3)			F_4 lines	DH 18-31 (T_4)		
	Seed cotton yield (kg/ha)	Superiority over SBMC	Inferiority over IBMC		Seed cotton yield (kg/ha)	Superiority over SBMC	Inferiority over IBMC		Seed cotton yield (kg/ha)	Superiority over SBMC	Inferiority over IBMC		Seed cotton yield (kg/ha)	Superiority over SBMC	Inferiority over IBMC
[DH 98-27 x (DB 533 x DB 534 F4 IPS 49)]	2884.26	78.36**	104.82**	[ZCH 8 x (DB 533 x DB 534 F4 IPS 49)]	2250.72	31.62	45.84	[178-24 x (DB 533 x DB 534 F4 IPS 49)]	2207.48	23.49	47.17	[DH 18-31 x (DB 533 x DB 534 F4 IPS 49)]	2515.91	56.01**	59.38**
[DH 98-27 x (DB 534 x DB 533 F4 IPS 22)]	2800.90	73.20*	98.90**	[ZCH 8 x (DB 534 x DB 533 F4 IPS 22)]	2112.13	23.51	36.86	[178-24 x (DB 534 x DB 533 F4 IPS 22)]	2099.11	17.42	39.95	[DH 18-31 x (DB 534 x DB 533 F4 IPS 22)]	2502.36	55.17**	58.52**
[DH 98-27 x (DB 533 x DB 534 F4 IPS 52)]	2636.78	63.06*	87.24*	[ZCH 8 x (DB 533 x DB 534 F4 IPS 52)]	2040.76	19.34	32.24	[178-24 x (DB 533 x DB 534 F4 IPS 52)]	2027.73	13.43	35.19	[DH 18-31 x (DB 533 x DB 534 F4 IPS 52)]	2490.38	54.42**	57.77**
[DH 98-27 x (DB 533 x DB 534 F4 IPS 105)]	2606.56	61.19*	85.10*	[ZCH 8 x (DB 533 x DB 534 F4 IPS 105)]	2015.23	17.85	30.58	[178-24 x (DB 533 x DB 534 F4 IPS 105)]	2026.17	13.34	35.09	[DH 18-31 x (DB 533 x DB 534 F4 IPS 17)]	2455.99	52.29**	55.59**
[DH 98-27 x (DB 533 x DB 534 F4 IPS 17)]	2433.59	50.49	72.81*	[ZCH 8 x (DB 533 x DB 534 F4 IPS 17)]	2001.68	17.05	29.71	[178-24 x (DB 533 x DB 534 F4 IPS 17)]	2025.13	13.28	35.02	[DH 18-31 x (DB 533 x DB 534 F4 IPS 16)]	2424.73	50.35**	53.61**
[DH 98-27 x (DB 533 x DB 534 F4 IPS 16)]	2384.62	47.46	69.34*	[ZCH 8 x (DB 533 x DB 534 F4 IPS 16)]	1985.01	16.08	28.63	[178-24 x (DB 533 x DB 534 F4 IPS 16)]	1983.45	10.95	32.24	[DH 18-31 x (DB 533 x DB 534 F4 IPS 48)]	2384.10	47.83**	51.03**
[DH 98-27 x (DB 533 x DB 534 F4 IPS 48)]	2380.97	47.24	69.08*	[ZCH 8 x (DB 533 x DB 534 F4 IPS 48)]	1908.42	11.60	23.66	[178-24 x (DB 533 x DB 534 F4 IPS 48)]	1980.84	10.81	32.06	[DH 18-31 x (DB 533 x DB 534 F4 IPS 25)]	2342.42	45.25*	48.39**
[DH 98-27 x (DB 533 x DB 534 F4 IPS 25)]	2152.77	33.12	52.87	[ZCH 8 x (DB 533 x DB 534 F4 IPS 25)]	1822.46	6.57	18.09	[178-24 x (DB 533 x DB 534 F4 IPS 25)]	1930.83	8.01	28.73	[DH 18-31 x (DB 533 x DB 534 F4 IPS 34)]	2340.33	45.12*	48.26**
[DH 98-27 x (DB 533 x DB 534 F4 IPS 34)]	2074.62	28.29	47.32	[ZCH 8 x (DB 533 x DB 534 F4 IPS 34)]	1815.69	6.18	17.65	[178-24 x (DB 533 x DB 534 F4 IPS 34)]	1902.69	6.44	26.85	[DH 18-31 x (DB 533 x DB 534 F4 IPS 55)]	2326.79	44.28*	47.40**
[DH 98-27 x (DB 533 x DB 534 F4 IPS 55)]	2074.10	28.26	47.29	[ZCH 8 x (DB 533 x DB 534 F4 IPS 55)]	1806.31	5.63	17.05	[178-24 x (DB 533 x DB 534 F4 IPS 55)]	1899.05	6.23	26.61	[DH 18-31 x (DB 533 x DB 534 F4 IPS 44)]	2322.62	44.02*	47.14*
[[DH 98-27 x (DB 533 x DB 534 F4 IPS 44)]	2029.82	25.52	44.14	[ZCH 8 x (DB 533 x DB 534 F4 IPS 44)]	1772.44	3.65	14.85	[178-24 x (DB 533 x DB 534 F4 IPS 44)]	1878.73	5.10	25.26	[DH 18-31 x (DB 533 x DB 534 F4 IPS 13)]	2321.06	43.92*	47.04*
[DH 98-27 x (DB 533 x DB 534 F4 IPS 13)]	2009.50	24.26	42.70	[ZCH 8 x (DB 533 x DB 534 F4 IPS 13)]	1758.90	2.86	13.97	[178-24 x (DB 533 x DB 534 F4 IPS 13)]	1859.97	4.05	24.01	[DH 18-31 x (DB 533 x DB 534 F4 IPS 8)]	2314.80	43.54*	46.64*
[DH 98-27 x (DB 533 x DB 534 F4 IPS 8)]	1999.08	23.62	41.96	[ZCH 8 x (DB 533 x DB 534 F4 IPS 8)]	1750.04	2.34	13.40	[178-24 x (DB 533 x DB 534 F4 IPS 8)]	1840.69	2.97	22.72	[DH 18-31 x (DB 533 x DB 534 F4 IPS 1)]	2297.61	42.47*	45.55*
[DH 98-27 x (DB 533 x DB 534 F4 IPS 1)]	1980.32	22.46	40.63	[ZCH 8 x (DB 533 x DB 534 F4 IPS 1)]	1734.41	1.43	12.39	[178-24 x (DB 533 x DB 534 F4 IPS 1)]	1828.71	2.30	21.92	[DH 18-31 x (DB 533 x DB 534 F4 IPS 14)]	2275.73	41.11*	44.17*
[DH 98-27 x (DB 533 x DB 534 F4 IPS 14)]	1955.83	20.95	38.89	[ZCH 8 x (DB 533 x DB 534 F4 IPS 14)]	1713.05	0.18	11.00	[178-24 x (DB 533 x DB 534 F4 IPS 14)]	1815.16	1.54	21.02	[DH 18-31 x (DB 533 x DB 534 F4 IPS 6)]	2273.64	40.98*	44.03*
[DH 98-27 x (DB 533 x DB 534 F4 IPS 6)]	1923.53	18.95	36.59	[ZCH 8 x (DB 533 x DB 534 F4 IPS 6)]	1706.28	-0.22	10.56	[178-24 x (DB 533 x DB 534 F4 IPS 6)]	1814.64	1.51	20.98	[DH 18-31 x (DB 533 x DB 534 F4 IPS 15)]	2271.56	40.85*	43.90*
[DH 98-27 x (DB 533 x DB 534 F4 IPS 15)]	1902.69	17.66	35.11	[ZCH 8 x (DB 533 x DB 534 F4 IPS 15)]	1693.25	-0.98	9.72	[178-24 x (DB 533 x DB 534 F4 IPS 15)]	1768.27	-1.08	17.89	[DH 18-31 x (DB 533 x DB 534 F4 IPS 71)]	2259.58	40.11*	43.14*

Contd.....

F_4 lines	DH98-27 (T_1)			F_4 lines	ZCH8 (T_2)			F_4 lines	178-24 (T_3)			F_4 lines	DH 18-31 (T_4)		
	Seed cotton yield (kg/ha)	Superiority over SBMC	Inferiority over IBMC		Seed cotton yield (kg/ha)	Superiority over SBMC	Inferiority over IBMC		Seed cotton yield (kg/ha)	Superiority over SBMC	Inferiority over IBMC		Seed cotton yield (kg/ha)	Superiority over SBMC	Inferiority over IBMC
[DH 98-27 x (DB 533 x DB 534 F4 IPS 71)]	1894.36	17.14	34.52	[ZCH 8 x (DB 533 x DB 534 F4 IPS 71)]	1674.49	-2.08	8.50	[178-24 x (DB 533 x DB 534 F4 IPS 71)]	1701.59	-4.81	13.45	[DH 18-31 x (DB 533 x DB 534 F4 IPS 26)]	2255.93	39.89*	42.91*
[DH 98-27 x (DB 533 x DB 534 F4 IPS 26)]	1878.73	16.18	33.41	[ZCH 8 x (DB 533 x DB 534 F4 IPS 26)]	1645.32	-3.78	6.61	[178-24 x (DB 533 x DB 534 F4 IPS 26)]	1651.57	-7.61	10.11	[DH 18-31 x (DB 533 x DB 534 F4 IPS 12)]	2120.47	31.49	34.33
[DH 98-27 x (DB 533 x DB 534 F4 IPS 12)]	1861.53	15.11	32.19	[ZCH 8 x (DB 533 x DB 534 F4 IPS 12)]	1630.73	-4.64	5.67	[178-24 x (DB 533 x DB 534 F4 IPS 12)]	1580.71	-11.58	5.39	[DH 18-31 x (DB 533 x DB 534 F4 IPS 38)]	2118.39	31.36	34.20
[DH 98-27 x (DB 533 x DB 534 F4 IPS 38)]	1859.97	15.02	32.08	[ZCH 8 x (DB 533 x DB 534 F4 IPS 38)]	1625.52	-4.94	5.33	[178-24 x (DB 533 x DB 534 F4 IPS 38)]	1568.73	-12.25	4.59	[DH 18-31 x (DB 533 x DB 534 F4 IPS 23)]	2111.61	30.94	33.77
[DH 98-27 x (DB 533 x DB 534 F4 IPS 23)]	1855.28	14.73	31.75	[ZCH 8 x (DB 533 x DB 534 F4 IPS 23)]	1622.92	-5.09	5.16	[178-24 x (DB 533 x DB 534 F4 IPS 62)]	1565.08	-12.45	4.35	[DH 18-31 x (DB 533 x DB 534 F4 IPS 62)]	2024.61	25.54	28.26
[DH 98-27 x (DB 533 x DB 534 F4 IPS 62)]	1819.33	12.51	29.19	[ZCH 8 x (DB 533 x DB 534 F4 IPS 62)]	1575.50	-7.87	2.09	[178-24 x (DB 533 x DB 534 F4 IPS 23)]	1565.08	-12.45	4.35	[DH 18-31 x (DB 533 x DB 534 F4 IPS 105)]	2024.61	25.54	28.26
[DH 98-27 x (DB 533 x DB 534 F4 IPS 36)]	1812.04	12.05	28.68	[ZCH 8 x (DB 533 x DB 534 F4 IPS 36)]	1520.28	-11.10	-1.49	[178-24 x (DB 533 x DB 534 F4 IPS 36)]	1512.98	-15.36	0.87	[DH 18-31 x (DB 533 x DB 534 F4 IPS 36)]	2007.93	24.51	27.20
[DH 98-27 x (DB 533 x DB 534 F4 IPS 30)]	1785.99	10.44	26.83	[ZCH 8 x (DB 533 x DB 534 F4 IPS 30)]	1514.03	-11.46	-1.89	[178-24 x (DB 533 x DB 534 F4 IPS 30)]	1486.41	-16.85	-0.90	[DH 18-31 x (DB 533 x DB 534 F4 IPS 30)]	2003.25	24.22	26.90
[DH 98-27 x (DB 533 x DB 534 F4 IPS 32)]	1761.50	8.93	25.09	[ZCH 8 x (DB 533 x DB 534 F4 IPS 32)]	1481.72	-13.35	-3.99	[178-24 x (DB 533 x DB 534 F4 IPS 32)]	1391.07	-22.18	-7.26	[DH 18-31 x (DB 533 x DB 534 F4 IPS 32)]	1975.11	22.47	25.12
[DH 98-27 x (DB 533 x DB 534 F4 IPS 24)]	1703.15	5.32	20.94	[ZCH 8 x (DB 533 x DB 534 F4 IPS 24)]	1474.43	-13.78	-4.46	[178-24 x (DB 533 x DB 534 F4 IPS 24)]	1298.85	-27.34	-13.40	[DH 18-31 x (DB 533 x DB 534 F4 IPS 24)]	1928.22	19.56	22.15
[DH 98-27 x (DB 533 x DB 534 F4 IPS 33)]	1642.19	1.55	16.61	[ZCH 8 x (DB 533 x DB 534 F4 IPS 33)]	1388.47	-18.81	-10.03	[178-24 x (DB 533 x DB 534 F4 IPS 33)]	**1146.20**	-35.88	-23.58	[DH 18-31 x (DB 533 x DB 534 F4 IPS 33)]	1899.57	17.79	20.34
Segregants	**28**				**20**				**20**				**28**		
Positive	**28**				**15**				**16**				**28**		
Negative	**0**				**5**				**4**				**0**		
SEm+	**63.48**				**39.53**				**48.24**				**34.41**		
CD at 5%	**934.90**				**802.60**				**808.29**				**551.2116**		
CD at 1%	**1263.249**				**1084.49**				**1092.18**				**744.8079**		
Straight crosses (Bench Mark Crosses)															
SBMC	**1617.11 (DB 533 x DH 98-27/T_1)**				**1710.04 (DB 533 x ZCH8/T2)**				**1787.64 (DB 533X 178-24/T3)**			**1612.70 (DB 533X DH 18-31/T4)**			
IBMC	**1408.22 (DB 534 x DH 98-27/T_1)**				**1543.25 (DB 534 x ZCH8/T2)**				**1499.90 (DB 534 x 178-24/T3)**			**1578.465 (DB 534 x DH 18-31/T4)**			

SBMC: Superior Bench Mark Crosses **IBMC:** Inferior Bench Mark Crosses

bench mark crosses (SBMC). This reflected the extent of transgressive segregation for combining ability occurring in desirable direction. Despite all, along with superior straight crosses, five derived F_1 crossess showed negative inferiority over inferior straight cross. This proved the transgressive segregation for combining ability occurring in undesirable direction also.

The heterosis values of derived F_1 crosses over MRC 6918 and DCH 32, non of the derived F_1 crosses were shown significant superior over the two commercial checks.

5.2.5.3 With tester T_3 (178-24)

With tester 178-24 (T_3), the per cent superiority of derived F_1 crosses over superior straight cross produced as many as 16 positive transgressive segregants. Among these, DB 533 x DB 534 F_4 IPS 49 (23.49), DB 534 x DB 533 F_4 IPS 22 (17.42) and DB 533 x DB 534 F_4 IPS 52 (13.43) F_4 lines have produced highest transgressive segregants. Whereas, the per cent inferiority of derived F_1 crosses over inferior straight cross revealed four negative transgressive segregants.

Comparing the mean yields of derived F_1 crosses over superior straight cross, it was evident that the derived F_1s expressed marginal amount of superiority over superior straight cross indicating presence of genetic diversity between the F_4 lines and the concerned tester. This indicated the extent of transgressive segregation for combining ability in desirable direction.

Two of the derived F_1 crosses were significantly superior over *Bt* check (MRC 6918) and one cross showed significantly superior over non *Bt* commercial check (DCH 32).

5.2.5.4 With tester T_4 (DH 18-31)

Along with tester DH 18-31 (T_4), the per cent superiority of derived F_1 crosses over superior straight cross had produced 28 positive transgressive segregants. Among these, eighteen F_4 lines have significant transgressive segregants and DB 533 x DB 534 F_4 IPS 49 (56.01), DB 534 x DB 533 F_4 IPS 22 (55.17) and DB 533 x DB 534 F_4 IPS 52 (54.42) F_4 lines recorded highest value of positive transgressive segregants. Whereas, there are no negative transgressive segregants for combining ability.

Comparing the mean yields of derived F_1 crosses and superior straight cross, it was evident that the derived F_1 crosses expressed substantially high amount of expression. This reflected the extent of transgressive segregation for combining ability occurring in desirable direction. Despite all, along with superior straight crosses, non of derived F_1 crosses hybrids showed negative inferiority over inferior straight cross. This proved the transgressive segregation for combining ability occurring in undesirable direction also.

The heterosis values of derived F_1 crosses over MRC 6918 and DCH 32, non of the derived F_1 crosses were shown significant superior over the two commercial checks.

In general, the derived F_1 crosses expressed substantially high amount of transgressive segregation for combining ability for DH 98-27 (T_1) and DH 18-31 (T_2) testers. Among the population used in the combining ability study, DB 533 x DB 534 F_4 IPS 49, DB 534 x DB 533 F_4 IPS 22 and DB 533 x DB 534 F_4 IPS 52 F_4 lines combined very well with all the four testers. Being F_4 lines productive with all the four testers over DB 533 and DB 534 itself indicates that when even good combiner parents can be used for creating recombinational variability. These parents reveal diversity in the identity of favourable alleles contained in them. We can expect segregation at more number of yield influencing dominant loci. As a result of this variability is released at more number of loci and thus recombinant lines having desirable blend of favourable alleles distributed between two parents are obtained such lines give rise to superior derived F_1 crosses.

It also indicated that in general, the segregants are genetically more diverse from tester as compared to the two parents. It can be taken to infer that segregants used as female plants have the genotypic constitution complimentary to that found in the tester(s). In other words, they accumulated more number of such dominant favourable alleles, which impart diversity to their genetic constitution as compared to the genetic constitution of the testers used. Thus, the difference in performance seen between straight crosses and derived F_1 crosses is attributed to greater genetic diversity existing between the tester(s) and segregants.

These results of present study are in confirmity with earlier studies in sorghum of Sridhar (1991) and Desai (1991), which also observed increased genetic diversity among the F_2 and F_3 segregants from a given tester as compared to the parents.

The genetic diversity is very essential in making the derived F_1 crosses or for that matter any F_1 heterotic (Falconer, 1981). The value of F_1 crosses depends on the magnitude of dominance and genetic diversity as revealed by the formula $HF_1 = \Sigma dy^2$, where 'd' is dominance effect and 'y' represents genetic diversity between the parents, when straight crosses and derived F_1 crosses are compared the difference in their performance is attributed to greater heterosis existing between the tester and segregants.

This study clearly depicts that by crossing two genotypes we can obtain many segregants which accumulate such favourable combinations of alleles which make them genetically more diverse from a tester than the two original parents involved.

There is a need to test the stability of combining ability of superior lines in succeeding advanced generations. In addition to this, it is required to confirm the superiority of the promising crosses for their yield potentiality by testing them in large scale plots.

5.2.6 Potential combiners and combinations developed from the study

In this part of the study nature and magnitude of variability for combining ability was assessed against four hirsutum tester included in the heterotic box.

The derived F_1 crosses (28 x 4) were compared with the bench mark crosses (two barbadense lines x 4 hirsutum testers) of the heterotic box, best *Bt* check hybrid (MRC 6918) and non *Bt* check (DCH 32). The derived F_1 crosses revealed considerable variability for *per se* performance measured in terms of productivity and fiber quality traits. Many derived F_1 crosses were found to be more productive than DCH 32 (48 hybrids) and MRC 6918 (35 hybrids).

The potential crosses like DH 98-27 X (DB 533 x DB 534 F_4 IPS 49), DH 98-27 X (DB 534 x DB 533 F_4 IPS 22) and DH 98-27 X (DB 533 x DB 534 F_4 IPS 52) recorded highest *per se* performance for seed cotton yield (Table 39 and Plate 11). These crosses also recorded high value for yield attributing characters like number of bolls per plant, mean boll weight, seed index and number of sympodia per plant. These potential crosses recorded highly significant heterosis over mid parent for seed cotton yield. They also recorded significant heterosis for other yield attributing characters in desirable direction.

Apart from showing high productivity the potential cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 49 showed higher value of photosynthetic rate, stomatal conductance and fiber quality parameters. This potential cross is example for blending of yield characters, physiological parameters and fiber quality.

The *gca* and *sca* status of superior crosses is given in the Table 36. Most of the potential crosses involved DH 98-27, DH 18-31, DB 533 x DB 534 F_4 IPS 49, DB 534 x DB 533 F_4 IPS 22, DB 533 x DB 534 F_4 IPS 52, DB 533 x DB 534 F_4 IPS 17 and DB 533 x DB 534 F_4 IPS 16 as a common parents, which had *gca* effect of 94.65, 35.44, -208.12, -346.19, -128.67, 311.05 and -179.86, respectively. These potential crosses also revealed the contribution of *sca* effect. This suggests that these crosses can be exploited either as hybrids or they can be subjected to the schemes aimed at improving combining ability. In cross pollinated crops, reciprocal recurrent selection schemes are adopted for exploiting both *gca* and *sca* effects and utilizing the improved lines obtained from the diverse sources for developing more potential inter plant type hybrids.

This scheme of reciprocal recurrent selection cannot be implemented as it is in cotton because of the difference in mating system of cotton. In maize, populations are subjected to natural random mating and this can be maintained with ease. The available populations are themselves random mating populations which can be subjected to procedures of reciprocal recurrent selection. In cotton, it is possible to identify opposite pairs of genotypes based on predicted or actual double cross performance. Segregating populations can be developed by utilizing opposite pairs of genotypes and they can be subjected to one cycle of recurrent selection for combining ability. A modification in this approach defined (Patil, 1995) as reciprocal selection for combining ability has been followed in cotton (Patil and Patil, 2003).

Hybrid breeding programs in cross pollinated crops implement population improvement programs aimed at improving combining ability. Improving combining ability in a primarily self pollinated crop such as cotton should work but the procedures need to be modified to suit the mating system of cotton. Two modified approaches of improving combining ability were tested in cotton. One method was practicing reciprocal selection for combining ability based on double cross performance. A second method is the triangular approach of improving combining ability against specific testers (Patil *et al*., 2007).

Table 39. Combining ability status of most potential derived F_1 crosses with respect to seed cotton yield (kg/ha)

Sl. No.	Potential crosses	Seed cotton yield (kg/ha)			
		Per se Performance	*gca* effect		*sca* effect
			gca of line	gca of tester	
1	[DH 98-27 x (DB 533 x DB 534 F4 IPS 49)]	2884.26	-208.12	94.65**	610.26*
2	[DH 98-27 x (DB 534 x DB 533 F4 IPS 22)]	2800.90	-346.19**	94.65**	680.34*
3	[DH 98-27 x (DB 533 x DB 534 F4 IPS 52)]	2636.78	-128.67	94.65**	450.45
4	[DH 98-27 x (DB 533 x DB 534 F4 IPS 105)]	2606.56	-72.66	94.65**	487.51
5	[DH 18-31 x (DB 533 x DB 534 F4 IPS 49)]	2515.91	-208.12	35.44	140.97
6	[DH 18-31 x (DB 534 x DB 533 F4 IPS 22)]	2502.36	-346.19**	35.44	245.30
7	[DH 18-31 x (DB 533 x DB 534 F4 IPS 52)]	2490.38	-128.67	35.44	210.00
8	[DH 18-31 x (DB 533 x DB 534 F4 IPS 17)]	2455.99	311.05*	35.44	289.59
9	[DH 98-27 x (DB 533 x DB 534 F4 IPS 17)]	2433.59	311.05*	94.65**	453.96
10	[DH18-31 x (DB 533 x DB 534 F4 IPS 16)]	2424.73	-179.86	35.44	203.57
11	[DH 98-27 x (DB 533 x DB 534 F4 IPS 16)]	2384.62	-179.86	94.65**	257.49
	Mean	**2557.83**			

DH 98-27 X (DB 533 X DB 534 F4 IPS 49)

DH 98-27 x (DB 534 x DB 533 F4 IPS 22)

Plate 11 : Most productive hirsutum testers included in recombinational variability study

5.3 Correlation co-efficient analysis

5.3.1 Phenotypic correlation co-efficient in derived F_1 crosses

Yield is a complex polygenically inherited character resulting from multiplicative interaction of its contributing characters. It is highly influenced by the environment, hence selection based on yield alone may limit the improvement.Whereas, the component characters of yield are less complex in inheritance and are influenced by the environment to a lesser extent. Thus, effective improvement in yield may be brought about through selection for yield component characters.

Yield component characters show association among themselves and also with yield. Favorable associations between desirable attributes will help improvement in a joint manner. Whereas, unfavorable associations between the desirable attributes under selection may limit genetic advance. Hence, knowledge of associations between the yield components and also among themselves are essential for planning a sound breeding programme.

Grafius (1959) reported that there may not be genes for yield as such, but operate only through its components. So, correlation analysis provides the information on nature and magnitude of the association of different components characters with seed yield, which is regarded as highly complex trait in which the breeder is ultimately interested. So, it is a matter of great importance to the plant breeders to find out as to which of the characters are correlated with yield and also how they are associated among themselves, if negative association between characters is due to pleiotropic effects it would be very difficult to obtain the desired combinations while if linkage is involved, special breeding programmes are needed to break these linkage blocks.

In the present investigation, character association among different quantitative characters in cross population study is estimated by using correlation co-efficient at phenotypic level.

At phenotypic level, seed cotton yield exhibited highest positive association with lint index, mean boll weight, number of monopodia per plant, number of bolls per plant, number of sympodia per plant, plant height, seed index, photosynthetic rate, ginning outturn and sympodial length at 50 per cent plant height. Similar results of association of these traits with seed cotton yield were reported by Bhatade (1982), Gulamov *et al.* (1974), Manivasakam (1985), Nazir and Khan (1974), Verma *et al.* (2006) and Muthu *et al.* (2004). Whereas seed cotton yield recorded negative correlation with stomatal conductance, inter branch distance, reproductive points on sympodia and transpiration rate. Negative correlation between seed cotton yield and stomatal conductance the same results confirmed with the findings of Penman and Schofield (1951), Jones (1977), Austin (1977) and Jing and Ma (1990).

The phenotypic correlation values also revealed that seed cotton yield per plant had highly significant and positive phenotypic correlation with bolls per plant. Similar results were represented by Musande *et al*. (1981), Govilla and Sharma (1981), Gill and Singh (1981), Bhatade (1982), Gawand *et al*. (1984), Kumar and Choudhary (1986), Shandhu *et al* .(1986). Significant and positive phenotypic correlation found between seed cotton yield per plant and mean boll weight. The same findings were reported by Griffee, Ligon and Brannon (1929).The association of seed cotton yield with monopodia appeared positive association was found by Singh *et al*. (1968 a).

Number of monopodia per plant recorded highly significant positive strong correlation with plant height. Number of sympodia per plant exhibited highly significant positive correlation with plant height and number of monopodia per plant. Number of sympodia per plant had highly significant positive strong correlation with plant height. Number of bolls per plant recorded highly significant positive correlation with plant height, number of monopodia per plant and number of sympodia per plant. Among these number of bolls per plant had highly significant positive strong correlation with number of sympodia per plant.

Mean boll weight exhibited highly significant positive correlation with plant height, number of monopodia per plant, number of sympodia per plant and number of bolls per plant. Among these, mean boll weight showed highly significant positive strong correlation with number of bolls per plant. Reproductive points on sympodia showed highly negative significant correlation with number of bolls per plant and mean boll weight, while reproductive points on sympodia recorded negative significant correlation with number of sympodia per plant. Sultan *et al.* (1999) and Jagtap and Kolhe (1984) reported the same results.

Sympodial length at 50% plant height exhibited highly positive significant correlation with plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant and reproductive points on sympodia. Among these, sympodial length at 50 % plant height recorded highly significant positive strong correlation with plant height. Inter branch distance exhibited significant positive correlation with sympodial length at 50% plant height.

Seed index recorded significant positive correlation with plant height, highly significant positive correlation with number of monopodia per plant, significant positive correlation with number of sympodia per plant and highly significant positive correlation with mean boll weight. Among these seed index showed highly significant positive strong correlation with mean boll weight. Ginning outturn showed significant negative correlation with reproductive points on sympodia. Similar results have been also reported by Sambamurthy *et al.* (1994).

Lint index exhibited highly significant positive association with number of monopodia per plant, number of sympodia per plant, mean boll weight, seed index and ginning outturn. Among these, lint index showed highly significant positive strong correlation with seed index. Lint index recorded significant negative correlation with reproductive points on sympodia. The same result of significant positive correlation between seed index and lint index confirmed by Sambamurthy *et al.* (1994).

seed cotton yield exhibited highly significant positive correlation with plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, mean boll weight, seed index, ginning outturn, lint index and photosynthetic rate in cross population. Among these, seed cotton yield exhibited highly significant positive strong association with lint index compare to other characters. Similar results of association of these traits with seed cotton yield were reported by Bhatade (1982), Gulamov *et al.* (1974), Manivasakam (1985), Nazir and Khan (1974), Verma *et al.* (2006) and Muthu *et al.* (2004).

Stomatal conductance showed highly negative significant correlation with number of monopodia per plant and number of bolls per plant, while stomatal conductance had highly significant positive strong correlation with photosynthetic rate. Stomatal conductance exhibited significant positive correlation with inter branch distance and ginning outturn.

Transpiration rate had highly significant negative correlation with plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, mean boll weight and seed index, while transpiration rate recorded highly significant positive correlation with inter branch distance, photosynthetic rate and stomatal conductance. Among these, transpiration rate showed highly significant positive strong correlation with stomatal conductance. Transpiration rate exhibited significant positive correlation with number of reproductive points.

5.3.2 Phenotypic correlation co-efficient in line x tester inter specific crosses (YHB)

The phenotypic correlation co-efficients among all characters related to seed cotton yield per plant were estimated and the results are presented below.

Seed cotton yield exhibited significant positive correlation with mean boll weight, ginning outturn and lint index. Among these, seed cotton yield recorded significant positive strong correlation with ginning outturn. Similar results of association of these traits with seed cotton yield were reported by Bhatade (1982), Gulamov *et al.* (1974), Manivasakam (1985), Ligon and Brannon (1929), Nazir and Khan (1974), Verma *et al.* (2006) and Muthu *et al.* (2004).

Number of monopodia per plant recorded non significant negative correlation with plant height. Number of sympodia per plant exhibited highly significant positive correlation with plant height.

Number of bolls per plant recorded highly significant positive correlation with number of sympodia per plant. Mean boll weight exhibited non significant correlation with other characters.

Reproductive points on sympodia showed highly significant positive correlation with plant height and number of sympodia per plant. Among these, reproductive points recorded highly significant positive strong correlation with plant height.

Sympodial length at 50% plant height exhibited highly significant positive correlation with plant height, number of sympodia per plant and reproductive points on sympodia. Among these, sympodial length at 50% plant height showed highly significant positive strong correlation with reproductive points on sympodia, while sympodial length at 50 per cent plant height showed highly significant negative correlation with number of monopodia per plant.

Inter branch distance exhibited highly significant positive correlation with plant height, number of sympodia per plant and sympodial length at 50% plant height. Among these, inter branch distance had highly significant positive strong correlation with plant height, while exhibited significant positive correlation with reproductive points on sympodia.

Seed index recorded highly significant positive correlation with number of bolls per plant and highly significant negative correlation with inter branch distance.

Ginning outturn showed non significant correlation with other characters.

5.3.3 Intergeneration (F_3-F5) correlation and heritability estimates

Intergeneration correlation co-efficients give an idea about the effectiveness of single plant selection and to some extent on nature of gene action. If the correlation co-efficient is high, it would mean high heritable portion and probably the additive component. Cahaner and Hillet (1980) indicted that heritability estimated based on regression method contains greater proportion of non additive variance in the numerator and hence it is less reliable. In the present study, Intergeneration correlation values revealed that, the barbadense lines in both generations exhibited highly significant positive correlation for 2.5% S/L and significant positive correlation for fibre uniformity ratio and fibre micronaire value. Non of barbadense in two generations exhibited significant correlation for fiber maturity ratio, fiber tenacity and fiber elongation.

The moderate heritability was noticed for fiber maturity ratio, fiber tenacity and fiber elongation.The high heritability was noticed for 2.5% S/L, fiber uniformity ratio and fiber micronaire value. Indicating this trait is mostly governed by additive gene action and suitability of this trait for selection on individual plant basis in the advanced generations of segregating progenies. These findings were supported by Kulkarni *et al*. (1976) and Reddy *et al*. (1985).

5.4 Path Co-efficient Analysis

5.4.1 Direct and indirect phenotypic effects of component characters on seed cotton yield in derived F_1 crosses

The relationship between yield and yield components may be negative or positive but it is the net result of direct effect of that particular trait and indirect effects *via* other traits. Hence, it is necessary to determine the path co-efficient which partition the observed correlation in to direct and indirect effects and also reveals the cause and effect relationship between yield and their related traits.

5.4.1.1 Plant height (cm)

The direct effect of plant height on seed cotton yield was positive. The contribution of other characters indirectly on seed cotton yield through plant height appeared to be positive value in respect of number of monopodia per plant, number of sympodia per plant, number of bolls per plant, mean boll weight, reproductive points on sympodia, sympodial length at 50% plant height, seed index, lint index and photosynthetic rate. The contribution had negative indirect effects *via* inter branch distance, ginning outturn, stomatal conductance and transpiration rate.

5.4.1.2 Number of monopodia per plant

It was observed that number of monopodia per plant appeared to influence seed cotton yield directly as positive value. Balakotaiah (1973), Gill and Singh (1981), Vijendaradradas (1981) represented the same result in their study. The contribution of other characters indirectly on seed cotton yield through number of monopodia per plant appeared to be positive value in respect of plant height, number of sympodia per plant, number of bolls per plant, mean boll weight, sympodial length at 50% plant height, seed index, lint index and photosynthetic rate. The association recorded negative indirect effects *via* reproductive points on sympodia, inter branch distance, ginning outturn, stomatal conductance and transpiration rate.

5.4.1.3 Number of sympodia per plant

The direct influence of number of sympodia per plant towards seed cotton yield was positive. Tomar and Singh (1992), Bhatade (1982) found the same result. The contribution of other characters indirectly on seed cotton yield through number of sympodia per plant showed to be positive value in respect of plant height, number of monopodia per plant, number of bolls per plant, mean boll weight, sympodial length at 50 % plant height, inter branch distance, seed index, ginning outturn, lint index

and photosynthetic rate. The contribution showed negative indirect effects *via* reproductive points on sympodia, stomatal conductance and transpiration rate. Similar results were represented by Gill and Singh (1981) and Choudhary *et al.* (1988).

5.4.1.4 Number of bolls per plant

The direct effect of number of bolls per plant on seed cotton yield was positive. The contribution of other characters indirectly on seed cotton yield through number of bolls per plant appeared to be positive value in respect of plant height, number of monopodia per plant, number of sympodia per plant, mean boll weight, sympodial length at 50% plant height, seed index and lint index. The contribution exhibited negative indirect effects *via* reproductive points on sympodia, inter branch distance, ginning outturn, photosynthetic rate, stomatal conductance and transpiration rate. The importance of number of bolls per plant towards seed yield has also been reported by Dedaniy and Pethani (1994), Tyagi *et al.* (1988), Muthu *et al.* (2004) and Verma *et al*. (2006). Therefore this trait appears to be most important in influencing seed cotton yield in cotton and selection should be oriented towards high boll number.

5.4.1.5 Mean boll weight (g)

The direct contribution of mean boll weight on seed cotton yield was positive. The highest contribution of mean boll weight has been reported by Balakotaiah (1973), Gill and Singh (1981), Vijendaradradas (1981), Salimath (1975) and Krishnarao and Mary (1990). This indicates that selection for high mean boll weight would contribute to increased seed yield. The contribution of other characters indirectly on seed cotton yield through mean boll weight appeared to be positive value in respect of plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, sympodial length at 50% plant height, seed index, ginning outturn, lint index and photosynthetic rate. The association exhibited negative indirect effects *via* reproductive points on sympodia, inter branch distance, stomatal conductance and transpiration rate.

5.4.1.6 Reproductive points on sympodia

It was observed that reproductive points on sympodia appeared to influence seed cotton yield directly as negative value. The contribution of other characters indirectly on seed cotton yield through reproductive points on sympodia to be positive value in respect of number of monopodia per plant, number of sympodia per plant, number of bolls per plant, mean boll weight, seed index, ginning outturn, lint index, photosynthetic rate and stomatal conductance. The association exhibited negative indirect effects *via* plant height, sympodial length at 50% plant height, inter branch distance and transpiration rate.

5.4.1.7 Sympodial length at 50%plant height (cm)

The direct effect of sympodial length at 50% plant height on seed cotton yield was positive. The indirect contribution to seed cotton yield through sympodial length at 50% plant height was positive value in respect of plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, mean boll weight, reproductive points on sympodia and inter branch distance. The association exhibited negative indirect effects *via* seed index, ginning outturn, lint index, photosynthetic rate, stomatal conductance and transpiration rate.

5.4.1.8 Inter branch distance (cm)

It expressed a considerably negative direct effect of inter branch distance on seed cotton yield. The indirect effect of inter branch distance was positive through plant height, number of monopodia per plant, number of bolls per plant, mean boll weight, seed index, lint index and photosynthetic rate. The association recorded negative indirect effects *via* number of sympodia per plant, reproductive points on sympodia, sympodial length at 50% plant height, ginning outturn, stomatal conductance and transpiration rate.

5.4.1.9 Seed index (g)

It was observed that this character appeared to influence seed cotton yield directly as positive value. The contribution of other characters indirectly on seed cotton yield through seed index to be positive value in respect of plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, mean boll weight, ginning outturn, lint index and photosynthetic rate. The association exhibited negative indirect effects *via* reproductive points on sympodia, sympodial length at 50% plant height, inter branch distance, stomatal conductance and transpiration rate. Similar results were also reported by Tyagi *et al.* (1988), Sumathi and Nandarajan (1995).

5.4.1.10 Ginning outturn (%)

Ginning out turn could be considered as one of the most important components owing to the fact that it influenced seed cotton yield via lint index in most of the crosses. The direct effect of ginning outturn on seed cotton yield was positive. The contribution of other characters indirectly on seed cotton yield through ginning outturn to be positive value in respect of number of sympodia per plant, mean boll weight, inter branch distance, seed index, lint index, photosynthetic rate, stomatal conductance and transpiration rate. The association exhibited negative indirect effects *via* plant height, number of monopodia per plant, number of bolls per plant, reproductive points on sympodia and sympodial length at 50% plant height.Similar findings of high indirect effect of ginning out turn in seed cotton yield is also reported by Tomar *et al.* (1992).

5.4.1.11 Lint index (g)

It expressed a considerably positive direct effect of lint index on seed cotton yield. Tomar and Singh (1992) found the same result. The indirect effect of lint index was positive through plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, mean boll weight, seed index, ginning outturn, photosynthetic rate and stomatal conductance. The association recorded negative indirect effects *via* reproductive points on sympodia, sympodial length at 50% plant height inter branch distance and transpiration rate. These findings are in line with the earlier findings of Dedaniya and Pethani (1994) and Tomar and Singh (1991).

5.4.1.12 Photosynthetic rate ($\mu molCO_2m^{-2}s^{-1}$)

The direct contribution of photosynthetic rate on seed cotton yield was positive. The contribution of other characters indirectly on seed cotton yield through photosynthetic rate appeared to be positive value in respect of plant height, number of monopodia per plant, number of sympodia per plant, mean boll weight, seed index, ginning outturn, lint index, stomatal conductance and transpiration rate. The association exhibited negative indirect effects *via* number of bolls per plant reproductive points on sympodia, sympodial length at 50 % plant height and inter branch distance.

5.4.1.13 Stomatal conductance ($\mu molm^{-2}s^{-1}$)

It was observed that this character appeared to influence seed cotton yield directly as negative value. Dhopte *et al.* (1988) recorded the same result. The contribution of other characters indirectly on seed cotton yield through stomatal conductance to be positive value in respect of plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, mean boll weight, reproductive points on sympodia, sympodial length at 50% plant height and seed index. The association exhibited negative indirect effects *via* inter branch distance, ginning outturn, lint index, photosynthetic rate and transpiration rate. Wong *et al*. (1979) and Kuroda and Kumura (1990) found the same result.

5.4.1.14 Transpiration rate (mmol $H_2Om^{-2}s^{-1}$)

It expressed a considerably negative direct effect of transpiration rate on seed cotton yield. The indirect effect of transpiration rate was positive through plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, mean boll weight, sympodial length at 50% plant height, seed index andlint index. The association recorded negative indirect effects *via* reproductive points on sympodia, inter branch distance, ginning outturn, photosynthetic rate and stomatal conductance.

5.4.2 Direct and indirect phenotypic effects of component characters on seed cotton yield in Line x Tester inter specific crosses (YHB)

The phenotypic path co-efficient analysis among all characters related to seed cotton yield per plant were estimated and the results are presented below.

5.4.2.1 Plant height (cm)

The direct effect of this character on seed cotton yield was positive, although plant height exhibited non significant positive association with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through plant height appeared to be positive value in respect of number of sympodia per plant, number of bolls per plant, reproductive points on sympodia, sympodial length at 50 % plant height, inter branch distance, seed index, ginning outturn and lint index. The contribution had negative indirect effects *via* number of monopodia per plant and mean boll weight.

5.4.2.2 Number of monopodia per plant

It was observed that this character appeared to influence seed cotton yield directly as positive value, although number of monopodia per plant recorded non significant positive correlation with seed cotton yield. Balakotaiah (1973), Gill and Singh (1981), Vijendaradradas (1981) represented the same result in their study. The contribution of other characters indirectly on seed cotton yield through number of monopodia per plant appeared to be positive value in respect of number of bolls per plant, ginning outturn and lint index. The association recorded negative indirect effects *via* plant height, number of sympodia per plant, mean boll weight, reproductive points on sympodia, sympodial length at 50 % plant height, inter branch distance and seed index.

5.4.2.3 Number of sympodia per plant

The direct influence of number of sympodia per plant towards seed cotton yield was positive.Tomar and Singh (1992), Bhatade (1982) found the same result. Number of sympodia per plant recorded non significant positive correlation with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through number of sympodia per plant showed to be positive value in respect of plant height, number of bolls per plant, mean boll weight, reproductive points on sympodia, sympodial length at 50 % plant height, inter branch distance, seed index, ginning outturn and lint index. The contribution showed negative indirect effect *via* number of monopodia per plant.

5.4.2.4 Number of bolls per plant

The direct effect of number of bolls per plant on seed cotton yield was negative, although number of bolls per plant exhibited non significant positive association with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through number of bolls per plant appeared to be positive value in respect of inter branch distance. The contribution exhibited negative indirect effects *via* plant height, number of monopodia per plant, number of sympodia per plant, mean boll weight, reproductive points on sympodia, sympodial length at 50 % plant height, seed index, ginning outturn and lint index. The importance of number of bolls per plant towards seed yield has also been reported by Dedaniy and Pethani (1994), Tyagi *et al.* (1988), Muthu *et al.* (2004) and Verma *et al*. (2006). Therefore this trait appears to be most important in influencing seed cotton yield in cotton and selection should be oriented towards high boll number.

5.4.2.5 Mean boll weight (g)

The direct contribution of mean boll weight on seed cotton yield was positive. The highest contribution of mean boll weight has been reported by Balakotaiah (1973), Gill and Singh (1981), Vijendaradradas (1981), Salimath (1975) and Krishnarao and Mary (1990). Mean boll weight showed significant positive association with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through mean boll weight appeared to be positive value in respect of number of sympodia per plant, number of bolls per plant, seed index and lint index. The association exhibited negative indirect effects *via* plant height, number of monopodia per plant, reproductive points on sympodia, sympodial length at 50 % plant height, inter branch distance and ginning outturn.

5.4.2.6 Reproductive points on sympodia

It was observed that this character appeared to influence seed cotton yield directly as negative value, reproductive points on sympodia recorded non significant negative correlation with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through reproductive points on sympodia to be positive value in respect of number of monopodia per plant, mean boll weight, seed index, ginning outturn and lint index. The association showed negative indirect effects *via* plant height, number of sympodia per plant, number of bolls per plant, sympodial length at 50 % plant height and inter branch distance.

5.4.2.7 Sympodial length at 50 %plant height (cm)

The direct effect of sympodial length at 50 % plant height on seed cotton yield was positive, although sympodial length at 50 % plant height recorded non significant negative correlation with seed cotton yield. The indirect contribution to seed cotton yield through sympodial length at 50 % plant height was positive value in respect of plant height, number of sympodia per plant, number of bolls per plant, reproductive points on sympodia and inter branch distance. The association exhibited negative indirect effects *via* number of monopodia per plant, mean boll weight, seed index, ginning outturn and lint index.

5.4.2.8 Inter branch distance (cm)

It expressed a considerably negative direct effect of inter branch distance on seed cotton yield and had non significant negative correlation with seed cotton yield. The indirect effect of inter branch distance was positive through number of monopodia per plant, number of bolls per plant, mean boll weight, seed index and lint index. The association recorded negative indirect effects *via* plant height, number of sympodia per plant, reproductive points on sympodia, sympodial length at 50 % plant height and ginning outturn.

5.4.2.9 Seed index (g)

It was observed that this character appeared to influence seed cotton yield directly as negative value, seed index recorded non significant negative correlation with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through seed index to be positive value in respect of number of monopodia per plant, reproductive points on sympodia, sympodial length at 50 % plant height, inter branch distance and ginning outturn. The association recorded negative indirect effects *via* plant height, number of sympodia per plant, number of bolls per plant, mean boll weight and lint index. Similar results were also reported by Tyagi *et al.* (1988), Sumathi and Nandarajan (1995).

5.4.2.10 Ginning outturn (%)

The direct effect of ginning outturn on seed cotton yield was negative, ginning outturn recorded significant positive correlation with seed cotton yield. The contribution of other characters indirectly on seed cotton yield through ginning outturn to be positive value in respect of mean boll weight, reproductive points on sympodia, sympodial length at 50% plant height and seed index. The association exhibited negative indirect effects *via* plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, inter branch distance -and lint index. Similar findings of high indirect effect of ginning out turn in seed cotton yield is also reported by Tomar *et al.* (1992).

5.4.2.11 Lint index (g)

It expressed a considerably positive direct effect of lint index on seed cotton yield and had significant positive correlation with seed cotton yield. Tomar and Singh (1992) found the same result. The indirect effect of lint index was positive through plant height, number of monopodia per plant, number of sympodia per plant, number of bolls per plant, mean boll weight, seed index and ginning outturn. The association recorded negative indirect effects *via* reproductive points on sympodia, sympodial length at 50 % plant height and inter branch distance.

5.5 Molecular marker study in cotton

DNA based molecular markers acted as a versatile tool to study variability and diversity in different plant species. The search for superior hybrid parents in cotton breeding programmes is commonly based on the estimation of the general combining ability (*gca*) and specific combining ability (*sca*) in inbred lines. However, the application of this procedure is expensive and time consuming. The development of DNA based markers represent an alternative procedure of the identification of promising parental lines for superior performances of hybrids. The microsatellite (SSR's) markers have been widely used for the estimation of variation among closely related individuals due to its multi allelic nature and high polymorphism. Molecular markers based on polymorphism of DNA are especially useful for this purpose because they are not affected by environment (Tatineni *et al.*, 1996 and Saghai-Maroof *et al*., 1984). Several examples of the application of molecular markers to estimate genetic distances have been reported in maize (Smith *et al.*, 1990) and rice (Zhang *et al.*, 1995). Thus, molecular markers like SSR's (microsatellite) could be used for germplasm classification and clustering to derive valuable information for heterosis prediction.

Analysis of microsatellites (SSR's) in 32 parents (28 barbadense lines and 4 hirsutum testers) using 40 primers. Of these, 23 primers revealed a high DNA polymorphism among parents, these 23 primers produced a total of 134 amplified profiles.

The similarity co-efficients involved in the line x tester study ranged from 57% to 96 %, with an average of 81%. Among the parental lines, the lines DB 533 x DB 534 F_4 IPS 8 and DB 533 x DB 534 F_4 IPS 1 showed highest similarity co-efficient value (96%).While, the lines DB 533 x DB 534 F_4 IPS 48 and DB 533 x DB 534 F_4 IPS 16 exhibited lowest similarity co-efficient value (57%). All the 32

genotypes showed diversity among themselves indicating that there is a considerable amount of variation, which can be exploited through appropriate breeding programme.

The dendrogram constructed from the pooled data revealed three distinct clusters. One cluster involved testers and in other clusters all barbadense lines were placed which are already having proven record in giving good hybrids.

The similarity co-efficient values between the line DB 533 x DB 534 F_4 IPS 49 and the tester DH 98-27 showed 67%. It revealed that DB 533 x DB 534 F_4 IPS 49 was closely related to DH 98-27 with 67 % similarity between parents. The hybrid between DB 533 x DB 534 F_4 IPS 49 and DH 98-27 exhibited the highest yield of 2884.26 kg/ha. Similarity co-efficient (88%) value between lines and testers showed between the line DB 533 x DB 534 F_4 IPS 52 and the tester ZCH8, the hybrid between these recorded an yield of 2040.757 kg/ha. Lowest similarity co-efficient value was noticed between the line DB 533 x DB 534 F_4 IPS 16 and tester DH 98-27 which revealed that they are far distinct from each other.This combination exhibited 2384.62 kg/ha yield.

Genetic distance (GD) based on SSR markers were computed. Genetic distance (GD) ranged from 0.041 to 0.429, with an average of 0.183. The result implied that each cluster dendrogram substantially reflected its own genetic relationship among parents. Overall, a low significant correlation of GD with hybrid performance and heterosis was detected. Highly significant positive correlation were found between genetic distance (GD) and ginning outturn (Fig. 17) for F_1 performance (0.277) and heterosis over MRC 6918 (0.279) and DCH 32 (0.279), while significant positive correlation were found between genetic distance (GD) and ginning outturn for mid parent heterosis (0.237). Highly significant positive correlation were found between genetic distance (GD) and seed cotton yield (Fig. 18) for F_1 performance (0.359) and heterosis over MRC 6918 (0.336) and over DCH 32 (0.362), while significant positive correlation were found between genetic distance (GD) and seed cotton yield for mid parent heterosis (0.226). Significant positive correlation were found between genetic distance (GD) and lint index (Fig. 19) for mid parent heterosis (0.227), F_1 performance (0.251) and heterosis over MRC 6918 (0.250) and DCH 32 (0.250), while significant positive correlation were found only between genetic distance (GD) and fiber micronaire value (Fig. 20) for F_1 performance (0.241).

5.6 *In planta* genetic transformation

Genetic engineering offers a directed method of plant breeding that selectively targets one or a few traits for introduction into the crop plant. The first transgenic cotton plants were obtained in 1987 (Umbeck *et al.*, 1987). The deployment of endotoxins for the protection of crops against insect pests requires the availability of proteins that cause high toxicity to target pests at low level of expression. It is also important to develop novel toxins that bind to different receptors and can therefore be valuable in pyramiding for durable pest resistant. Since crops are damaged by a variety of herbivores, it is desirable to identify endotoxins that can cause mortality or growth inhibition of different target pest species. In this respect, the development of *Cry1Ec* in this work is important since both Spodoptera and Helicoverpa are common agricultural pests and serious bollworms of cotton. Several proteins, especially *Cry1Ac* cause very high toxicity to Helicoverpa sp. Other proteins with satisfactory activity against Helicoverpa are *Cry1Ab, Cry1Ia*$_5$*, Cry2Ab2* etc. (Chambers *et al.,* 1991; von Tersch *et al*., 1991; Lambert *et al.,* 1996; Selvapandiyan *et al.*, 1998; Perlak *et al*., 2001). The *Cry1C* has been reported to show significant toxicity to Spodoptera sp. (Hone´e *et al.,* 1988; Hofte and Whiteley, 1989; Gill *et al*., 1992; Kalman *et al*., 1993) at reasonably low level in larval diet. Within the subgroup of *Cry1 d*-endotoxins, a few other proteins that resemble *Cry1C* (Visser *et al*., 1990; Kalman *et al*., 1993) and *Cry1F* (Chambers *et al.,* 1991) have been reported to show toxicity to Spodoptera sp., though at relatively higher LC_{50} values. The *Cry1E* resembles the *Cry1C* subgroup to the extent of about 70%. It does not cause significant toxicity to *S. exigua* (Visser *et al*., 1990; Masson *et al*., 1992; Bosch *et al.,* 1994) but appears to bind to receptors different from *Cry1C.* Therefore, modification of *Cry1E* and search for proteins with high toxicity to Spodoptera sp. have been objectives in several earlier studies.

Recent advances in transgenic technology now make it possible to transfer and express various genes in agriculturally important species like cotton. The rapid development of cotton transformation technology not only provides a valuable method for introducing useful genes into cotton to improve important agronomic traits, but also helps in the study of gene function and regulation. Although transformation rates have been significantly improved since the first report of success in the transformation of cotton (Firoozabady *et al*., 1987; Umbeck *et al*., 1987), increase in transformation efficiency is still needed.

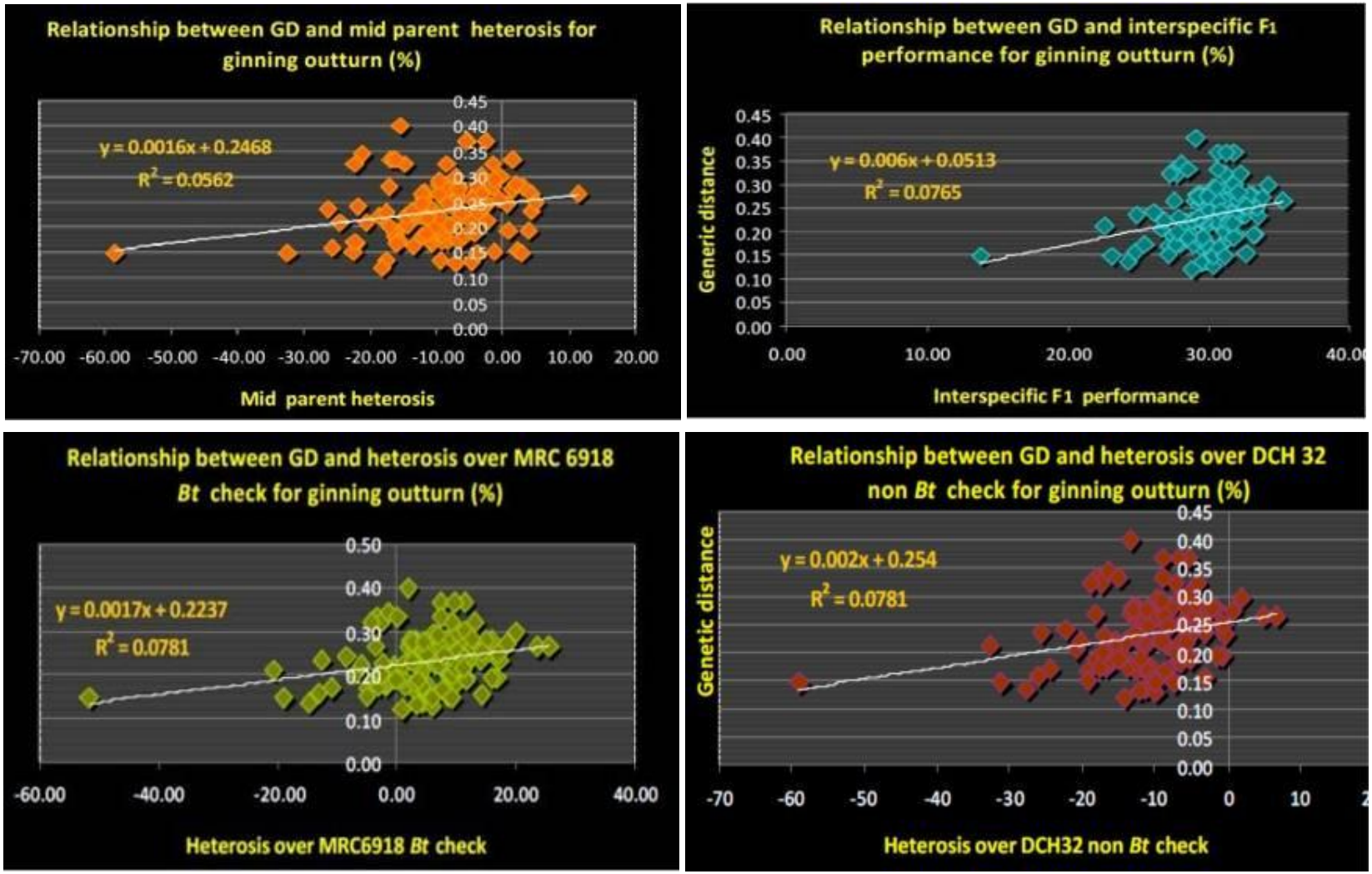


Fig 17 : Relationship between genetic distance (GD) and inter specific F_1 performance, mid parent heterosis and heterosis over MRC 6918 and DCH 32 checks for ginning outturn (%)

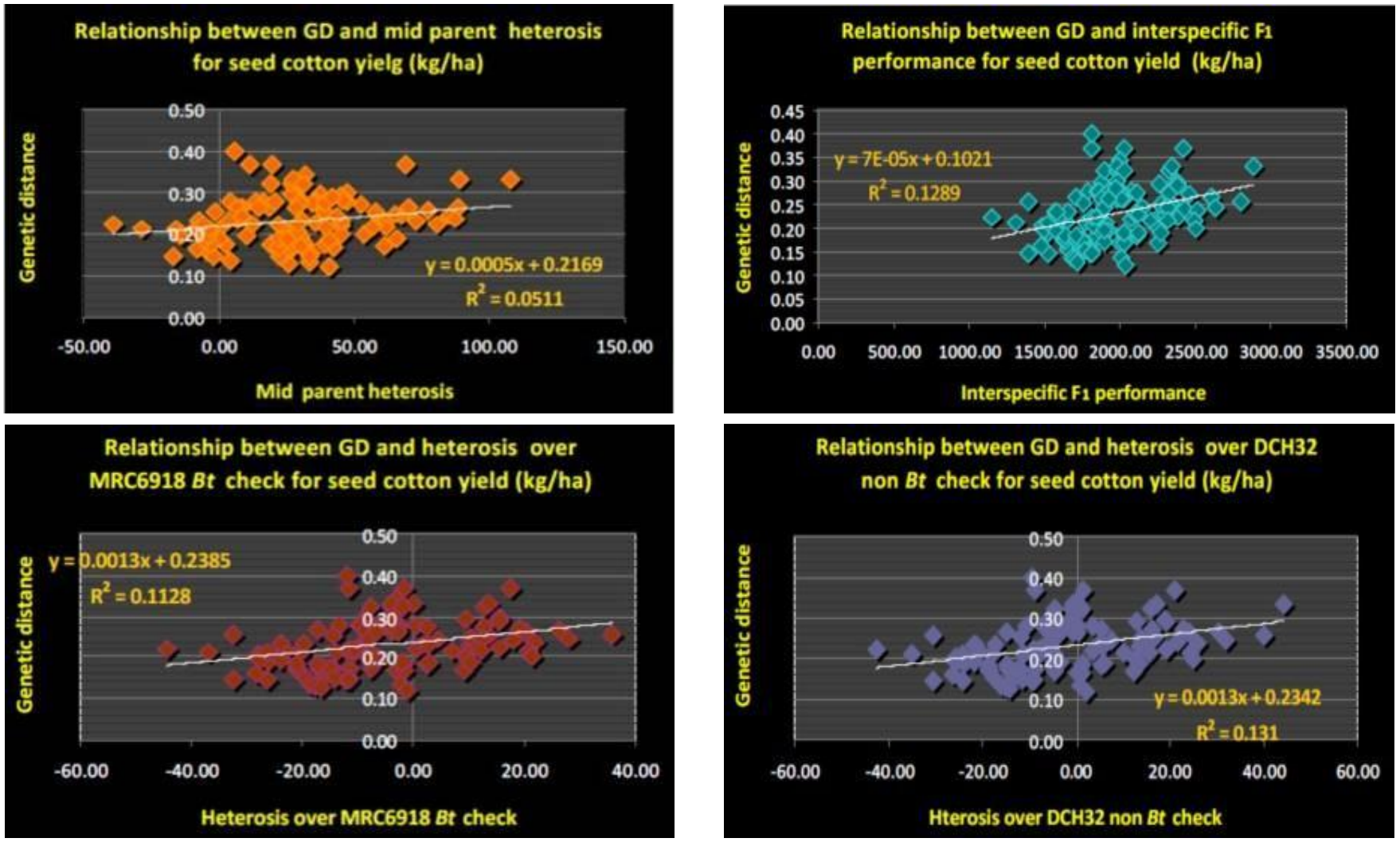


Fig 18 : Relationship between genetic distance (GD) and inter specific F_1 performance, mid parent heterosis and heterosis over MRC 6918 and DCH 32 for seed cotton yield (kg/ha)

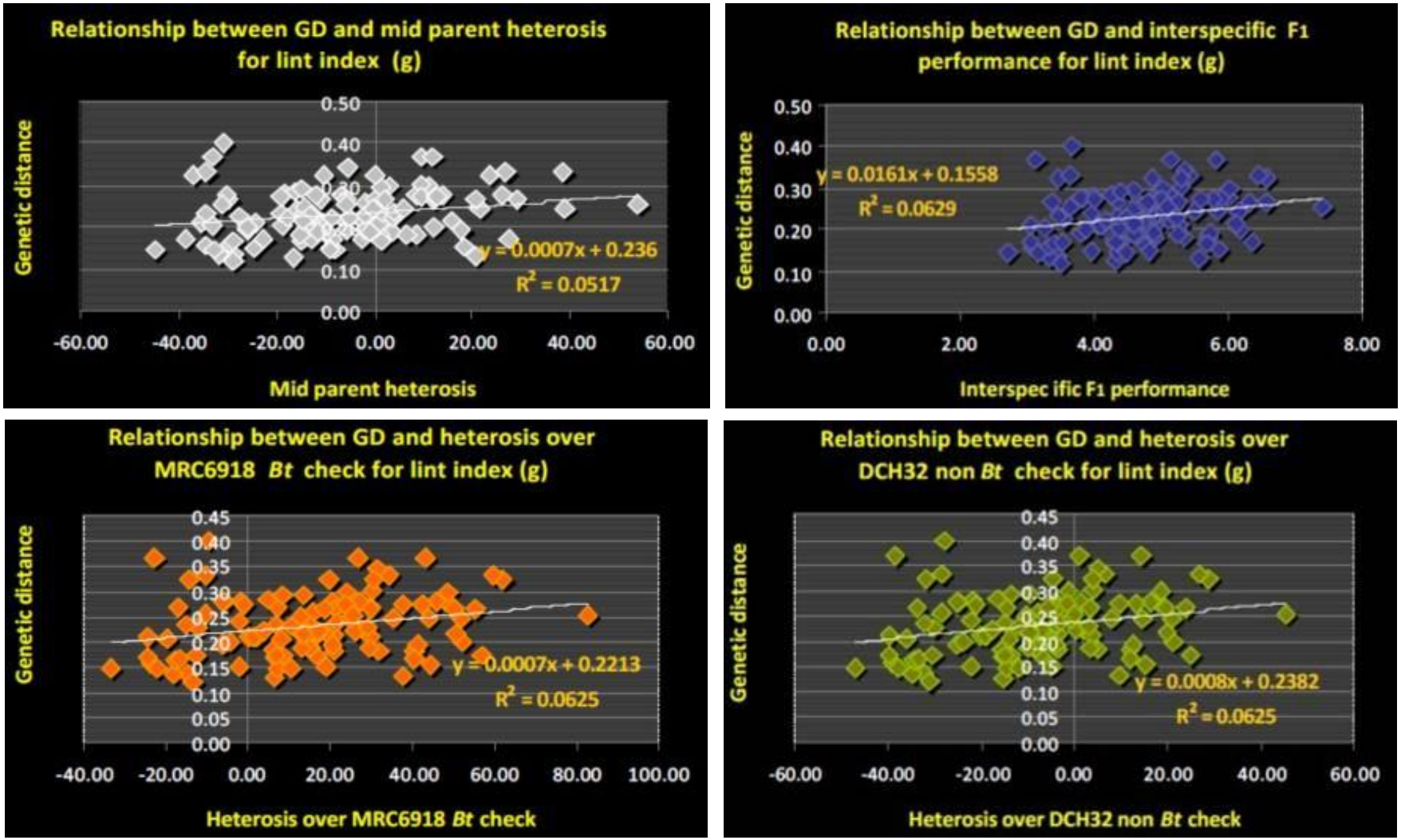


Fig 19 : Relationship between genetic distance (GD) and inter specific F_1 performance, mid parent heterosis and heterosis over MRC 6918 and DCH 32 checks for lint index (g)

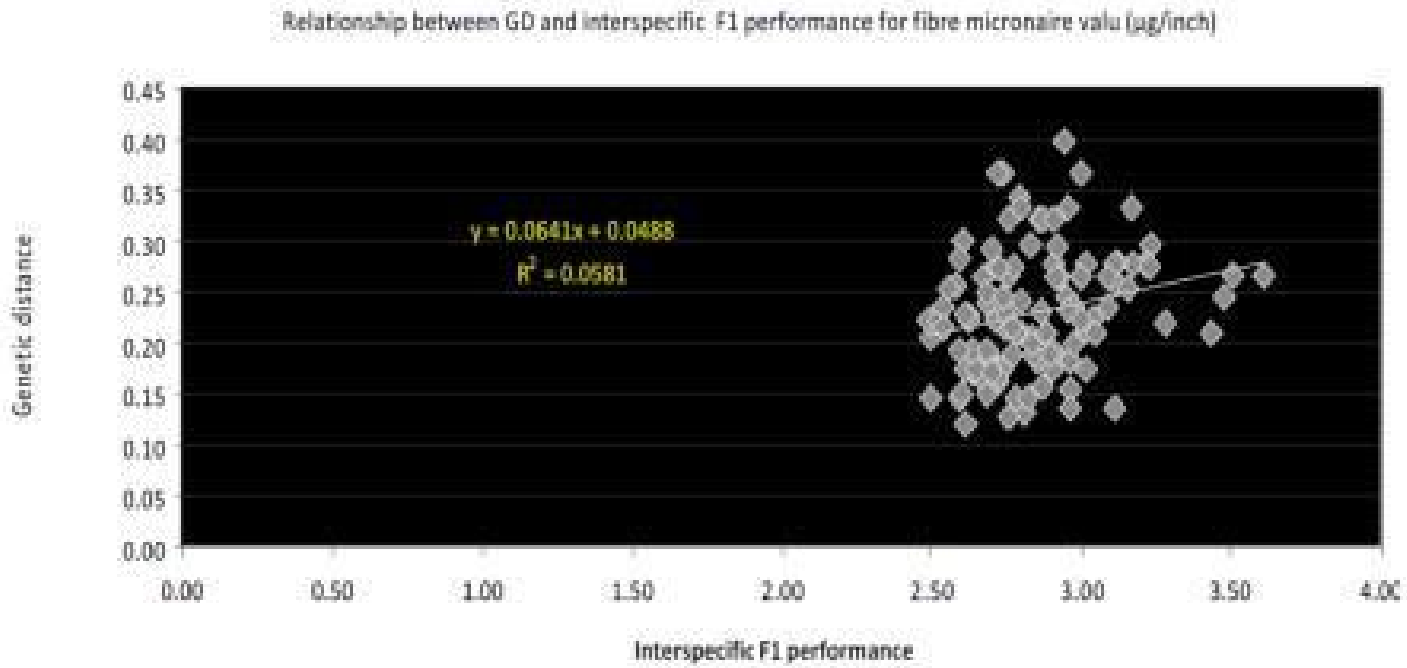


Fig 20 : Relationship between genetic distance (GD) and inter specific F_1 performance for fibre micronaire value (µg/inch)

Transformation techniques that evade tissue culture (Graves and Goldman, 1986) therefore become important in recalcitrant crops such as cotton. In the present study, *in planta* transformation protocol was used to develop transformants (Rohini and Sankara Rao, 2000a; Rohini and Sankara Rao, 2000b; Rohini and Sankara Rao, 2001). In this method, the seedling shoot is embedded in the stem between the cotyledons, break off one cotyledons to expose shoot apex and cut the tissue in the shoot apex to make wound and *Agrobacterium* is targeted to the wound. Therefore, *Agrobacterium tumefaciens* transfers the gene into the genome of diverse cells which are already destined to develop into specific organs and the meristematic cells still to be differentiated. This results in the primary transformants (T_0) being chimeric in nature. This is the reason for the analysis of the transgenic plants to be carried out in the T_1 generation.

In *in planta* method of transformation, invariably the transformation of afew cell/cells happen and such cell/cells of targetted tissue (like shoot apical) will become part of the regenerated shoot where in the transformed cells prevail as chimeric. These plants/ shoots are refered as primary transformed and such transformed chimeric becomes flowers and seeds are harvested, they will have whole germ transformed status. In the present study the tissue choosen for transformation status was basically chimeric / mosaic in related for transformation status and it would be likely that a non-transformed tissue resulted in no PCR amplified with gene specific primers.

Future line of work

1. As a first part of this study (hirsutum vs barbadense) heterotic groups were identified the most productive crosses *viz.,* ZCH 8 x DB 533, DH 98-27 x DB 534, DH 18-31 x DB 533, ZCH 8 x DB 534, 178-24 x DB 533, DH 98-27 x DB 533, DH 18-31 x DB 534 and 178-24 x DB 534 were considered forming heterotic boxes of two barbadense lines DB 533 and DB 534 and four hirsutum testers DH 98-27, ZCH 8, 178-24 and DH 18-31. The cross of barbadense lines was advanced to F_4 generation and these F_4 lines were crossed to these above mentioned hirsutum testers. Thus in this study recombinational variability for combining ability was evaluated on barbadense side. Out of the four hirsutum testers, two testers DH 98-27 and DH 18-31 gave more potential crosses combinations. Hence, these testers need to be crossed and advanced to further selfing generations and cross with two barbadense lines DB 533 x DB 534.This future work mark the reciprocal selection for combining ability on hirsutum side.
2. In the study on recombinational variability for combining ability the most potential crosses were identified *viz*., DH 98-27 X (DB 533 x DB 534 F_4 IPS 49), DH 98-27 X (DB 534 x DB 533 F_4 IPS 22) and DH 98-27 X (DB 533 x DB 534 F_4 IPS 52) will be tested in multi location trials on larger plot size to confirm their yield potential and to know their stability of performance over different agro-climatic situations. It is possible to release them based on confirmation of their potentiality.
3. The potential barbadense line DB 533 x DB 534 F_5 IPS 18 showed superior than Suvin line for seed cotton yield, mean boll weight, seed index, ginning outturn, lint index, fiber micronaire value, fiber strength and S/L ratio can be used for developing separate trait based populations with other barbadense lines for yield components and fibre quality. Confirmation of its superiority will enable release of this new line as an alternative for Suvin variety of barbadense.
4. The two barbadense lines *viz.*, DB 533 x DB 534 F_4 IPS 49 and DB 534 x DB 533 F_4 IPS 22 with high *gca* against four hirsutum testers. These can be used for creating second phase of variability for combining ability. This cross can be advanced to F_4 generation and utilized for crossing against these four hirsutum testers.
5. Since, the study on molecular diversity was restricted to only few selected SSR primers, there is a need to use more number of primers specifically linked to different quantitative traits for assessment of genetic diversity in order to relate molecular diversity.
6. *In planta* genetic transformation needs to be tested by refining the protocol meant for cotton.

SUMMARY AND CONCLUSIONS

In the present scenario it is necessary to increase production of ELS (Extra Long Stable) cottons. Present study aimed at developing heterotic groups of hirsutum *vs* barbadense cottons, based on a detailed line x tester (4 barbadense lines x 23 hirsutum testers). DB 533 and DB 534 the selected barbadense elite combiners were utilized to create recombinational variability for combining ability. These two barbadense varietal lines were crossed and advanced to F_4 generation for creating recombinational variability for combining ability against the hirsutum testers (DH 98-27 (T_1), ZCH 8 (T_2), 178-24(T_3) and DH 18-31 (T_4)).

6.1 Development of heterotic groups and heterotic box

The line x tester study was planned to assess the relative potential of the barbadense and hirsutum in developing inter specific hybrid combinations. Barbadense were used as lines and hirsutum were used as testers.

Among four barbadense lines, positive *gca* effects for seed cotton yield was recorded by DB 533 and DB 534 confiriming the potential of these barbadense lines in developing productive inter specific hybrids. Among 23 hirsutum testers, four testers DH 18-31, ZCH 8, DH 98-27 and 178-24 exhibited good positive values of *gca* effects for seed cotton yield and were located among top ten testers ranks 2, 8, 1 and 7 respectively when compared to other hirsutum testers.

Among these different inter specific hybrids, the mean performance of eight crosses DH 18-31 x DB 533, DH 98-27 x DB 533, 178-24 x DB 533, ZCH 8 x DB 533, DH 18-31 x DB 534, DH 98-27 x DB 534, 178-24 x DB 534 and ZCH 8 x DB 534 associated with this heterotic box was found to be 2336 kg/ha as compared to the overall mean of Line x Tester crosses which was 2036 kg/ha. This accounted for 15% superiority over the mean of all crosses.

6.2 Confirmation of the potential of heterotic box

Study on this set of crosses was denoted as best HB trial. The data generated on 49 best HB crosses of this study is utilized to confirm the performance of eight crosses of the heterotic box. The potential of 8 bench mark crosses of heterotic box ZCH 8 x DB 533, DH 98-27 x DB 534, DH 18-31 x DB 533, ZCH 8 x DB 534, 178-24 x DB 533, DH 98-27 x DB 533, DH 18-31 x DB 534 and 178-24 x DB 534 recorded higher *per se* performance for seed cotton yield ranking 1, 2, 4, 6, 8, 10, 11 and 14 out of 49 crosses. These crosses also recorded superior value for yield attributing characters like number of bolls and mean boll weight. The mean performance of these crosses associated with this heterotic box was found to be 2174 kg/ha as compared to the overall mean of best HB inter specific hybrids which was 1921kg/ha.

The crosses namely ZCH 8 x DB 533, DH 98-27 x DB 534, DH 18-31 x DB 533, ZCH 8 x DB 534 and 178-24 x DB 533 recorded highest yield combining good fibre micronaire and fibre length. These crosses are examples for blending of both quality and yield.

6.3 Exploitation of heterotic groups

The elite barbadense combiners namely DB 533 and DB 534 were indentified for creation and exploitation of recombinational variability for combining ability. In 2007- 2008 this cross was made and early segregating generations were raised during 2008- 2009 / 2009-2010, out of 171 F_3 lines 53 were identified based on productivity and fiber quality and advanced to succeeding generations. In F_4 generation 28 barbadense lines were utilized to assess recombinational variability for combining ability. These selected F_4 lines were crossed with 4 hirsutum testers figuring in the heterotic box identified in this study. This became the base material (28 barbadense lines x 4 hirsutum testers) for evaluation of recombinational variability for combining ability.

6.3.1 Evaluation of *per se* potential of barbadense lines

This study also focused attention on determining whether these barbadense lines can straight away be utilized as varieties for producing ELS cottons. Hence, 53 F_5 barbadense lines were evaluated for productivity traits and fiber quality traits and compared with Suvin known to be standard barbadense variety in international market.

The potential barbadense line DB 533 x DB 534 F5 IPS 18 showed superiority over Suvin line for seed cotton yield, mean boll weight, seed index, ginning outturn, lint index, fiber micronaire value,

fiber strength and S/L ratio and can be used for developing separate trait based populations with other barbadense lines for yield components and fibre quality. Confirmation of their superiority will enable release of these new lines as an alternative for Suvin variety of barbadense.

6.3.2 Evaluation of recombinational variability for combining ability

In this part of the study nature and magnitude of variability for combining ability was assessed against four hirsutum tester included in the heterotic box.

The derived F_1 crosses (28 x 4) were compared with the bench mark crosses (two barbadense lines x 4 hirsutum testers) of the heterotic box, best *Bt* check hybrid (MRC 6918) and non *Bt* check (DCH 32). The derived F_1 crosses revealed considerable variability for *per se* performance measured in terms of productivity and fiber quality traits. Many derived F_1 crosses were found to be more productive than DCH 32 (48 hybrids) and MRC 6918 (35 hybrids). The potential crosses like DH 98-27 X (DB 533 x DB 534 F_4 IPS 49), DH 98-27 X (DB 534 x DB 533 F_4 IPS 22) and DH 98-27 X (DB 533 x DB 534 F_4 IPS 52) recorded highest *per se* performance for seed cotton yield. These crosses also recorded high value for yield attributing characters like number of bolls per plant, mean boll weight, seed index and number of sympodia per plant. These potential crosses recorded highly significant heterosis over mid parent for seed cotton yield. They also recorded significant heterosis for other yield attributing characters in desirable direction.

Apart from showing high productivity the potential cross DH 98-27 X (DB 533 x DB 534 F_4 IPS 49 showed higher value of photosynthetic rate, stomatal conductance and fiber quality parameters. This potential cross is example for blending of yield characters, physiological parameters and fiber quality.The overall combining ability status of F_4 barbadense lines was determined by working out pooled *gca* score. Three methods namely simple *gca* score, per cent *gca* and weighted *gca* method were used in arriving at the best general combiner lines. The overall ranking from these approaches differed and the weighted *gca* approach helped in preciese identification of potential combiners. Based on weighted *gca* method ,the most potential combiners were found to be the lines DB 533 x DB 534 F_4 IPS 26, DB 533 x DB 534 F_4 IPS 17, DB 533 x DB 534 F_4 IPS 8 and DB 533 x DB 534 F_4 IPS 32 . Among the testers, the tester DH 18-31 based on weighted *gca* method is the most potential parent

The set of 28 lines distinguished for the ability to combine with each tester. The efficiency of tester in distinguishing of these F_4 lines was determined based on mean seed cotton yield of 28 crosses and co-efficient of variability. In derived F_1 crosses, tester DH 98-27 (T_1) revealed high mean and also higher co-efficient of variance as compared to the other three testers for seed cotton yield. Both DH 98-27 and DH 18-31 were found to be efficient testers on the basis of high mean and high co-efficient variance. Considering mean and co-efficient variance as parameters T_1 was found to be more efficient in distinguishing the barbadense F_4 lines for their combining ability for utilized to distinguish lines.

A method of sub grouping the F_4 lines against each tester was done. Based on this elite combiner F_4 lines were identified against each tester. This approach helped in sub grouping the F_4 lines against a pair of hirsutum testers and identifying lines for deriving sub populations against hirsutum testers. Both the lines DB 533 x DB 534 F_4 IPS 49 and DB 534 x DB 533 F_4 IPS 22 have combined very well with four hirsutum testers.This suggests that these two barbadense lines can recombined to initiate second phase of creating recombinational variability for combining ability. The segregating F_4 lines obtained from this cross can be crossed to these four hirsutum testers and especially DH 18-31 and DH 98-27 because the mean of crosses with these testers (T_1 and T_4) was very high.

The F_4 lines which gave more potential crosses than bench mark crosses were identified as transgressive segregants for combining ability (positive). Among the population used in the combining ability study, DB 533 x DB 534 F_4 IPS 49, DB 534 x DB 533 F_4 IPS 22 and DB 533 x DB 534 F_4 IPS 52 F_4 lines combined very well with all the four testers and revealed transgressive positive segregation for combining ability. These parents reveal diversity with respect to the identity of dominant favourable alleles contained in them. We can expect segregation at more number of yield influencing dominant loci. As a result of this variability is released at more number of loci and thus recombinant lines having desirable blend of favourable alleles distributed between two parents are obtained. Such lines give rise to superior derived F_1 crosses.

6.4 Correlation co-efficient and path co-efficient analysis

The measure of association and path co-efficient analysis was done in the study of derived F_1 crosses and in line x tester inter specific crosses (YHB) studies. It is necessary to work out path co-efficient analysis which partitions the observed correlation into direct and indirect effects and also reveals the cause and effect relationship between yield and their related traits.

In derived F_1 study at phenotypic level, seed cotton yield exhibited highest positive association with lint index, mean boll weight, number of monopodia per plant, number of bolls per plant, number of sympodia per plant, plant height, seed index, photosynthetic rate, ginning outturn and sympodial length at 50 per cent plant height, whereas seed cotton yield recorded negative correlation with stomatal conductance, inter branch distance, reproductive points on sympodia and transpiration rate.

In the line x tester inter specific crosses study (YHB) at phenotypic level, seed cotton yield exhibited significant positive correlation with mean boll weight, ginning outturn and lint index. Among these, seed cotton yield recorded significant positive strong correlation with ginning outturn.

Intergeneration correlation co-efficients give an idea about the effectiveness of single plant selection and to some extent on nature of gene action. If the correlation co-efficient is high, it would mean high heritable portion and probably the additive component. In the present study, Intergeneration correlation between two generations (F_3 and F_5) for fiber quality values revealed that, the barbadense lines in both generations exhibited highly significant positive correlation for 2.5% S/L and significant positive correlation for fibre uniformity ratio and fibre micronaire value. Non of barbadense in two generations exhibited significant correlation for fiber maturity ratio, fiber tenacity and fiber elongation.

The moderate heritability was noticed for fiber maturity ratio, fiber tenacity and fiber elongation. The high heritability was noticed for 2.5% S/L, fiber uniformity ratio and fiber micronaire value. Indicating this trait is mostly governed by additive gene action and suitability of this trait for selection on individual plant basis in the advanced generations of segregating progenies

6.5 Evaluation of molecular diversity

DNA based molecular markers acted as a versatile tool to study variability and diversity in different plant species. The search for superior hybrid parents in cotton breeding programmes is commonly based on the estimation of the general combining ability (*gca*) and specific combining ability (*sca*) in inbred lines. However, the application of this procedure is expensive and time consuming. The development of DNA based markers represent an alternative procedure of the identification of promising parental lines for superior performances of hybrids. The 28 of F_4 barbadense lines along with four hirsutum testers DH 98-27, ZCH8, 178-24 and DH 18-31 were subjected to diversity analysis using SSR molecular marker system.

Analysis of microsatellites (SSR's) in 32 parents (28 barbadense lines and 4 hirsutum testers) using 40 primers. Of these, 23 primers revealed a high DNA polymorphism among parents, these 23 primers produced a total of 134 amplified profiles.

The similarity co-efficients involved in the line x tester study ranged from 57% to 96 %, with an average of 81%. Among the parental lines, the lines DB 533 x DB 534 F_4 IPS 8 and DB 533 x DB 534 F_4 IPS 1 showed highest similarity co-efficient value (96%).While, the lines DB 533 x DB 534 F_4 IPS 48 and DB 533 x DB 534 F_4 IPS 16 exhibited lowest similarity co-efficient value (57%). All the 32 genotypes showed diversity among themselves indicating that there is a considerable amount of variation, which can be exploited through appropriate breeding programme.

The dendrogram constructed from the pooled data revealed three distinct clusters. One cluster involved testers and in other clusters all barbadense lines were placed which are already having proven record in giving good hybrids.

The similarity co-efficient values between the line DB 533 x DB 534 F_4 IPS 49 and the tester DH 98-27 showed 67%. It revealed that DB 533 x DB 534 F_4 IPS 49 was closely related to DH 98-27 with 67 % similarity between parents. The hybrid between DB 533 x DB 534 F_4 IPS 49 and DH 98-27 exhibited the highest yield of 2884.26 kg/ha. Similarity co-efficient (88%) value between lines and testers showed between the line DB 533 x DB 534 F_4 IPS 52 and the tester ZCH8, the hybrid between these recorded an yield of 2040.757 kg/ha. Lowest similarity co-efficient value was noticed between

the line DB 533 x DB 534 F_4 IPS 16 and tester DH 98-27 which revealed that they are far distinct from each other.This combination exhibited 2384.62 kg/ha yield.

Genetic distance (GD) based on SSR markers were computed. Genetic distance (GD) ranged from 0.041 to 0.429, with an average of 0.183. The result implied that each cluster dendrogram substantially reflected its own genetic relationship among parents. Overall, a low significant correlation of GD with hybrid performance and heterosis was detected. Highly significant positive correlation were found between genetic distance (GD) and ginning outturn for F_1 performance (0.277) and heterosis over MRC 6918 (0.279) and DCH 32 (0.279), while significant positive correlation were found between genetic distance (GD) and ginning outturn for mid parent heterosis (0.237). Highly significant positive correlation were found between genetic distance (GD) and seed cotton yield for F_1 performance (0.359) and heterosis over MRC 6918 (0.336) and over DCH 32 (0.362), while significant positive correlation were found between genetic distance (GD) and seed cotton yield for mid parent heterosis (0.226). Significant positive correlation were found between genetic distance (GD) and lint index for mid parent heterosis (0.227), F_1 performance (0.251) and heterosis over MRC 6918 (0.250) and DCH 32 (0.250), while significant positive correlation were found only between genetic distance (GD) and fiber micronaire value for F_1 performance (0.241).

6.6 *In planta* genetic transformation

Inter specific hybrids are known to be more susceptible to biotic stress. It is hence important to develop *Bt* version for inter specific hybrid. Presently, the *Bt* gene commercialized are owned by private sector. It is necessary to develop public sector's *Bt* event and commercialize them. UAS Dharwad is involved the developing public sector of *Bt* cotton genotypes.

Production of transgenic plants is a routine process for many crop species. Transgenes are introduced into plants to confer novel traits such as improved nutritional qualities, tolerance to pollutants, resistance to pathogens and for studies of plant metabolism. Nowadays, it is possible to insert genes from plants evolutionary distant from the host plant, as well as from fungi, viruses, bacteria and even animals. Genetic transformation requires penetration of the transgene through the plant cell wall, facilitated by biological or physical methods (Electroporation, Biolistics, Vacuum infiltration, Ultrasound-mediated transformation, Shock wave-mediated transformation, Silicon carbide whisker-mediated transformation, Microinjection, Macroinjection, Lasermicrobeams and Electrophoresis).

Several methods of injuring the plant for transformation and regeneration were examined in an effort to improve the efficiency of production of transgenic cotton. *Agrobacterium tumefaciens* strain carrying *Cry1 Ac- Cry1Ec* was used for transformation study. The effect of wounding on established seedling, effect of vertical cut on well established seedling and regeneration was studied.

The seedlings in pots were co-cultivated with solid *Agrobacterium* culture after cutting the meristematic tip with sharp knife. PCR was performed to confirm the presence of the transgene in the plants that were selected to be advanced further. The results showed that non of plants had trangenes *Cry1Ac- Cry1Ec* through PCR amplification. *In planta* genetic transformation needs to be tested by refining the protocol meant for cotton.

In *in planta* method of transformation, invariably the transformation of a few cell/cells happen and such cell/cells of targetted tissue (like shoot apical) will become part of the regenerated shoot where in the transformed cells prevail as chimeric. These plants/ shoots are refered as primary transformed and such transformed chimeric becomes flowers and seeds are harvested, they will have whole germ transformed status. In the present study the tissue choosen for transformation status was basically chimeric / mosaic in related for transformation status and it would be likely that a non-transformed tissue resulted in no PCR amplified with gene specific primers.

REFERENCES

Abel, B. C. and Pollak, L. M., 1991, Rank comparison of unadopted maize populations by testers and per se evaluation. *Crop Sci.,* **31** : 650-655.

Abdallah, A. M. A., Abou-El-Zahab, A. A. and Radwan, S. R. H., 1999, Combining ability for yield and earliness of Pima x Egyptian cotton cultivars crosses. Proceedings-Beltwide-Cotton-Conferences, Orlando, Florida, -USA., **1** : 473-477.

Abdel-Hafez, A. G., El-Keredy, M. S., El-Okkia, A. F. and Gooda, B. M. R., 2007, Estimates of heterosis and combining ability for yield, yield components and fiber properties in Egyptian cotton (*Gossypium barbadense* L.). *Egyptian. J. Pl. Breeding.,* **11** (1) : 423-435.

Ackerson, R. C. and Humbert, R. R., 1981, Osmoregulation in cotton in response to water stress. I-Alteration in photosynthesis, leaf conductance, translocation and ultra structure. *Plant Physiol.,* **67** : 484-488.

Adamczyk, J. J. and Gore, J., 2004, Laboratory and field performance of cotton containing *Cry* 1Ac, *Cry* 1F and both against beet armyworm, fall armyworm larvae. *Florida Entomologist.,* **87** (4) : 427-432.

Agrawal, D. C., Banerjee, R. R., Kolala, A. B., Dhage, A. V., Kulkarni, A. V., Nalawade, S. H. and Krishnamurthy, K. V., 1997, *In vitro* induction of multiple shoots and plant regeneration in cotton (*Gossypium hirsutum* L.). *Plant Cell Rep.,* **16** : 647-652.

Ahmed, M. F., 2007, Cotton diallel cross analysis for some agronomic traits under normal and drought conditions and biochemical genetic markers for heterosis and combining ability. *Egyptian. J. Pl. Breeding.,* **11** (1) : 57-73.

Ahuja, S. L. and Tuteja, O. P., 2000, Variability and association analysis for chemical components imparting resistance to *Gossypium hirsutum L.* cotton. *J. Cotton Res. Develop.,* **14** (1) : 19-22.

Ahuja, S. L. and Tuteja, O. P., 2003, Line X tester analysis for combining ability in upland cotton. *J. Indian Soc. Cotton Improv.,* **11** (2) : 25-30.

Akhmedov, K. K., 1991, Directional selection and the development of plant height and economically useful characters in cotton. *Genetika Selecktsii Tashkent USSR*.

Akumuradov, S. and Chapau, A., 1992, Response of varieties to irradiation. *Khlopok.,* **1** : 36-38.

Alam, A. K. M. R. and Islam, H., 1991, Correlation and path co-efficient analysis of yield and yield contributing characters in upland cotton (*Gossypium hirsutum* L.). *Ann. Bangladesh Agric.,* **1** : 87-90.

Allard, R. W., 1960, Principles of Plant Breeding, John Wiley and Sons, New York., pp. 75-98.

Allison, J. C. S. and Curnow, R. N., 1966, On the choice of tester parent for the breeding of synthetic varieties of maize (*Zea mays* L.). *Crop Sci*, **6** : 541-544.

Altaher, A. F. and Singh, R. P., 2003, Yield components analysis in upland cotton (*Gossypium hirsutum* L.). *J. Indian Soc. Cotton Improv.,* **28** (3) : 151-157.

Amalraj, S. F. A. and Gawande, M. C., 1985, Genetics of yield and ginning characters in inter-varietal hybrids of *Gossypium hirsutum* L. *J. Indian Soc. Cotton Improv.,* **10** : 100-106.

Amalraj, S. F. A., 1989, Combining ability studies on *Gossypium hirsutum* × *Gossypium barbadense* hybrids. *Indian J. Agri. Res.,* **23** (2) : 65-69.

Amolik, V. L., Aher, R. P., Mehetre, S. S. and Darade, R. S., 1997, Heterosis for seed cotton yield and fibre properties in *desi* cotton *(G. hirsutum* L.). *J. Cotton Res. Dev.,* **11**(1) : 1-8.

Amudha, K. and Raveendran, T, S., 1997, Combining ability for yield components and fibre characters in coloured limited cotton (*Gossypium hirsutum* L.). *J. Indian Soc. Cotton Improv.,* **22** : 101-104.

Annapurve, S. N., Deshmukh, G. S., Kausale, S. P. and Kale, U. N., 2007, Correlation study of yield contributing characters in American cotton. *J. Cotton Res. Dev.,* **21** (1) : 16-20.

Anonymous, 2013, *Annual Report,* All India Coordinated Cotton Improvement Project, held at Maharana Pratap University of Agriculture and Technology, Udaipur during 8th – 10th April, 2013., pp. A-2.

Ansingkar, A. S. and Bhale, N. L., 1984, Evaluation of Hayman's and Griffings biometrical approaches in genetic studies of *Gossypium arboreum* L. *Indian J. Agric. Sci.,* **54** : 1004-1007.

Anthony, T. T., Stephen, H. B., Igor, V. K., Ignacio, E. M. M., Wayne, K. V., Laura, A. B., Heungsop, S., Tzyy, J. C., Hiroaki, K., Gary, R. D., Detlef, W. and Maria, J. H., 2000, Transformation of *Medicago truncatula* via infiltration of seedlings or flowering plants with *Agrobacterium*. *The Plant. J.,* **22** (6) : 531- 541.

Anuradha, B., 1998, Genetic studies in compact cotton genotypes (*Gossypium hirsutum* L.) *M. Sc. (Agri.) Thesis*, Univ. *Agric. Sci.,* Dharwad, Karnataka (India).

Arceo, A. J. M. and Molina, J. D., 1991, Study of maize lines as testers for general combining ability. *Revista Chapingo.,* **15** : 7-11.

Armes, N. J., Jadhav, D. R. and Desouza, K. R., 1996, A survey of insecticide resistance in *Helicoverpa armigera* in the Indian subcontinent. *Bulletin Ent. Res.,* **86** : 499-514.

Arshad, M., Hanif, F., Noor Hani and Shah, S. M., 1993, Correlation studies on some commercial cotton varieties of (*Gossypium hirsutum* L.). *Sarhad J. Agric.,* **1** : 49-53.

Arunachalam, V. and Bandopadhyay, 1979, Are "Multiple cross - multiple pollen" an answer for productive population in *Brassica campestiris* var. brown Sarson. *Theor. Appl. Genet.,* **54** : 203-207.

Ashok Kumar, K. and Ravikesavan, R., 2008, Genetic studies of combining ability estimates for seed oil, seed protein and fibre quality traits in upland cotton (*Gossypium hirsutum* L.). *Res. J. Agriculture Biol. Sci.,* **4** (6) : 798-802.

Ashok, R. Patankar, Patil, B. C., Khadi, B. M. and Salimath, P. M., 2004, Correlation of yield and plant type traits of diploid cotton in rainfedand protective management situations. *Sympo In Strategies for Sustainable Cotton Production*. (Eds.) Patil, Nov. 23-25, 2004, UAS, Dharwad., 467pp.

Aslam, M., Hrzog, C. A. and Chalfant, R. B., 2000, Different cotton strains screened for resistance to *Heliothis spp*. (*Lepidoptera : Noctuidae*) in the field. *Pak. J. Biol. Sci.,* **3** (8) : 1290-1291.

Atkins, R. E., 1979, Yield comparisons among short statured seed parents of grain sorghum. *Iowa State. J. Res.,* **53** : 269-272.

Austin, R. B., 1977, Improvement of barely for dryland forming. In : *Proc. symp plant improv for arid zone.* Ahwaz, Iran., pp. 12-27.

Balakotaiah, K., 1973, Path co-efficient analysis in upland cotton (*Gosypium hirsutum* L.). *Indian J. Agric. Sci.,* **43** (7) : 681-683.

Basal, H., Unay, A., Canavar, O. and Yavas, I., 2009, Combining ability for fiber quality parameters and within boll yield components in intra specific and inter specific cotton populations. *Spanish J. Agri. Res.,* **7** (2) : 364-374.

Basu, A. K. and M. G. Bhat, 1987, Variability for harvest index in upland cotton. *Indian J. agric. Sci.,* **57** : 236-40.

Bernardo, R., 1992, Relationship between single-cross performance and molecular marker heterozigosity. *Theor. Appl. Genet.,* **83** : 628-634.

Betran, F. J., J. M. Ribaut, D. Beck, and D. Gonzalez De Leon, 2003, Genetic diversity, specific combining ability, and heterosis in tropical maize under stress and nonstress environments. *Crop Sci.,* **43** : 797-806.

Bevan, M., Barnes, W. M. and Chilton, M. D., 1983a, Structures and transcription of nopaline synthase gene region of T-DNA. *Nucleic Acids Res.,* **11** : 369-385.

Bhandari, D. R., 1978, Line × tester analysis of combining ability and its interactions with environment in American cotton. *Madras Agri. J.,* **64** : 218-225.

Bhandari, D. R., 1980, Studies on combining ability for vegetative characters and its interaction with locations in American cotton (*G. hirsutum* L.). *J. Indian Soc. Cotton Improv.,* **5** : 29-31.

Bhardwaj, S. N., Saini, A. D., Singh, M. and Singh, K. P., 1988, Relation between specific leaf weight, leaf conductance, carbon exchange rate and chlorophyll contens in genotypes of upland cotton (*G. hirsutum L.). Indian J. Plant PhysioL.,* **31** : 102-104.

Bhardwaj, S. N., Saini, A. D., Singh, M. and Singh, K. P., 1988b, Effect of temperature and photosynthetically active radiation on boll weight in upland cotton (*G. hirsutum L.) Indian J. Agri. Sci.,* **58** : 556-557.

Bhat, J. G. and Rao, M. R. K., 1980, Heterosis in growth and photosynthetic rate in hybrids of cotton. *Euphytica.,* **30** : 129-133.

Bhatade, S. S., 1982, Studies on character association and path analysis in F_2 generation of some crosses in cotton. *Madras Agric. J.,* **69** : 367-371.

Bhatade, S. S. and Bhale, N. L., 1983, Combining ability for seed and fibre characters and its interaction with locations in (*G. arboreum* L.). *Indian J. Agri. Sci.,* **53** : 418-422.

Bhatade, S. S. and Rajeshwar, S. R., 1994, Heterobeltiosis and standard heterosis for yield and quality characters in some *Gossypium hirsutum* crosses. *Madras Agri. J.,* **81** : 34-35.

Bhatade, S. S., Reddy, V. G., Rajeswar, S. R. and Nadre, N. R., 1992, Diallel analysis of combining ability in certain inter specific crosses of *Gossypium hirsutum* L. *J. Indian Soc. Cotton Improv.,* **17** : 26-32.

Bhatade, S. S., Shobhabe, M. R. and Unchegoankar, P. K., 1980, Heterosis and combining ability in *Gossypium arboreum* L. *Indian J. Agri. Sciences.,* **50** : 310-316.

Bodar, D. G., Mor, B. R., Kukadia, M. V. and Fatteh, U. G., 1988, Genetic parameters and path co-efficient analysis in upland cotton (*Gossypium hirsutum* L.). *Cotton Dev.,* **18** : 12-14.

Bos, I., 1977, More arguments against intermating F_2 plants of a self fertilizing crop. *Euphytica.,* **26** : 33-46.

Bosch, D., Schipper, B., Van Der Klei, H., De Maagd, R. A. And Stiekema, W. J., 1994, Recombinant Bacillus thuringiensis crystal proteins with new properties : possibilities for resistance management. *Bio/Tech.*, **12** : 915–918.

Bowman, W. D., 1989, The relationship between leaf water status, gas exchange and spectral reflectance in cotton leaves. *Remote sensing of Environment.,* **30** : 249-255.

Broer, I., Droge-Laser, W., Barkers, R. F., Neumann, K., Klipper, W. and Puhler., 1995, Identification of *Agrobacterium tumefaciens* C58 T-DNA genes c and f and their impact on crown gall tumor formation. *Plant Mol. Biol.,* **27** : 41-57.

Brubaker, C. L., Wendel J. F., 1994, Reevaluating the origin of domesticated cotton (*Gossypium hirsutum* L.) using nuclear restriction fragment length polymorphism (RFLPs). *American. J. Bot.*, 81 : 1309-1326.

Butany, W. T., Singh, M. and Mehra, R. B., 1968, Path analysis of yield components in cotton. *Indian J. Genet.,* **28** (1) : 40-43.

Buttery, B. R., Tan, C. S., Buzzell, R. T., Gaynor, J. D and Mac Tavish., 1992, Stomatal number of soybean and response to water stress plant and soil., **149** : 283-288.

Cahaner, A. and Hillet, J., 1980, Estimating heritability and genetic correlation between traits from generations F2 and F3 of self fertilizing species : A comparison of three methods. *Theor. Appl. Genet.,* **58** : 33-38.

Candida, H. C., Demagalhaes, B., Schuster, I., Sediyama, T., De Barros, E. G. and Moreira, M. A., 2005, Characterization and genetic diversity analysis of cotton cultivars using microsatellites. *Genet. Mol. Biol.,* **29** (2) : 321-329.

Cano-Rios, P. and Davis, D. D., 1981, Breeding for early maturing and verticillium wilt tolerance in upland cotton. *Crop Sci.,* **21** : 319-321.

Cano-Rios, P., 1987, Performance of intra and inter specific cotton hybrids across environments. Dissertation Abstracts *International, Science and Engineering.,* **47** : 3584-3585.

Cantrel, R. G., Liu, S., Mc Carty, J. C. Jr. and Stewart, J., Mcd., 2000, Simple Sequence Repeat-Based Assessment of Genetic diversity in Cotton Race Stock Accessions. *Crop Sci.,* **40** : 1459-1469.

Carvalho, L. P. De., Moraes, C. F. De. and Cruz, C. D., 1994, Combining ability and heterosis in upland cotton. *Capacidade de Combinacaoe Heterose Revistaceres.,* **41** : 514-527.

Cervera, M., Pina, J. A., Juarez, J., Navarro, L. and Pena L., 1998, *Agrobacterium* mediated transformation of citrange : factors affecting transformation and regeneration. *Plant Cell Rep.,* **18** : 271-278.

Cetin Karademir, Oktay Gencer, Emine Karademir and Remzi Ekinci., 2009, Combining ability estimates and heterosis for yield and fibre quality of cotton in line X tester design. *Notulac Botanicae Horti Agrobotanici Cluj-Napoca.,* **37** (2) : 228-233.

Chahal, G. S., 1971, Diallel analysis of some quantitative characters in *desi* cotton (*G. arboreum* L.). *M. Sc. Thesis*, Punjab Agric. Univ, Ludhiana.

Chakresh Kumar, Joshi, P. and Bhardwaj, R. P., 1984, Combining ability analysis for yield and other quantitative characters in upland cotton (*G. hirsutum* L.), *ISCR. J.,* **3** : 10-13.

Chambers, J. A., Jelen, A., Gilbert, M. P., Jany, C. S., Johnson, T. B. and Gawron-Burke, C., 1991, Isolation and characterization of a novel insecticidal crystal protein gene from Bacillus thuringiensis subsp. aizawai. *J Bacteriol.,* **173** : 3966–3976.

Chandramathi, P. S. and Menon, P. M., 1973, Diallel analysis of yield and its components and halo length in cotton (*Gossypium barbadense* L.). *Madras. Agri. J*., **60** : 1560-1566.

Channadorai, K., 1973, Heterosis in diallel crosses of cotton *(G. hirsutum* L.). *Madras Agri. J.,* **60** : 1555-1559.

Chee, P. P., Fober, K. A. and Slighton, J. L., 1989, Transformation of soybean (*Glycine max*) by infecting germinating seeds with *Agrobacterium tumefaciens*. *Plant Physiol.,* **91** : 1212-1218.

Cherry JP, Katterman frh, Endrizzi je., 1972, Seed esterases, leucine, and catalases of species of the genus *Gossypium*. *Theor. Appl. Genet.,* **42** : 218–226.

Chinchane, B. N., Nandeshwar, S. B., Deshpande, L. A. AND Chinchane, V. N., 2004, *Agrobacterium* mediated transformation and regeneration in *Gossypium arboretum* L. cotton (cv. PV-255*). International Symposium on "Strategies for Sustainable Cotton Production- A Global Vision" 1. Crop Improv.,* pp. 23-24.

Choudhary, P. N., Borole, D. N., Patil, S. D. and Narkhede, B. N., 1988, Path analysis in desi cotton. *J. Maharashtra. Agri. Univ.,* **13** : 54-55.

Christou, P., 1995, Strategies for variety independent genetic transformation of important cereals, legumes and woody species utilizing particle bombardment. *Euphytica.,* **85** : 13-27.

Comstock, R. E., 1964, Selection procedure in corn improvement. *Proc. Ann. Corn Sorghum Research Conference.,* **19** : 87-97.

Comstock, R. E., 1979, Inbred lines versus the population as testers in reciprocal recurrent selection. *Crop Sci.,* **19** : 881-886.

Cousins, Y. L., Lyon, B. R. and Lleusellyn, T., 1992, Transformation of an Australian cotton cultivar. Prospects for cotton improvement through genetic engineering. *Aust. J. Plant Physiol.,* **18** : 481-494.

Cress, C. E., 1966, Heterosis of the hybrid related gene frequency difference between two populations. *Genetics.,* **53** : 269-274.

Dagaonkar, V. S. and Malkandale, J. D., 1993, Diallel analysis using fixed effect model in upland cotton. *J. Indian Soc. Cotton Improv*, **18** : 50-53.

Davis, R. L., 1927, Report of the plant breeder, *Report Puerto Rico Federal Agricultural Experimental Station.,* pp. 14-15.

Dedaniya, A. D. and Pethani, K. V., 1994, Genetic variability, correlation and path analysis in desi cotton (*Gossypium arboreum* L.). *Indian J. Genet.,* **54** (3) : 229-234.

Deepakbabu, H., 2007, Evaluation of recombinational variability for combining ability in F5 generation of cotton (*Gossipium hirsutum* L.). *M. Sc. (Agri.) Thesis,* Univ. Agric. Sci., Dharwad.

Deosarkar, D. B., Jadhav, D. S. and Patil, S. G., 2009b, Combining ability studies for yield and quality traits in cotton (*Gossypium hirsutum* L.). *J. Cotton Res. Develop.,* **23** (2) : 183-187.

Desai, M. G. S., 1991, Studies on recombinational variability for combining ability in B × R crosses of sorghum [*Sorghum bicolor* (L.) Moench]. *M. Sc. (Agri.) Thesis,* Univ. Agric. Sci., Dharwad.

Deshpande, L. A. and Baig, K. S., 2003, Combining ability analysis for yield, economic and morphological traits in American cotton *(G. hirsutum* L.). *J. Res*, Acharya N. G. Ranga Agric. Univ., **31** (3) : 28-34.

Deshpande, L. A. and Bhale, N. L., 1984, Combining ability and inheritance of ginning out-turn and contributing traits in upland cotton (*G. hirsutum* L.). *J. Indian Soci. Cotton Improv.,* **9** : 46-54.

Dever, J. K. and Gannaway, J. R., 1992, Relative fibre uniformity between parents and F_1 and F_2 generations in cotton. *Crop Sci.,* **32** : 1402-1408.

Dewey, D. R. and Lu, K. H., 1959, A correlation and path co-efficient analysis of components of crested wheat grass seed production. *Agron. J.,* **51** : 515-518.

Dhaliwal, H. S., Kawai, M. and Uchimiya, H., 1998. Genetic engineering for abiotic stress tolerance in plants. *Plant Biotech.*, **15** : 1-10.

Dhanda, S. S., Tyagi, A. P. and Jatasra, D. S., 1987, Character association among quantitative and qualitative attributes of upland cotton. *Indian. J. of Agric. Sci.,* **54 :** 24-29.

Dhopte, A. M., Mohod, V. K., Potkile, N. N and Wankhde, S. T., 1988, Influence of leaf morphology on stomatal conductance, transpiration, leaf temperature in isolines of ten cotton varieties under optimum soil moisture and their association with productivity. *Ann. plant physiol.,* **2 :** 140-148.

Diers, B. W., P. B. E. Mcvetty, and T. C. Osborn, 1996, Relationship between heterosis and genetic distance based on RFLP markers in oilseed rape (*Brassica napus L.). Crop Sci.,* **36 :** 79-83.

Dillen, W., Declercq, J., Kapila, J., Zambre, M., Van Mantagu, M. and Angerm, G., 1997, The effect of temperature on *Agrobacterium tumefaciens* mediated gene transfer to plants. *Plant J.,* **12** : 1459-1463.

Doggett, H. and Eberhart, 1968, Recurrent selection in sorghum. *Crop Sci*, **8** : 119-121.

Donaldson``, P. A. and Simmonds, D. H., 2000, Susceptibility of *Agrobacterium tumefaciens* and cotyledonary node transformation in short season soybean. *Plant Cell Rep.,* **19** : 478-484.

Dongre, A. B., Gabhiye, A. and Bhandarkar, M., 2004, Development of insect resistant cotton with indigenously synthesized *cry* 1Aa3 gene. In : *Proceedings of International symposium on "Strategies for sustainable cotton production – A global vision"* 23- 25 Nov, 2004 held at UAS, Dharwad, p. 475.

Doss and Kadambavanasundaram, M., 1997, Heterosis in intra and inter specific hybrids in tetraploid cotton. *J. Indian Soc. Cotton Improv,* **22** (2) : 110-117.

Dudley, J. W., Saghai-Maroof, M. A. and Rufener, G. K. 1991, Molecular markers and the grouping of parents in maize breeding programs. *Crop Sci.,* **31** : 718–723.

Duhoon, S. S., Basu, A. K. and Sahni, V. M., 1983, Heterosis and combining ability studies in cotton (*G. hirsutum* L.). *J. Indian Soc. Cotton Improv*, **8** : 19-27.

East, E. M., 1908, Inbreeding in corn. *Report Connecticut Agriculture Experimental Station.,* **1907** : 407-429.

Echekwu, C. A. and Alabi, S. G., 1995, Genetic effects of yield and its components in inter specific crosses of cotton. *Discovery and Innovation.,* **7** : 395-399.

Edwards, K., Johnstone, C. and Thompson, C., 1991, A simple and rapid method for the preparation of plant genomic DNA for PCR analysis. *Nucleic Acid Res.,* **19** : 1349.

El-Adl, A. M. and Miller, P. A., 1971, Transgressive segregation and the nature of gene action for yield in an intervarietal cross of upland cotton. *Crop Sci.,* **11** : 381-384.

El-Adl, A. M., El-Diasty, Z. M., Awad, A. A., Zeina, A. M. and El-Bary, A. M. A., 2001, Inheritance of quantitative traits of Egyptian cotton (G. barbadense L.). A - yield and yield component traits. *Egyptian J. Agric. Res,* **79** (2) : 625-646.

El-Gohary, A. A., Shallam, A. A. and El-Mogaazi, M., 1985, Breeding potential of some cultivated Egyptian cotton varieties. *Agri. Res. Rev.,* **59** : 1-17.

El-Mansy, Y. M., Rokia, M. Hassan, and M. E. Abdel-Salam, 2010, Estimation of genetic components and genetic divergence in diallel hybrids of cotton. *J. Agric. Res. Kafer El-Sheikh Univ.,* **36** (1) : 17 -32.

El-Sheikh, M. H., 1993, Comparative efficiency of high and low yielding testers in evaluating S_1 line of maize. *J. Agri. Sci.,* **18** : 3139-3145.

El-Zik, K. M. and Thaxton, P. M., 1989, Genetic improvement for resistance to pests and stresses in cotton. In : Integrated Pest Management Systems and Cotton Production. R. E. Frisbie, K. M. El-Zik and L. T. Wilson (eds.). John Wiley & Sons, NY., pp. 191-224.

Enriquez-Obregon, G. A., Vazquez-Padron, R. I., Prietsosansonov, D. L., Delariva, G. A. and Selman-Housein, G., 1998, Herbicide resistant sugarcane (*Saccharum officinarum* L.) plants by *Agrobacterium* mediated transformation. *Planta.,* **6** : 20-27.

Falconer, D. S., 1981, *Introduction of Quantitative Genetics*, Longman Inc. Ltd., New York., p. 340.

Fan, X. M., J. Tan, B. H. Huang, and F. Liu. 2001, Analyses of combining ability and heterotic patterns of quality protein maize inbreds. *Acta Agron. Sin.,* **27** : 986–992.

Fawzi, A. L., 1962, Effectiveness of early testing method of breeding in isolating better inbred lines of maize. *Agri. Res,* Egypt., **40** : 85-96.

Fehr, W. R., 1987, Principles of Cultivar Development, *Theory and Technique.,* **1** : 432-433.

Firoozabady, E., Deboer, D. L., Merlo, D. J., Halk, E. L., Amerson, L. N., Rashka, A. E. and Murray, E. E., 1987, Transformation of cotton *(Gossypium hirsutum* L.) by *Agrobacterium tumefaciens and* regeneration of transgenic plants. *Plant Mol. Biol.,* **10** : 105-116.

Fischer, S., Maurer, H. P., Wurschum, T., Mohring, J., Piepho, H. P., Schon, C. C., Thiemt, E. M., Dhillon, B. S., Weissmann, E. A., Melchinger, A. E., and Reif, J. C., 2010, Development of heterotic groups in triticale, *Crop Sci.,* **50** : 584-590.

Fisher, R. A. and Yates, F., 1963, *Statistical Tables for Biological Agriculture and Medical Research*, Oliver and Boyd. Edinburgh.

Fraley, R. T., Rogers, S. G. and Horsch, R. B., 1983, Expression of bacterial genes in plant cells. *Proceedings of National Academy of Sciences*, USA., **80** : 4803-4807.

Fredrick, J. R., Randy, W. D., Tony, A. A., Roy, L. F., Stewin, R. S., Hohnson, T., Gand Davis, A. F., 1990, Insect resistant cotton plant. *Biotechnology.,* **11** : 1151-1156.

Gawand, P. B., Thombre, M. V. and Jadhav, M. G., 1984, Correlation and path co-efficient analysis in cotton. *J. Maharashtra. Agric. Univ.,* **9** : 221-222.

Gaziyants, S. M. and Zhalilov, O. S. H., 1983, Genetic analysis of economically useful characters in cotton varieties and lines. *Selektsiya I. Semenovodstvo., USSR*, **8** : 27.

Geetha, N., Venkatachalam, P. and Lakshmi Seta, 1999, *Agrobacterium* mediated genetic transformation of pigeonpea (*Cajanus cajan* L.) and development of transgenic plants via direct organogenesis. *Plant Biotech*, **16** : 213-218.

Gerasenkov, B. I. and Goncharova, L. P., 1972, Evaluation of combining ability in maize inbred lines in early stages of inbreeding. *Referativnyl Zhurnal.,* **3** : 27-39.

Gesos, K. and Pulatov, M., 1986, Production of *Gossypium barbadense* varieties with high fibre outturn. *Khlopkovodstva.,* **10** : 24-25.

Gesos, K. and Torev, D., 1986, Regional breeding or genetic evaluation of characters. *Khlopok.,* **1** : 36-38.

Gill, S. S. and Singh, T. H., 1981, Correlation and path co-efficient analysis of yield with yield components in upland cotton. *Crop Improv.,* **8** : 23-27.

Gill, S. S. and Singh, T. H., 1982, Heterosis in upland cotton *(G. hirsutum* L.). *J. Indian Soc. Cotton Improv.,* **7** : 57-61.

Gill, S. S., Cowles, E. A. and Pietrantonio, P. V., 1992, The mode of action of Bacillus thuringiensis endotoxins. *Ann Rev Entomol.,* **37** : 615–636.

Girase, V. S. and Mehetre, S. S., 2002, Correlation and Path analysis in cotton. *J. Cotton Res. Dev.,* **16** : 1-7.

Godshalk, E. B., M. Lee, and K. R. Lamkey. 1990, Relationship of restriction fragment length polymorphisms to single-cross hybrid performance of maize. *Theor. Appl. Genet.,* **80** : 273–280.

Gopinath, G. and Madalageri, B. B., 1985, A note on the heredity of leaf area and stomatal frequency in egg plant (*Solanum melongena*). *Current Res.,* **14** : (4/6) : 36-37.

Goudar, P. V. K., Kataraki, B. H., Salimath, P. M. and Chetti, M. B., 1996, Genetics of yield, yield attributes and their implications in breeding of cotton *(G. hirsutum* L.). *Indian J. Genet. Plant Breed.,* **56** : 147-151.

Gould, J. and Maria Magallenes-Cedeno, 1998, Adaptation of cotton shot apex to *Agrobacterim* mediated transformation. *Plant Mol. Boil. Rep.,* **16 :** 1-10.

Gould, J., Devey, M., Ulian, E. C., Hasegawa, O., Peterson, G. and Smith, G, H., 1991a, Transformation of *Zea mays* L. using *Agrobacterium tumefaciens* and the shoot apex. *Plant Physiol.,* **95** : 426-434.

Govilla, O. P. and Sharma, S. B., 1981, Path analysis and its implications in breeding for early maturity and high yield in cotton. *J. Indian Soci. Cotton Improv.,* **6** : 69-71.

Grafiaus, J. E., 1959, Correlation and path analysis in barley. *Agron. J,* **51** : 551-554.

Grakh, S. S. and Choudhary, M. S., 1983, Heterosis for yield and yield contributing characters in desi cotton (*Gossypium arboreum* L.). *Indian J. Agric. Res.,* **17** : 73-78.

Graves, A. C. F., and S. L. Goldman, 1986. The transformation of *Zea mays* seedlings with *Agrobacterium tumefaciens*, *Plant Mol. Biol.*, **7** : 43-50.

Green, J. M., 1948, Relative value of two testers for estimating top cross performance in segregating maize populations. *J. American Soc. Agron.,* **40** : 45-57.

Gridley, H. E., 1975, Breeding implication from a diallel analysis in two environments of yield and component characters in upland cotton (*G. hirsutum* L.). *Theor. Appl. Genet.,* **46** : 401-406.

Griffee, F., Ligon, L. L. and Brannon, L. H., 1929, Biometrical analysis of Upland grown at still water, Oklahoma, Oklahoma *Agric. Exp. Sta. Bull.,* **1987 :** PP. 32. (From Sikka and Joshi, 1960).

Gulamov, K., Nasimov, S., Atazhanov, M., Azimara, A. and Azizov, B., 1974, The study of correlations between characters in varieties and radiation induced mutants of cotton (*Gossypium hirsutum* L.). *Khlopchatnika.,* **2** : 176-186.

Gunasheelan, T. and Krishnaswamy, R., 1988, Heterosis and inbreeding depression in the inter vacial crosses of (*G. hirsutum* L.). *J. Indian Soc. Cotton Improv.,* **13** : 5-10.

Guo, X., Huang, C., Jin, S., Nie, Y. and Zhang, X., 2007, *Agrobacterium* mediated transformation of *Cry* 1C, *Cry* 2A and *Cry* 9C genes into *Gossypium hirsutum* and plant regeneration. *Biol. Planta.,* **51 :** 242-248.

Gupta, P. K., Balyan H. S., Sharma, P. C., Ramesh, B., 1996, Microsatellites in plants : a new class of molecular markers. *Current Sci.,* **70** : 45-53.

Gupta, S. P. and Singh, T. H., 1986, Combining ability in the F_1 and advanced generations of a diallel cross in upland cotton *(G. hirsutum* L.). *Indian J. Genet. Plant Breed.,* **46** : 345-347.

Gupta, S. P. and Singh, T. H., 1987, Heterosis and inbreeding depression of seed cotton yield and some seed and fibre attributes in upland cotton (*G. hirsutum* L.). *Crop Improv.,* **14** : 14-17.

Gururaj, 2006, Genetic studies on compact and robust plant types of cotton (*Gossypium hirsutum L.*). *M. Sc. (Agri) Thesis*, Univ. Agric. Sci., Dharwad, Karnataka (India).

Gururajan, K. N., 2000, Yield component analysis in Egyptian cotton(*Gossypium barbadense* Linn.). *J. Indian Soc. Cotton Improv.,* **25** (2) : 17-22.

Gururajarao, M. R., Hiremath, K. G. and Virupakshappa, K., 1977, Genetic analysis of ginning and fibre properties in upland cotton-graphic analysis of six quantitative traits. *Mysore. J. Agri. Sci.,* **11** : 444-452.

Gutierrez, O. A., S. Basu, S. Saha, J. N. Jenkins, D. B. Shoemaker, C. L. Cheatham, and J. C. Mccarty, 2002, Genetic distance among selected cotton genotypes and its relationship with F2 performance. *Crop Sci.,* **42 :** 1841-01847.

Gynheung, W. S., 1985, High efficiency transformation of cultured tobacco cells. *Plant Physiol.,* **79** : 568-570.

Hallauer, A. R. and Miranda, J. B., 1981, Quantitative genetics in maize breeding. *Iowa State University Press, Ames.,* pp. 267-298.

Hanamaraddi., 2010, Genetic investigation in cotton (*Gossypium hirsutum* L.). *M. Sc. (Agri.) Thesis,* Univ. Agric. Sci., Dharwad, Karnataka (India).

Hansen, G., Shillito, R. D. and Chilton, M. D., 1997, T- strand integration in maize protoplants after co delivery of a T-DNA substrate and virulence genes. *Proc. of the Nation. Acad. of Sci. of USA.,* **94 :** 11726-11730.

Hapase, R. S., Aher, R. P. and Thombre, M. V., 1987, Line × tester analysis of combining ability in desi corron. *J. Maharashtra. Agri. Univ.,* **12** : 195-197.

Harland, S. G., 1939, The Genetics of Cotton. Jonthan cape London., pp. 1-193.

Hayes, H. K., Immer, F. F. and Smith, D. L., 1956, *Methods of Plant Breeding*. McGraw Hill Book Publishing Company, Inc., New Delhi., pp. 21-34.

Hayes, H. K., Immer, I. R. and Smith, D. C., 1955, *Methods of Plant Breeding*. McGraw Hill Book Company International Corporation, New York.

Hayes, J. D. and Foster, C. A., 1976, Heterosis in self pollinated crops with particular reference to barley. Heterosis in plant breeding. *Proc of 7th Congress EUCARPIA*, pp. 239-256.

Hazra, S., Sathaye, S. S., Mascarenhas, A. F., 1989, Direct somatic embryogenesis in peanut (*Arachis hypogaea* L). *Bio/Technol.*, **7** : 949-951.

Hemphill, J. K, Maier, C. G. A. and Chapman, K. D., 1998, Rapid *in vitro* plant regeneration of cotton. *Plant Cell Rep.,* **17 :** 273-278.

Herrnstadf, C., Soanres, G. G., Wilcox, E. R. and Edward, D. L., 1986, A new strain of *Bacillus thuringiensis* with activity against coleopteran insects. *Biotech.,* **4** : 305-308.

Hofte, H. and Whiteley, H. R., 1989, Insecticidal crystal protein of Bacillus thuringiensis. *Microbiol Rev.,* **53** : 242–255.

Hoftey, H. and Whiteley, H. R., 1989, Insecticidal crystal protein of *Bacillus thuringiensis*. *Microbiol Rev.,* **53** : 242-255.

Hone´e, G., Van Der Salm, T, and Visser, B., 1988, Nucleotide sequence of crystal protein gene isolated from B. thuringiensis subspecies entomocidus 60. 5 coding for a toxin highly active against. *Spodoptera species Nucleic Acids Res.,* **16** : 6240.

Horner, E. S., Lundy, H. W., Lutrick, M. C. and Chapman, W. H., 1973, Comparison of three methods of recurrent selection in maize. *Crop Sci.,* **13** : 485-489.

Horsch, R., Fry, J., Hoffman, N., Wallroth, M., Ekhholtz, D., Roger, S. and Fraley, R., 1985, A single and general method for transferring genes into plants. *Sci.,* **227** : 1229-1231.

Huang, Y. Q., and J. S. Li. 2001, Classifi cation of heterotic groups with RFLPs among 45 maize inbred lines. *Agric. Sin*. China., **34** (3) : 244–250.

Hull, F. H., 1945, Recurrent selection for specific combining ability in corn. *J. American Soc. Agron.,* **37** : 134-145.

Hutmacher, R. B. and Krieg, D. R., 1983, Photosynthetic rate control in cotton. Stomatal and non-stomatal factors. *Plant Physiol.,* **73** : 658-661.

Idris, H. A., 2006, Evaluation of some egyptian cotton hybrids using augmented randomized complete block design. *Bulletin. Fac. Agri.,* **57** (4) : 621-628.

Iftikhar, Ahmed Khan, Manzoor, Ahmad Khan and Muhammad Iqbal, 1985, Study of heterosis and combining ability in cotton (*G. hirsutum* L.). *Pakistan Cotton.,* **29** : 77-84.

Ikram-Ul-Haq, 2004, *Agrobacterium* mediated transformation of cotton via vacuum infiltration. *Plant Mol. Biol. Rep.,* **22 :** 279-288.

Jagtap, D. R. and Kolhe, A. K., 1984, Correlation studies in cotton (*Gossypium hirsutum*). *Madras Agric. J.,* **71** (7) : 470-471.

Jagtap, D. R., 1986, Combining ability in upland cotton. *Indian J. Agri. Sci.,* **56** : 833-840.

Jagtap, D. R. and Kolhe, A. K., 1987, Graphical and combining ability analysis in upland cotton. *Indian J. Agri. Sci.,* **57** : 456-464.

Jagtap, D. R., and Mehetre, S. S., 1998, Genetic variability in intervarietal crosses of upland cotton (*Gossypium hirsutum* L.). *Ann. Agri. Res.,* **19** (2) : 130-132.

Jagtap, J. G., Holkar, S. and Teland, S. W., 1992, Line × tester analysis for some attributes in upland cotton. *J. Indian Soc. Cotton Improv.,* **17** : 109-114.

Jenkins, M. T., 1935, The effect of inbreeding and of selection within inbred lines of maize upon the hybrids made after successive generations of selfing. *Iowa State J. Sc. i*, **3** : 429-450.

Jing, J. H. and Ma, S. S., 1990, Response of leaf gas exchange to water stress in maize, upland rice, cowpeas and cotton. *Acta Agronomica Silica.,* **16** : 342-348.

Jones, H. G., 1977, Aspects of water relations of spring wheat (Triticum aestivum L.) in response to induced drought. *J. Agri. Sci.,* **88** : 267-282.

Jorge L. Morre, Hugo R. Permingeat, Maria V. Romagnoli, Cintia M. Heisterborg and Ruben H. Vallejos., 1998, Multiple shoot induction and plant regeneration from embryonic axes of cotton. *Plant Cell Tissue Organ Cul.,* **54** : 131–136.

Joshi, N. V., 1960, Review of mathio cotton improvement scheme in Saurashtra. *Indian Cotton Growing Review.,* **14** : 192-198.

Kadapa, S. N. and Prajapati, R. M., 1990, Heterosis and line × tester analysis of intra *Gossypium barbadense* L. hybrids. *Indian J. Genet. Plant Breed.,* **50** : 320-328.

Kajjidoni, S. T., 1982, Heterosis, combining ability and gene action for earliness, yield components in 2 × 10 crosses of *Gossypium herbaceum* L. × *Gossypium arboreum* L. cotton. *M. Sc. (Agri.) Thesis*, Univ. Agric. Sci., Bangalore, Karnataka (India).

Kajjidoni, S. T., Patil, S. J., Khadi, B. M. and Salimath, P. M., 1999, A comparative study of heterosis in GMS based and conventional intra arboreum cotton hybrids. *Indian J. Genet.,* **59** (4) : 493-504.

Kalman, S., Kiehne, K. L., Libs, J. L. and Yamamoto, T., 1993, Cloning of a novel cryIC-type gene from a strain of Bacillus thuringiensis subsp. galleriae. *Appl Environ Microbiol.,* **59** : 1131–1137.

Kalpande, H. V., Mukewar, A. M. and Kalpande, V. V., 2008, Combining ability analysis in upland cotton (*Gossypium hirsutum* L.). *J. Cotton Res. Dev.,* **22** (1) : 10-13.

Kalsy, H. S. and Garg, H. R., 1980, Combining ability analysis in cotton. *Crop Improv.,* **7** : 113-118.

Kalsy, H. S. and Vithal, B. M., 1980, Inheritance of some quantitative characters in upland cotton. *J. Res*, Punjab Agric. Univ., **17** : 1-4.

Kalsy, H. S., Garg, H. R., Vithal, B. M. and Singh, T. H., 1981, Comining ability w Ezstudies in a diallel cross of cotton. (*Gossypium hirsutum* L.). *J. Indian Soc. Cotton Improv.,* **6** : 73-79.

Kappel, V. and Tsiger, G., 1984, Importance of the divergence of interchanged testers for successful international collaboration in breeding hybrid maize II. Methods of Evaluating Divergence. *Informatsiony Byulltin, Po. Kukurur.,* **3** : 33-37.

Kar, S., Tony, M. J., Pritilata Nayak and Sen, S. K., 1 996, Efficient transgenic plant regeneration through *Agrobacterium* – mediated transformation of chickpea (*Cicer arietinum* L.). *Plant Cell Rep.,* **16** : 32-37.

Karande, S. S., Wandhare, M. R., Ladole, M. Y., Waode, M. M. and Meshram, L. D., 2004, Heterosis and combining ability studies in inter specific diploid cotton hybrids for fibre quality parameters. *Int. Symp. on Strategies Sustainable Cotton Production – A Global Vision 1. Crop Improv.,* 23-25 November, 2004, Univ. Agric. Sci., Dharwad (India), Karnataka, India.

Katageri, I. S. and Kadapa, S. N., 1989, Heterosis for yield and its component characters in bollworm tolerance in *Gossypium hirsutum* L. x *Gossypium barbadense* L. cotton hybrids. *Indian J. Genet. Plant Breed.,* **49** (1) : 107-112.

Katageri, I. S., Vamadevaiah, H. M., Udikeri, S. S., Khadi, B. M. and Kumar, P. A., 2007, Genetic transformation of an elite Indian genotype of cotton (*Gossypium hirsutum* L.) for insect resistance. *Current Sci.,* **93** (12) : 1843-1847.

Katarki, B. H., Patil, S. A. and Allayanavarmath, S. B., 1970, Utilization of heterosis in cotton production. *Mysore. J. Agri. Sci.,* **14** : 278-284.

Kaushik, L. S., Singh, D. P. and Paroda, R. S., 1984, Line × tester analysis for fixed effect model in cotton *(G. hirsutum* L.). *Theor. Appl. Genet.,* **68** : 487-491.

Kempthorne, O., 1957, *An Introduction to Genetic Statistics,* John Wiley and Sons, New York.

Kenchanagoudar, P. V., 1983, Genetics of earliness, yield and its components in cotton *(G. hirsutum* L.). *M. Sc. (Agri.) Thesis*, Univ. Agric. Sci, Bangalore, Karnataka (India).

Keshall, J., Cantrell, R. and Axtell, T., 1985, Variation in agronomic traits of B lines developed from random mating sorghum populations. *Agronomy Abstract*, p. 71.

Khadi, B. M., Prakash Rao, Yenjerappa, S. T. and Janagodar, B. S., 1996, Combining ability studies and identification of superior inter specific desi cotton hybrids. *Mysore. J. Agri. Sci*, **30** : 1-9.

Khan, A. A., Ali, M. M., Mahamood, A. and Khan, M. A., 1989, Manifestation of heterosis and combining ability in upland cotton. *Pakistan J. Scientific and Industrial Res.,* **32** : 629-632.

Khan, S. A., Hussain, D., Askari, E., Stewart, J. M., Malik, K. A., and Zafar, Y., 2000, Molecular phylogeny of *Gossypium* sp. by DNA fingerprinting. *Theor. Appl. Genet.,* **101** : 931-938.

Khan, W. S., Gill, A. R. and Din, F., 1986, Hybrid vigour in relation to development in upland cotton *(G. hirsutum* L.). *J. Agri. Res. Pakistan.,* **22** : 203-208.

Killi, F., 1995, Path co-efficient analysis and correlation for cotton (*Gossypium hirsutum L.*) yield and some yield components in the east Mediterranean and South eastern Anatolian Project regions. *Turkish. J. Agric. Foresty.,* **19** : 379-382.

Knowles, B. H., 1994, Mechanism of action of *Bacillus thuringiensis* insecticidal deltaendotoxins. *Adv. Insect Physiol.,* **24** : 275-308.

Kolte, T. P. and Thombre, M. V., 1984, Heterosis and combining ability studies in *Gossypium* species. *J. Maharashtra. Agric. Univ.,* **9** : 252-254.

Konez, C., Nemeth, K., Redei, G. P. and Scel, J., 1994, Homologous recombination and gene silencing in plants. *Plant Cell Rep.,* **22** : 167-174.

Koodalingam, K., Rajashekaran, S. and Ramalingam, A., 1991, Heterosis and inbreeding depression in intra specific upland cotton. *Ann. Agri. Res.,* **12** : 288-291.

Kowasalya, R. and Raveendran, T. S., 1996, Heterosis in intra-specific *Gossypium* hybrids possessing *harknessi* and *hirsutum* plasmons. *Ann. Plant Physiol.,* **10** : 114-117.

Krattiger, K. and Anatole, F., 1997, Insect resistance in crops : a case study of *Bacillus thuringiensis* (*Bt*) and its transfer to developing countries. *ISAAA Briefs*. pp. 42.

Krieg, A., Huger, A., Langenbuch, G. and Schneter, W., 1983, *Bacillus thuringiensis* var. tenebrionis : a new pathoype effective against larvae of Coleoptera. *J. Appl. Entomol.,* **96** : 500-508.

Krishnamurthy, K. V., Suhasini, K., Sagare, M. M., Kathen, A. De, Pickard, T. and Schieder, O., 2000, *Agrobacterium* mediated transformation of chickpea (*Cicer arietinum* L.) embryo axes. *Plant Cell Rep.,* **19** : 235-240.

Krishnadas, D. and Kadambavanasundaram, 1997, Heterosis in intra and inter specific hybrids in tetraploid cotton. *J. Indian Soc. Cotton Improv.,* **22** : 110-117.

Krishnamurthy, R. and Kothandaraman, R., 1977, Heterosis in inter specific hybrids of *Gossypium*. *Indian J. Genet. Plant Breed.,* **37** (1) : 40-45.

Krishnarao, K. V. and Mary, T. N., 1990, Variability correlation and path analysis of yield and fibre traits in upland cotton. *Madras Agric. J.,* **77** (3&4) : 146-151.

Krishnaswamy, R. and Gunaseelan, T., 1985, Heterosis and combining ability in the inter racial hybrids of *Gossypium hirsutum* L. *Phytobreedon.,* **1** : 23-30.

Kulkarni, R. S, Swamy Rao, T. and Virupakshappa, 1976, Gene action in bhendi. *Agri. Res. J. Kerala.,* **14** (1) : 13-20.

Kumaraswamy, G. K, 2005, Expression of *cry*1Ac from native *Bacillus thuringiensis* D1 in *Escherichia coli*, M. Sc. (Agri) *Thesis*, Univ. Agricl. Sci., Dharwad.

Kumar, P., Singh, K., Vikal, Y., Radhawa, L. S. and Chahal, G. S., 2003, Genetic diversity studies of elite cotton germplasm lines using RAPD markers and morphological characteristics. *Indian J. Genet.,* **63** (1) : 5-10.

Kumar, V. and Choudhary, M. L., 1986, Correlation of certain quantitative characters with yield in (*Gossypium hirsutum* L.) cotton. *Cotton Dev.,* **16** : 21-22.

Kumboh, N., Baloch, M. J., Kumbhar, M. B., Khanzada, S. and Jatoi, W. A., 2008, Diallel analysis for estimating combining ability in upland cotton (*Gossypium hirsutum* L.). *Pakistan J. Agril. Engin. and Veter. Sci.,* **24** (1) : 27-33.

Kuroda, E. and Kumura, A., 1990, Difference in single leaf photosynthesis between ola and new rice cultivars. I. Single – leaf photosynthesis and its dependence on stomatal conductance. *Japanese J. Crop Sci.,* **59 :** 283-292.

Laxman, S. and Ganesh, M., 2003, Combining ability for yield components and fibre characters in cotton *(G. hirsutum* L.). *J. Res*, Acharya N. G. Ranga Agric. Univ., **31** (4) : 19-23.

Lambert, B., Buysse, L., Decock, C., Jansens, S., Piens, C. and Saey, B., 1996, A Bacillus thuringiensis insecticidal crystal protein with a high activity against members of the family noctuidae. *Appl Environ Microbiol.,* **62** : 80–86.

Lawrence, P. K. and Koundal, K. R., 2001, *Agrobacterium tumefaciens* mediated transformation of pigeonpea (*Cajanus cajan* L. Millsp.) and molecular analysis of regenerated plants. *Current Sci.,* **80** : 1428-1432.

Lee, J. A., Miller, P. A. and Rawlings, J. O., 1967, Interaction of combining ability effects with environments in diallel crosses of upland cotton *(G. hirsutum* L.). *Crop Sci.,* **7** : 477-481.

Leelavathi, S., Sunnichan, V. G., Kumaria, R., Vijaykanth, G. P., Bhatnagar, R. K. and Reddy, V. S., 2004, A simple and rapid *Agrobacterium* mediated transformation protocol for cotton (*Gossypium hirsutum* L.) : embryogenic calli as a source to generate large no. of transgenic plants. *Plant Cell Rep.,* **22** : 465-470.

Lee, M., Godshalk, E. B., Lambey, K. R. and Woodman, W. l., 1989, Association of restriction length polymorphism among maize inbreds with agronomic performance of their crosses. *Crop Sci.,* **29** : 1067-1071.

Litt, M. and Lutty, J. A., 1989, A hypervariable microsatellite revealed by in vitro amplification of a dinucleotide repeat within the cardiac muscle actin gene. *Am. J. Hum. Genet.,* **44** : p. 397.

Liu, S., Saha, S., Stelly, D., Burr, B. and Cantrell, R. G., 2000, Chromosomal assignment of Microsatellite loci in cotton. *The J. Heredity.,* **91** (4) : 326-332.

Lopez-Perez, E., 1979, Comparisons among five different testers for the evaluation of unselected lines of maize (*Zea mays* L.). *Dissertation Abstracts International.,* **40** : 1989B.

Ludlow, M. M. and Mukhow, R. W., 1990, Improving crop yield in water limited environments. *Adv. Agron.,* **43** : 110-153.

Lycett, G. W. and Grierson, D., 1990. Genetic engineering of crop plants. Butter worth, London.

Lyer, V. N., Klee, H. J. and Nester, E. W., 1982, Units of genetic expression in the virulence region of a plant tumor inducing plasmid of *Agrobacterium tumefaciens*. *Mol. Gen. Genet.,* **188** : 418-424.

Madhusudhana, R., 1993, Combining ability in segregating generation of sorghum (*Sorghum bicolor* L. Moench). *M. Sc. (Agri.) Thesis*, Univ. Agric. Sci., Dharwad, India.

Ma, F. C., Zhou, Y. Y., Wang, R. T. and Liu, C. G., 1983, Genetic analysis of characters in the progeny of an intervarietal hybrids of upland cotton. *Acta Agriculturae.,* **9** : 27-34.

Mahalakhmi, A. and Kurana, P., 1997, *Agrobacterium* mediated cereal transformation : A critical appraisal. *Indian J. of Exp. Biol.,* **35** : 416-426.

Mahantesh Shastri, 2004, Genetic evaluation of diverse cotton (*Gossypium hirsutum* L.). plant types and their segregating generations. *M. Sc. (Agri.) Thesis*, Univ. Agric. Sci., Dharwad, Karnataka (India).

Mahdy, E. E., Hassaballa, E. A., Khlifa, M. A. and Ounis, F. G., 1987, Comparative studies on three selection procedures in an inter specific population of cotton. *Australian. J. Agri. Sci.,* **18** : 179-195.

Maisuria, A. T., Patel, J. C., Patel, K. G. and solanki, B. G., 2006, Study of best per se performance, heterosis and combining ability effects for seed cotton yield and its component characters through GMS system in Asiatic cotton. *J. Indian Soc. Cotton Improv*. (August)., pp. 88-91.

Maizer, M., Pannetie, C., Tourneur, J., Jouanin, L. and Giband, M., 1997, Expression of Bt toxin genes in plant cells. *Biotech. Annu. Rev.,* **3** : 313-347.

Maksudov, Z. Yu and Engalychev, O. K. H., 1984, Combining ability and correlations of cotton characteristics in crosses between varieties differing in age. *Skokhozyaistvenykh Nauk Imani V. I. Lenin No. 5*, pp. 19-22

Mallikarjun, H. B., 2005, Evaluation of recombinational variability for combining ability in cotton. *Ph. D. (Agri). Thesis*, Univ. Agric. Sci., Dharwad.

Mandloi, K. C., Kotu, G. K., Mishra, U. S., Pandey, S. C. and Julka, R., 1998, Combining ability analysis and inheritance of fibre quality characters in cotton. *J. Indian Soc. Cotton Improv.,* **23** (2) : 147-153.

Manickam, S. and Gururajan, K. N., 2004, Combining ability analysis for fibre quality in upland cotton (*Gossypium hirsutum* L.). *J. Indian Soc. Cotton Improv.,* **8**(1) : 86-91.

Manivasakam, P. and Kamalanathan, N. S., 1987, Variability in yield and other quantitative characters in *Gossypium barbadense* L. *Madras Agri. J.,* **74** : 360-364.

Manivasakam, P. and Kamalanathan, S., 1985, Association of characters in segregating populations of *G. barbadense* L. *Cotton Develop.,* **15** (1) : 29-30.

Manoharan, M., Sree Vidya, C. S. and Lakshmi Sita, G., 1998, *Agrobacterium* mediated genetic transformation in hot chilli (*Capsicum annuum* L. var Pusa Jwala). *Plant Sci.,* **131** : 77-83.

MaqbooL, S. B., Zhong, H., El-Maghraby, Y., Ahmad, A., Chai, B., Wang, W., Sabzikar, R and Sticklen, M. B., 2002, Competence of oat (*Avena sativa* L.) shoot apical meristems for integrative transformation, inherited expression, and osmotic tolerance of transgenic lines containing hva1. *Theor. Appl. Gene.,* **105** : 201–208.

Marani, A., 1963, Heterosis and combining ability for yield and components of yield in a diallel cross of two species of cotton. *Crop Sci.,* **3** : 352-355.

Martin, J. M., Talbort, L. E., Lanning, S. P. and Blake, N. K., 1995, Hybrid performance in wheat as related to parental diversity. *Crop Sci.,* **35** : 104–108.

Masson, L., Moar, W. J., Van Frankenhuyzen, K., Bosse, M. and Brousseau, R., 1992, Insecticidal properties of a Crystal protein gene product isolated from Bacillus thuringiensis subsp. kenyae. *Appl Environ Microbiol.,* **58** (2) : 642–646.

Md Liakat, Ali and Tepora, N. M., 1986, Comparative performance of four types of testers for evaluating corn inbred lines from two population. *Crop Sci.,* **11** : 175-179.

Medford, J. I., 1992, Vegetative apical meristems. *Plant Cell.,* **4** : 1029-1039.

Mehla, A. S., Mor, B. R. and Naidu, M. R., 1988, Genetic analysis of earliness characters in upland cotton *(G. hirsutum* L.). *Crop Improv.,* **15** : 156-159.

Mehla, A. S., Verma, S. S., Lather, B. P. S. and Verma, U., 1988, Genetic variability and heritability for yield and its components in upland cotton *(G. hirsutum* L.). *Cotton Dev.,* **18** : 15-17.

Melchinger, A. E., and R. K. Gumber. 1998, Overview of heterosis and heterotic groups in agronomic crops. p. 29–44. *In* K. R. Lamkey and J. E. Staub (ed.) Concepts and breeding of heterosis in crop plants. CSSA, Madison, WI.

Menkir, A., A. Melake-Berhan, A. C., Ingelbrecht, I. and A. Adpoju, 2004, Grouping of tropical mid-altitude maize inbred lines on the basis of yield data and molecular markers. *Theor. Appl. Genet.,* **108** : 1582–1590.

Meredith, W. R., JR, and J. S. Brown, 1998, Heterosis and combining ability of cotton originating from different regions of the United States . *J. Cotton Sci.,* **2 :** 77-84.

Miller, P. A. and Marani, A., 1963, Heterosis and combining ability in diallel crosses of upland cotton. *Crop Sci.,* **3** : 441-444.

Millr, P. A., Williams, J. C., H. F. and Comstock R. R., 1958, Estimates of genotypic and environment variance and co-variance in upland cotton and their implications in selections. *Agron. J.,* **50** : 126-131.

Mirakhamedov, S., Stakov, V. and Rakhimov, M., 1987, Transgressive selection for fibre length. *Khlopkovodstvo.,* **7** : 30-33.

Mohammad Ilyas, Muhammad Naveed, Tariq Manzoor Khan and Iftikhar Ahmad Khan 2007, Combining ability studies in some quantitative and qualitative traits of cotton (*Gossypium hirsutum* L.). *J. Agril. Soc. Sci.,* **3** (2) : 39-42.

Mohammadi, S. A., Prasanna, B. M., Sudan, C. and Singh, N. N., 2008, SSR heterogenic patterns of Maize parental lines and prediction of hybrid performance. *J. Biotechnol. Biotechnol Equip.,* **22** (1) : 541-547.

Mohammad Reza Zangi and Nadali Babaein Jelodar, 2010, Cytoplasmic and combining ability effects on agro-morphological characters in intra and inter crosses of pima and upland cottons *(G. barbadense* and *G. hirsutum). Internat. J. Biol.,* **2**(1) : 94-102.

Mohan Rao, A., 2001, Heterosis as a function of genetic divergence in sunflower (*Helianthus annuus* L.). *Ph. D. thesis* submitted to Acharya N. G. Ranga Agric. Univ, Hyderabad.

Mohiuddin, S. B., 1996, Genetic analysis of yield and yield components of intra specific hybrids of cotton *(G. hirsutum* L.). *Ph. D. (Agri) Thesis*, Acharya N. G. Ranga. Agric. Univ, Hyderabad.

Moralejo, M., Rochange, F., Boudet, A. M. and Teulieres, C., 1998, Generation of transgenic *Eucalyptus globulus* plant lets through *Agrobacterium tumefaciens* mediated transformation. *Austra. J. of Plant Physiol.,* **25** : 207-212.

Muhammad Iqbal, 2006, Correlation and path co-efficient analysis for earliness and yield traits in cotton (*G. hirsutum* L.*). Asian J. Sci*. Hyderabad, 208pp.

Mullis, K. B., 1990, The unusual origins of the polymerase chain reaction. *Scientific American.,* **262** : 56-65.

Multani, D. S. and Lyon, B. R., 1995, Genetic fingerprinting of Australian cotton cultivars with RAPD markers*. Genome*, **38** : 1005-1008.

Munasov, K., Alikho Dzhaeva, S. S. and Lemeshev, N. R., 1990, Variability and heritability of fibre length F_1-F_3 hybrids and their parents. *Refretivinya Zhurnal.,* **9** : 3378.

Murthy, J. S. V. S. and Ranganathacharyulu, N., 1998, Studies on combining ability in boll worm tolerant lines of upland cotton *(G. hirsutum* L.). *Ann. Agri. Res.,* **19** (2) : 227-228.

Musande, V. G., Chavan, B. N., Sondge, V. D. and Borulkar, D. N., 1981, Simple correlation and regression studies between seed cotton yield and yield attributing characters in cotton. J*. Maharashtra Agric. Univ.,* **6** : 163-165.

Muthukumar, Mariamma, M., Veluthambi, K. and Gnanam, A., 1996, Genetic transformation of cotyledon explants of cowpea (*Vigna unguiculata* L. Warp) using *Agrobacterium tumefaciens*. *Plant Cell Rep.,* **15** : 980-985.

Muthu, R., Kandasamy, G. and Jayarama, M., 2004, Correlation and path co-efficient analysis for yield and fibre quality traits in cotton (*G. hirsitum*). *J. Indian Soc. Cotton Improv.,* **29** (4) : 17-20.

Muthuswamy, A. and Vivekanandan, P., 2004, Correlation studies on seedcotton yield and its components in hirsutum cotton (*Gossypium hirsutum* L.). *J. Indian Soc., Cotton Improv.,* **29** (1) : 7-9.

Muthuswamy, A., Vivekanandan, P. and Jayaramachandran, M., 2003, Combining ability and gene action for fibre characters in upland cotton (*Gossypium hirsutum* L.). *J. Indian Soc. Cotton Improv.,* **28** (2) : 127-131.

Nadarajan, N. and Sree rangaswamy, S. R., 1991, Genetic analysis of some economic characters in *Gossypium hirsutum* L. *J. Indian Soc., Cotton Improv.,* **15** : 15-18.

Nagarajan, N., 1986, Genetic analysis of fibre characters in *Gossypium hirsutum* L. *Ph. D. Thesis (Agri)*, Tamil Nadu Agric. Univ, Coimbatore, India.

Nagarajan, P., 1989, A study on seed genetics in cotton *(G. hirsutum* L.). *M. Sc. (Agri.) Thesis*, Tamil Nadu Agric. Univ, Coimbatore, India.

Nagarajan, P., Kadambavanasundaram, M. and Bangaswamy, S. R., 1994, Combining ability for yield and fibre properties of cotton (*G. hirsutum* L.). *Madras Agric. J.,* **81** : 253-255.

Naqib, U. K., Khan, B. M., Gul, H., Farhatullah, M. B., Aisha, P., Umm-E-Aiman, Muhammad, Z. K. and Zahoor A. S., 2009, Diallel analysis of some quantitative traits in *Gossypium hirsutum* L. *Pakistan J. Bot.,* **41** (6) : 3009 -3022.

Narisireddy, A. and Satyanarayana, A., 2004, Combining ability studies for yield and yield components over environments in American cotton (*Gossypium hirsutum* L.). *Madras Agric. J.,* **91**(1-3) : 75-78.

Nawar, A. A. and El-Hosary, A. A., 1984, Evaluation of eleven testers of different genetic resources of corn. *Egyptian. J. Genet. Cytolo.,* **13** : 227-237.

Nazir, C. M. and Khan, S. I., 1974, Effect of gamma irradiation on yield in cotton (*Gossypium hirsutum* L.). *Agri. Pakistan Publ.,* **24** (2) : 159-166.

Neelam, G. and Potdukhe, N. P., 2002, Studies on variability and correlations in upland cotton for yield and its components. *J. Indian Soc. Cotton Improv.,* **27** (3) : 148-152.

Neelima, S., 2002, Heterosis and combining ability analysis for yield and yield components in cotton *(G. hirsutum* L.). *M. Sc. (Agri.) Thesis*, Acharya N. G. Ranga Agric. Univ., Hyderabad.

Neelima, S. and Chenga Reddy, V., 2008, Genetic parameters of yield and fibre quality traits in American cotton (*Gossypium hirsutum* L.). *Indian J. Agric. Res.,* **42** (1) : 67-70.

Nei, M., and W. Li, 1979, Mathematical model for studying genetic variation terms of restriction endonucleases. Proc. Natl Acad. Sci. USA., **6 :** 5269-5273.

Omara, M. K, El-Defrawy, M. M., Awad, H. Y. and El-Ameen, T. M., 1996, Genetic analysis of tability and control of variation in Egyptian cotton (*Gossypium barbadense* L.) fiber fineness and strength. *Australian. J. Agri. Sci.,* **26** : 23-27.

Otte, C. E., Ross, W. M., Sullivan, C. Y., G. T. R. L. and Miller, F. R., 1984, Evaluation of R lines from the sorghum random mating population, No. 3R. *Crop Sci.,* **24** : 9-12.

Ouma, J. P., Young, M. M. and Reichert, N. A., 2004, Optimization of *in vitro* regeneration of multiple shoots from hypocotyl sections of cotton (*Gossypium hirsutum* L.). *African J. Biotech.,* **3** (3) : 169-173.

Panchal, S. S., Patel, S. A., Saiyad, M. R. and Patel, S. B., 1995, Line × tester analysis of combining ability in Egyptian cotton (*G. hirsutum* L.). *Gujarat. Agri. Univ. Res. J.,* **20** : 58-63.

pannetier, C., Giband, M., Couzi, P., Le Tan, V., Maizier, M., Tourneur, J. and Hau. B., 1997, Introduction of new traits into Cotton through genetic engineering : insect resistance as example. *Euphytica.,* **96** : 163-166.

Panse, V. G. and Sukhatme, V. P., 1961, *Statistical Methods for Agricultural Workers*, ICAR, New Delhi, p. 145.

Patel, A. D., Patel, U. G. and Kumar, V., 2009, Diallel analysis for combining ability for seed cotton yield and its component traits in upland cotton. *J. Cotton Res. Develop.,* **23** (2) : 222-225.

Patel, C. S., 1984, Genetic analysis of yield and fibre characters in *desi* cotton (*G. arboreum* L.). *Cotton Dev.,* **14** : 41-45.

Patel, K. G., Patel, U. G., Patel, J. C., Patel, D. H. and Patel, R. D., 2005, Line x Tester analysis for combining ability of introgresed Asiatic cotton. *J. Indian Soc. Cotton Improv.,* pp. 105-109.

Patel, U. G., Patel, J. C., Patel, P. G., Vadodaria, K. V. and Sutaria, C. M., 1997, Combining ability analysis for seed cotton yield and mean fibre length in upland cotton *(G. hirsutum* L.). *Indian J. Genet Pl. Breed.*, **57** : 315-318.

Pathak, R. S. and Prakashkumar, 1976, A study heterosis in upland cotton *(G. hirsutum* L.). *Theor. Appl. Genet.,* **47** : 45-49.

Pathak, R. S. and Singh, R. B., 1970, Genetics of yield characters in upland cotton. *Indian J. Genet Pl. Breed.,* **30** : 679-689.

Patil, M. S., 1973, Heterosis for some agronomic characters in diploid cotton (*G. herbaceum* L.). *Indian J. Agri. Sci.,* **43** : 595-601.

Patil, M. S., 1974, Association between some quantitive characters in 6x6 diallel cross population of *(G. herbaceum* L.). *Mysore J. Agric. Sci.*, **8** : 90-96.

Patil, R. A. and Chopde, P. R., 1983, Diallel cross analysis for combining ability in upland cotton. *J. Indian Soc. Cotton Improv.,* **8** : 54-60.

Patil, S. A., 1975, Seven parent diallel analysis of yield and yield contributing characters *(G. hirsutum* L.). *M. Sc. (Agri.) Thesis*, Univ. Agric. Sci, Bangalore, Karnataka (India).

Patil, S. A., 1989, Genetics of yield, yield related physiological and morphological characters and their breeding implications in cotton *(G. hirsutum* L.). *Ph. D. (Agri.) Thesis*, Univ. Agric. Sci, Dharwad, Karnataka (India).

Patil, S. A., Ravikumar, R. L. and Prameshwarappa, K. G., 1997, Effect of combining hybridization and mutation on character association in safflower (*Carthamus tinctorius* L.) 1997 communicated to IVth International Safflower Conference, BARI (Italy), 2-7, 1997.

Patil, S. S., 1995, *Report on the Work Done in the Area of Hybrid Research CIMMYT*. The International maize and Wheat Improvement centre El Batan Mexico.

Patil, S. S., 1997, "Exploiting variability for important economic traits resulting from combinations of early and medium duration pigeon pea varieties" *Annual Report 1997 of ICAR ADHOC Scheme.*

Patil, S. S. and Pandit, V. V., 1991, Use of B × R cross for improving combining ability in sorghum. *Golden Jubilee Symposium on Research and Education : Current Trends and the Next Fifty Years,* held at New Delhi, p. 397.

Patil, S. S. and Patil, S. A., 2003, Role of improving combining ability in increasing performance of cotton hybrids. *Third World Cotton Research Conference*, 9-13 March 2003, held at Cape Town South Africa, pp. 234-238.

Patil, S. S., Mallaya, C. K., Patil, S. A. and Somashekhar, 2004, Developing hybrids and hybrid oriented populations in compact cotton. *Proceedings of International Symposium on Sustainable Cotton Production - A Global Vision,* held at Dharwad from 23 Nov- 25th Nov. 2004, pp. 130-134.

Patil, S. S., Pandit, V. V. and Shashidhar, L. S., 1991, Exploitation of induced variability for combining ability in developing new hybrids I sorghum. *Golden Jubilee Symposium on genetic Research and Education, Current Trends and the Next Fifty Years*, held at New Delhi, p. 668.

Patil, S. S., Patil, S. A., Ramakrishna, V., Deepakbabu, H. and Mallikarjun, H. B., 2007, Approaches of improving combining ability for enhancing performance of cotton hybrids. *Fourth World Cotton Research Conference*, 10-11th September 2007, held at Lubbock, Texas, U. S. A.

Patil, S. S., Ramakrishna, V., Manjula, S. M., Swati, P., Ranganatha, H. M., Kencharaddi, H. C. and Deepakbabu, H., 2011, Deploying reciprocal selection for combining ability for improving performance of hybrids in cotton (*Gossypium hirsutum*). *Indian J. Genet.,* **71** (2) : 180-184.

Paulo Antonio De Aguiar, Julio Cesar Viglioni Penna, Eleusio Curvelo Freire and Leonardo Cunha Melo, 2007, Diallel analysis of upland cotton cultivars. *Crop Breed. Appl. Biotechnol.,* **7**(1) : 353-359.

Pavasia, M. J., Shukla, P. T. and Patel, U. G., 1998, Combining ability studies for yield and its components over environments in upland cotton. *J. Indian Soc. Cotton Improv.,* **23** (2) : 140-143.

Pavasia, M. J., Shukla, P. T. and Patel, U. G., 1999, Combining ability analysis over environments for fibre characters in upland cotton. *Indian J. Genet Pl. Breed.,* **59** (1) : 77-81.

Pavasia, M. J., Shukla, P. T. and Patel, U. G. 1999b, Heterobeltiosis in multiple environments for seed cotton yield and related characters in cotton *(Gossypium hirsutum* L.). *J. Indian Soc. Cotton Improv.,* **24** (1) : 14-17.

Pederson, D. G., 1974, Arguments against intermating before selection a self fertilizing species. *Theor. Appl. Genet.,* **45** : 157-162.

Penman, H. L. and Schofield, R. K., 1951, Some physical aspects of assimilation and transpiration. *Sympo. Soc. Experiment Biol.,* **5** : 115-129.

Percival, E. and Kohel, R. J., 1990, Distribution collection and evaluation of *Gossypium. Adv. Agron.,* **44** : 225-228.

Perlak, F. J., Oppenhuizen, M., Gustafson, K., Voth, R., Sivasupramaniam, S. and Heering, D., 2001, Development and commercial use of Bollgard cotton in the USA – early promises versus today's reality. *Plant J.,* **27** : 489–501.

Pollock, K., Barfield, D. G. and Shields, R., 1983, The toxicity of antibiotics to plant cell cultures. *Plant Cell Rep.,* **2** : 36-39.

Potdukhe, N. R., 2002, Level of heterosis for quantitative traits in upland cotton. *J. Indian Soc. Cotton Improv.,* **27** (3) : 200-214.

Potrykus, I., 1990, Gene transfer to cereals. An assessment. *Biotech*. **8** : 535-542.

Potrykus, I., 1991, Gene transfer to plants : assessment of published approaches and results. *Ann. Review of Plant Physiol. Plant Molec. Biol.,* **42** : 205-225.

Prasad, K. V. S. K., Sharmila, P., Kumar, P. A. and Pardha Saradhi, P., 2000, Transformation of *Brassica juncea* (L.) Czern with bacterial cod A gene enhancer its tolerance to salt-stress. *Mol. Breed.,* **6** : 489-499.

Pretha, S. and Raveendran, T. S., 2008, Combining ability studies for yield and fibre quality traits in line x tester crosses of upland cotton (*Gossypium hirsutum* L.). *Int. J. Plant Breed. Genet.,* **2** (2) : 64-67.

Puech- Suanzes, I., Hasaio, T. C., Perers, E. and Henderson, D. W., 1989, Water stress effects on the carbon exchange rates of 3 upland cotton (*G. hirsutum L.*) cultivars in the field. *Field Crop Res.,* **21** : 239-255.

Rafalski, J. A., 1997, Randomly amplified polymorphic DNA (RAPD) analysis. In : DNA markers : Protocols, Applications and Overviews (eds. G. C. Anolles and P. M. Gresshoff), Wiley-Liss, Inc. USA, p. 364.

Rajput, J. B., Meshram, L. D., Kalpande, H. V., Golhar, S. R. and Swati, B., 1997, Heterosis studies in Asiatic cotton (*Gossypium* spp.). *J. Soils and Crops.,* **7** : 166-170.

Ramakrishna, V., 2008, Reciprocal selection for improving combining ability in cotton. *Ph. D. Thesis*, Univ. Agric. Sci, Dharwad, Karnataka (India).

Ramalingam, A., 1996, Genetics of seed cotton yield and its components in upland cotton *(G. hirsutum* L.) diallel and triallel analysis. *Ph. D. (Agri) Thesis*, Tamil Nadu. Univ. Agric. Sci., Coimbatore, India.

Rana, M. K., Singh, S. and Bhat, K. V., 2004, amplified fragment length polymorphism (AFLP) based diversity in advanced breeding lines of cotton (*Gossypium hirsutum* L.) *Indian J. Genet.,* **64** (2) : 91-93.

Rao, G. N. and Reddy, M. S. S., 2001, Studies on heritability and variability for yield and its components in *hirsutum* cottons. *J. Cotton. Res. Dev.,* **15** : 84-86.

Raut, R. S. and Misalkar, V. M., 1988, Combining ability studies in F_2 generation of cotton. *PKV. Res. J.,* **12** : 95-97.

Raut, R. S., Shakhare, S. B. and Ghorpade, P. B., 1989, Line $\times$ tester analysis of combining ability and heterosis in cotton. *J. Maharashtra. Agric. Univ.,* **14** : 214-215.

Ravi, M., Geethanjali, S., SameeyAfarheen, F. and Maheshwaran, M., 2003, Molecular marker based genetic diversity analysis in rice (oryza sativa L.) using RAPD and SSR markers. *Euphyfica.,* **133** : 243-252.

Rawlings, J. O. and Thompson, D. L., 1962, Performance level as criterion for the choice of maize testers. *Crop Sci.,* **2** : 217-220.

Reddy, A. N., 2001, Heterosis, combining ability and stability analysis of hybrids for yield and yield components in cotton (*Gossypium hirsutum* L.). *Ph. D. Thesis*, Acharya N. G. Ranga Agric. Univ., Rajendranagar, Hyderabad (India).

Reddy, K. R., Singh, R. P. and Rao, A. K., 1985, Variability and association analysis in okra. *Madras Agric. J.,* **72** (8) : 478-480.

Reif, J. C., A. R. Hallauer, and A. E. Melchinger. 2005a. Heterosis and heterotic pattern in maize. *Maydica.,* **50** : 215–223.

Riaz, A., G. Li, Z. Quresh, M. S. Swati, and C. F. Quiros, 2001, Genetic diversity of oilseed *Brassica napus* inbred lines based on sequence – related amplified polymorphism and its relation to hybrid performance. *Plant Breed.,* **120 :** 411-415.

Richey, F. D. and Mayer, L. S., 1925, The productiveness of successive generations of self fertilized lines of corn and of cross between them. *United State Department of Agriculture Bulletin*, p. 1454.

Rissi, R. De, and Hallauer, A. R., 1991, Evaluation of four testers for evaluating maize (*Zea mays* L.) lines in a hybrid development programme. *Revista Brasileria de Genetica.,* **14** : 467-481.

Robinson, H. F., Comstock, R. E. and Harvey, P. H., 1949, Estimates of heritability and degree of dominance in corn. *Agron. J.,* **41** : 353-359.

Rohini, V. K. and K. Sankara Rao, 2000a. Transformation of peanut (*Arachis hypogeae* L.) : a non-tissue culture based approach for generating transgenic plants, *Plant Sci*., **150 :** 41-49.

Rohini, V. K., and K. Sankara Rao, 2000b. Embryo transformation, a practical approach for realizing transgenic plants of safflower (*Carthamus tinctorius* L.), *Ann. Bot.* **86** : 1043-1049.

Rohini, V. K., and K. Sankara Rao, 2001. Transformation of peanut (*Arachis hypogaea* L.) with tobacco chitinase gene : variable response of transformants to leaf spot disease, *Plant Sci*., **160** (5) : 883-892.

Rohlf, F. J., 2001, NTSYS-PC Numerical Taxonomy and Multivariate Analysis System. Exeter Publ, Setauket.

Rungis, D., Liewellyn, D., Dennis, E. S., Lyon B. R., 2005, Simple sequence repeat (SSR) markers reveal low levels of polymorphism between cotton (*Gossypium hirsutum* L.) cultivars. *Australian J. Agri. Res.,* **56** : 301-307.

Russell, W. A., Eberhart, S. A. and Vega, V. A., 1973, Recurrent selection for specific combining ability for yield in two maize populations. *Crop Sci.,* **13** : 257-261.

Russell, W. A. and Eberhart, S. A., 1975, Hybrid performance of selected maize lines from reciprocal recurrent selection and test cross selection programmes. *Crop Sci.,* **15** : 1-4.

Sadykhova, L. D. and Makhamudov, T. K., 1986, Combining ability of cotton variety. *Referatinyi Zhurnal No. 5*, pp. 11-17.

Saeed, N. A, Zafar, Y and Malik, K. A., 1997, A simple procedure of *Gossypium* meristem shoot tip culture. *Organ Cult.,* **51** : 201–207.

Saeed R., Hafeez-Ur-Rahman. and Khan, T. M., 2004, Effect of kinetin on multiple shoot induction in cotton (*Gossypium hirsutum* L.) cv. NIAB-999. *Iranian J. Biotech.,* **2** (4) : 279-282.

Saghai-Maroof, M. A., Soliman, K. M., Jorgensen, R. A. and Allard, R. W., 1984, Ribosomal DNA spacer length polymorphism in barley : Mendelian inheritance, chromosomal location and population dynamics. *Proc Natl Acad Sci,* USA., **81** : 8014-8018.

Saha, S., Mehmet Karaca, Johnie N., Jenkins, Allan E., Zipf, O., Umesh, K. Reddy and Ramesh V. Kantetty, 2003, Simple sequence repeats as useful resources to study transcribed genes of cotton. *Euphylica.,* **130** (3) : 355-364.

Salimath, P. M., 1975, A study of genetic variability formulation of cotton *Gossypium hirsutum* L. *M. Sc. (Agri.) Thesis*, Univ. Agric. Sci., Bangalore, Karnataka (India).

Sambamoorhty, J. S. V., Gopinath, N. and Mukundan, S., 1994, Association of characters and path co-efficient analysis in upland cotton. (*Gossypium hirsutum* L.). *Madras Agric. J.,* **81** : 308-311.

Sambamurthy, J. S. V., Hopinath, N. and Mukandan, S., 1994, Association of characters and path co-efficient analysis in upland cotton (*Gossypium hirsutum* L.). *Madras Agric. J.,* **81** (6) : 308-311.

Sambamurthy, J. S. V., Ratnakumari, S., Chamundeshwari, N. and Shiva Reddy, K. V., 2004, Studies on nature of genetic divergence in diploid cotton (*G. herbaceum* L.). *International Symposium on Strategies for Sustainable Cotton Production – A Global Vision*, 23-25 November, 2004, held at University of Agricultural Sciences, Dharwad, pp. 187-189.

Sambamurthy, J. S. V., Reddy, D. M. and Reddy, K. H. G., 1995, Genetic variability, correlation and path analysis in cotton (*Gossypium hirsutum* L.). *J. Indian Soc. Cotton Improv.,* **20** : 133-138.

Sandhu, B. S. and Kooner, A. S., 1979, Inheritance of yield and its components in cotton (*G. arboreum* L.). *Crop Improv.,* **6** : 43-52.

Saravanan, N. A., Gopalan, A. and Sudhagar, R., 2003, Genetic analysis of quantitative characters in cotton (*Gossypium* spp.) *Madras Agric. J.,* **90** (4-6) : 236-238.

Sarsar, S. M., Patil, R. A. and Bhatade, S. S., 1986, Heterosis and combining ability in upland cotton. *Indian J. Agric. Sci.,* **56** : 567-573.

Satyavathi, V. V., Prasad, V., Gita Lakshmi, B. and Lakshmi Sita, G., 2002, High efficiency transformation protocol for three Indian cotton varieties via *Agrobacterium tumefaciens*. *Plant Sci.,* **162** : 215-223.

Sautter, C., Leduc, N., Bilang, R., Iglesiass, V., Pisel. A., Wen, X. and Potrykus, I., 1995, Shoot apical meristems as a target for gene transfer by microballistics. *Euphytica.,* **85** : 45-51.

Sawant, S. V., Kiran, K., Singh, P. K. and Tuli, R., 2001, Sequence architecture downstream of the initiator codon enhances gene expression and protein stability in plants. *Plant Physiol.,* **126** : 1630–1636.

Schrammeijer, B., Sijmons, P. C., Vanden Elzan, J. M. and Hoekema, L., 1990, Meristematic transformation of sunflower via *Agrobacterium*. *Plant Cell Rep*., **9** : 55-60.

Selvapandiyan, A., Reddy, V. S., Kumar, P. A., Tewari, K. K. and Bhatnagar, R. K., 1998, Transformation of Nicotiana tabacum with a native cry1Ia5 gene confers complete protection against Heliothis armigera. *Molec. Breed.,* **4** : 473–478.

Shaikh, A. R. and Upadhyaya, U. C., 1982, Correlation and path analysis in rainfed cotton (*Gossypium hirsutum* L.). *Cotton Dev.,* **12** : 17-18.

Shallam, A. A., Elgohary, A. A. and El-Mogazi, M., 1986, Breeding potentials of some cultivated Egyptian cotton varieties 2. Heterosis and combining ability of lint yield and fibre properties. *Agri. Rese. Rev.,* **59** : 19-31.

Shandhu, B. S., Mangat, N. S. and Arora, R. L., 1986, Characters associations in segregating populations of desi cotton. *Cotton Dev.,* **16** : 26-31.

Shanti, N. and Selvaraj, U., 1995, Combining ability studies for quantitative characters in cotton (*Gossypium hirsutum* L.). *Madras Agric. J.,* **82** : 162-164.

Shashidhar, L. S., Patil, S. S. and Gouda, J. V., 1989, use of induced mutations in improving combining ability in sorghum. *6th International Congress of SABRA*, held at Tokyo, Japan.

Sheng, J. X., G. Y. Lu, T. D. Fu, and G. S. Yang, 2002, Relationships between genetic diversity and hybrid performance in Oilseed rape (*Brassica napus*). *Acta Agron. Sin.,* **28 :** 622-627.

Shimshi, D. and Ephrat, J., 1975, Stomatal behavior of wheat cultivars in relation of their translocation, photosynthesis and yield. *Agron. J.,* **67** : 326-246.

Shuangxia Jin, Xianlong Zhang, Shaoguang Liang, Yichun Nie, Xiaoping Guo and Chao Huang, 2005, Factors affecting transformation efficiency of embryogenic callus of upland cotton with *Agrobacterium tumefaciens. Plant Cell Tissue Organ Cult.,* **81** : 229-2237.

Shull, G. H., 1909, A pure-line method of corn breeding. *AM Breeder's Association Report.,* **5** : 51-59.

Shull, G. H., 1914, Methods of Plant Breeding by Hayes H. K., Immes, F. R. and Smith, D. C., 1955, *McGraw Hill Book Company*, New York, p. 53.

Simongulyan, N. G. and Kim, V. L., 1990, Variation in quantitative characters I an irradiated cotton population. *Genetika.,* **26** : 1815-1821.

Singh, M. and Raut, R. N., 1983, Genetical Researches in Cotton and Jute : *In Genetical Research in India*. Ed. Jaiswal, P. L., ICAR, New Delhi.

Singh, M., Bharadwaj, S. N., Saini, A. B. and Singh, V. P., 1988, Yield improvement through simultaneous improvement of yield components in upland cotton (*G. hirsutum* L.). *Indian J. Agric. Sci.,* **58** : 425-428.

Singh, P. and Narayanan, S. S., 1993, Role of review on breeding aspects of plant type in cotton. *J. Indian Soc. Cotton Improv.,* **18** : 1-13.

Singh, P. and Singh, H. G., 1980, Line × tester analysis in upland cotton. *Crop Improv.,* **7** : 88-96.

Singh, P. and Singh, H. G., 1981, Gene action, heritability and genetic advance in upland cotton. *Indian J. Agric. Sci.,* **51** : 209 -213.

Singh, P., 1982, Note on useful heterosis in upland cotton. *Indian J. Agric. Sci.,* **52** : 29-31.

Singh, P. K., Sarangi, B. K., and Tuli R., 1996, A facile method for the construction of synthetic genes. *J Biosc.,* **21** : 735–741.

Singh, P., Loknathan, T. R. and Dinesh, K. A., 2003, Heterosis for fibre properties in intra *hirsutum* crosses *(G. hirsutum* L.). *Indian J. Genet Pl. Breed.,* **63** (4) : 325-327.

Singh, R. B. and Gupta, M. P., 1970, Multivariate analysis of divergence in upland cotton. *Indian J. Genet Pl. Breed.,* **30** : 608-618.

Singh, R. B., Kasly, H. S. and Rana, B. S., 1968, Variability and correlation studies in Punjab American cotton- (*Gossypium hirsutum* L.). *J. Res.,* **6 :** 139-144.

Singh, R. K. and Chaudhary, B. D., 1996, Biometrical methods in quantitative genetic analysis. Kalyani publishers, Ludhiana, pp. 191-200.

Singh, T. H., Quader, M. A. and Chahal, G. S., 1983, Estimates of gene effects for some quantitative characters in upland cotton (*Gossypium hirsutum* L.). *Cotton Fibres Tropical.,* **38** : 319-320.

Singh, V. V. and Bhat, M. G., 1984, Role of poor and average parents in heterosis in cotton. *Indian J. Agri. Sci.,* **54** : 370-373.

Singh, V. V., Singh, P. and Bhat, M. C., 1987, Study of yield components in rainfed American cotton. *J. Indian Soci. Cotton Improv.,* **12** : 1-4.

Sinha, P. D., Amudha, J. and Balasubramani, G., 2008, *Indian J. Crop Sci,* **3** (1) : 71-75.

Siruguppa, A. R. S. and Parameshwarappa, S. G., 1998, Heterosis and inbreeding depression in intra hirsutum crosses of cotton. *J. Indian Soc. Cotton Improv.,* **23** (1) : 124-125.

Sivaprasad, U., 2003, Heterosis and combining ability studies for yield and yield components in cotton (*Gossypium hirsutum* L.). *M. Sc. (Ag) Thesis,* Acharya N. G. Ranga Agricultural University, Rajendranagar, Hyderabad.

Sivaprasad, U., Chenga Reddy, V. and Narisireddy, A., 2004a Combining ability studies for yield and yield components in American cotton. Paper presented in International symposium on "Strategies for Sustainable Cotton Production – A Global Vision" held at University of Agricultural Sciences, Dharwad 23rd – 25th November, 2004.

Smith, O. S., Smith, J. S. C., Bowen, S. L., Tenborg, R. A. and Wall, S. J., 1990, Similarities among a group of elite maize inbreeds as measured by pedigree, F1 grain yield, grain yield, heterosis and RFLPs. *Theor. Appl. Genet.,* **80** : 833-840.

Sohu, V. S., Chahal, G. S., Singh, T. H. and Sohu, R. S., 1993, Heterosis for earliness and yield in unpland cotton (*Gossypium hirsutum*). In : Heterosis breeding in crop plants, theory and application. Eds. Verma, M. M., Virk, D. S. and Chahal, G. S. *Symposium*, 23-24 February, 1993, Ludhiana, India, pp. 78-79.

Somashekhar, D., 2006, Genetic studies on reciprocal selection for combining ability to improve hybrid performance in cotton. *Ph. D (Agri.) Thesis,* Univ. Agric. Sci, Dharwad, Karnataka (India).

Soomre, B. A., Mohinuddin Ahmed and Soomre, A. R., 1982, Heterosis studies in inter specific crosses of cotton (*G. hirsutum* L.). *Pakistan Cottons.,* **26** : 53-61.

Sprague, G. F. and Tatum, L. A., 1942, General versus specific combining ability in single crosses corn. *J. American Soc. Agron.,* **34** : 923-932.

Sridhar, B., 1991, Studies on combining ability in segregating generations of sorghum [*Sorghum bicolor* (L.) Moench]. *M. Sc. (Agri.) Thesis,* Univ. Agric. Sci., Dharwad, Karnataka (India).

Srivastiav, D. K., Kolganva, T. V., Mtt, V. L. and Piruzion, E. S., 1991, Genetic transformation of *Gossypium hirsutum* L. *Plant Biotech.,* **289** : 263-264.

Stachel, S. E. and Nester, E. W., 1986, The genetic and transcriptional organization of the vir region of the A6T plasmid of *Agrobacterium tumefaciens*. *Embo. J.,* **4** : 891-898.

Stuber, C. W., S. E. Lincoln, D. W. Wolff, T. Helentijars, and E. S. Lander, 1992, Identification of genetic factors contributing to heterosis in a hybrid from two elite maize inbred lines using molecular markers. *Genetics.,* **132** : 823-839.

Subramanian, A., Ravikesavan, R., Iyanar, K., Thangaraj, K. and Vindhyavarman, P., 2005, Combining ability analysis in upland cotton (*Gossypium hirsutum* L.). *Plant Archives.,* **5** (1) : 23-28.

Subramanyam, Y., Patel, J. C., Mehta, N. P., Masurla, A. T., Bhalad, M. C. and Janakl, L, K., 1991, Combining ability and inheritance of fibe fineness in diploid cottons. A comparison for F_1 and F_2 generations. *Indian J. Genet Pl. Breed.,* **54** : 424-428.

Sultan, M. K., Mitra, B. N., Chaudhary, R., Kamruzzama, M. M. and Matin, M. A., 1999, Correlation and path analysis in upland cotton (*Gossypium hirsutum* L.). *Bangladesh J. Scientific Indus. Res.,* **34** (1) : 55-58.

Sumathi, P. and Nandarajan, N., 1995, Character association and component analysis in upland cotton. *Madras Agric. J.,* **82** (4) : 255-258.

Sunilkumar, G. and rathore, K. S., 2001, Transgenic cotton : factors influencing *Agrobacterium*-mediated transformation and regeneration. *Mol. Breed.,* **8**(1) : 37-52.

Sun-Junling, Du-Xiongming, Zhou-Zhongli, Pan-Zhoe. and Pang- Baoyin, 2006, genetic variation in the progeny of upland cotton irradiated with gamma rays. *Acta Agriculturae Boreali Sinica.,* **21** (2) : 27-33.

Syiam, M. M., Awad, H. Y., El-Gharbawi, M. A. and Atta, Y. T., 1982, Heterosis and potence ratio of the technological characters. in : inter specific and intra specific crosses of cotton. *Plant Breeding Abstracts.,* **58** : 841-852.

Tabarah, T. A. M 1970, *Ph. D. Thesis*, Oklahoma State University., USA.

Tabar, M. V., Chandrashekaran S, Rana, M., K. and Bhat, K. V., 2004, RAPD analysis of genetic diversity in Indian tetraploid and diploid cotton (*Gossypium* sp.). *J. Plant Biochem. Biotechnol.,* **13** : 81- 84.

Tagiev, A. A., 1991, Variation in cotton induced by chemical mutagens. In : *Khimicheskii Mutagene Selecletsii.,* pp. 214-217.

Tanksley, S. D., 1983, Molecular markers in plant breeding. *Plant Mol. Biol. Rep.*, **1** : 3-8.

Tatineni, V., Cantrell, R. G. and Davis, D. D., 1996, Genetic diversity in elite cotton germplasm determined by morphological characteristics and RAPDs. *Crop Sci.,* **36** : 186-192.

Taware, S. P., Patil, V. P. and Deodikar, G. B., 1987, Hybrid vigour in (*G. arboreum* L.). *Indian J. Agri. Sci.,* **57** : 434-435.

Thombre, M. V., Pathade, S. V. and Patil, F. B., 1982, Genetic studies on seed cotton yield and its major components in upland cotton. *J. Maharashtra. Agri. Univ.,* **7** : 48-50.

Tinland, B., 1996, The integration on T-DNA into plant genomes. *Trends in Plant Sci.,* **1** : 178-184.

Tomar, S. K. and Singh, S. P., 1991, Genetic variability and association of characters in *desi* cotton (*G. arboreum* L.). *Indian J. Agri. Sci.,* **62** : 255-258.

Tomar, S. K. and Singh, S. P., 1992, Combining ability analysis over environments in Asiatic cotton (*G. arboreum* L.). *Indian J. Genet Pl. Breed.,* **52** : 264-269.

Tommar, S. K. and Singh, S. P., 1992, Correlation and path co-efficient studies over environments in desi cotton (*Gossypium arboretum* L.). *Indian J. Genet.,* **52** (2) : 187-191.

Turner, J. H., 1953, A study of heterosis in upland cotton II. Combining ability and inbreeding effects. *Agron. J.,* **45** : 487-490.

Tuteja, O. P., Singh, A. K. and Senapathi, B. K., 1996, Combining ability in relation to heterosis for quantitative characters in cotton. *J. Cotton Res. Dev.,* **10** : 139-145.

Tyagi, A. P., more, B. R. and Singh, D. P., 1988, Path analysis in upland cotton (*Gossypium hirsutum* L.). *Indian J. Agric. Res.,* **22** (3) : 137-142.

Umbeck, P., Johnson, G., Barton, K. and Swain, W., 1987, Genetically transformed cotton (*Gossypium hirsutum* L.) plants. *Bio/Tech.,* **5** : 263-266.

Vahtin, J. U. B., 1958, The inheritance of combining ability in maize when self-pollinated and selected for earliness. *Bulletin de Academic de Sccence White Russia*, pp. 209-216.

Valarmathi, M. and Jehangir, K. S., 1998, Line × tester analysis for combining ability in *(Gossypium hirsutum* L.). *Madras. Agri. J.,* **85** (2) : 103-105.

Valaramathi, M. and Jhangir, K. S., 1998b, Line x tester analysis for combining ability in cotton (*Gossypium hirsutum* L.*)*. *Madras. Agri. J.,* **85** (2) : 103-105.

Vaman, B. M., Nadarajan, N. and Pater, S. D., 1985, A note on the evaluation of genetic stock of *Gossypium barbadense* L. *Madras. Agri. J.,* **72** : 116-117.

Vande, N. N. and Thombre, M. V., 1983, Variability studies in Egyptian cotton. *Cotton Improv.,* **13** : 1-3.

Vande Roovart, E. and Fuller, G. D., 1935, Stomatal frequency in cereals. *Ecologia.,* **16** : 69-87.

Veluthambi, K., Gupta, K. A. and Sharma, A., 2003, The current status of plant transformation technologies. *Current Sci.,* **84** (3) : 368-380.

Venkataraman, N. and Santhanam. V., 1962, Correlation studies on yield components in Cambodia cotton (*Gossypium hirsutum* L.). *Indian Cott. Gr. Rev.,* **16** : 131-137.

Verma, S. K., Ahuja, S. L., Tuteja, O. P., Sunil Kumar, Mahender Singh, Monga, D. and Ram Prakash, 2004, Line × tester analysis of yield, its components and fibre quality traits in cotton (*Gossypium hirsutum* L.). *J. Indian Soc. Cotton Improv*, pp. 151-157.

Verma, S. K., Tuteja, O. P., Koli, N. R., Jal Singh and Monga, D., 2006, Assessment of genetic variability nature and magnitude of character association in cytotype genotypes of uplan cotton (*Gosyspium hirsutum* L.). *J. Indian Soc. cotton Improv.,* **31** (3) : 129-133.

Vfaie-Tabar, M., Chandshekaran, S., Singh, R. P. and Rana, M. K., 2003, evaluation of genetic diversity in Indian tetraploid and diploid cotton (*gossypium spp.)* by morphological characteristics and RAPDs. *Indian J. Genet.,* **63** (3) : 230-234.

Vijindradas, L. D., 1981, Studies on Egyptian cottons *Gossypium barbadense* L. and their yield components. *Cotton Dev.,* **11** : 17- 24.

Vijendradas, L. D., 1982, Heterosis in inter specific hybrids between cultivars of *Gossypium hirsutum* L. and *Gossypium barbadense* L. *Cotton Dev.,* **12** : 47-50.

Virk, P. S. and Kalsy, H. S., 1982, Combining ability analysis for some metric traits in upland cotton (*Gossypium hirsutum* L.). *Crop Improv.,* **9** : 152-155.

Virk, P. S., Kalsy, H. S., Virk, D. S. and Pooni, H. S., 1991, An assessment of the breeding potential of a *Gossypium hirsutum* L. *Crop Improv.,* **18** : 7-13.

Visser, B., Munsterman, E., Stoker, A. and Dirkse, W. G., 1990, A novel Bacillus thuringiensis gene encoding a Spodoptera exigua – specific crystal protein. *J Bacteriol.,* **172** : 6783– 6788.

Von Tersch, M. A., Robbins, H. L., Jany, C. S. and Johnson, T. B., 1991, Insecticidal toxins from Bacillus thuringiensis subsp. kenyae : gene cloning and characterization and comparison with B. thuringiensis subsp. kurstaki CryIAI toxins. *Appl Environ Microbiol.,* **57** : 349–358.

Waldia, R. S., 1980, Heterosis in *desi* cotton (*G. arboreum*). *J. Res*, Haryana Agric. Univ., **10** : 169-174.

Waldia, R. S., Mor, B. R. and Jatasara, D. S., 1980, Line × tester analysis for yield and its economic attributes in *Gossypium arboreum* L. *Indian J. Agri. Sci.,* **50** : 745-747.

Walejko, R. N. and Russell, W. A., 1977, Evaluation of recurrent selection for specific combining ability in two open-pollinated maize cultivars. *Crop Sci.,* **17** : 647-651.

Wang, W., chen, W., Gao, Y. and Zhu, Z., 1998, Obtaining insect resistant cotton by transformation with *Agrobacterium*. *Proceedings of the World.*

Wang, X. D. and Pan, J. J., 1991, Genetic analysis of heterosis and inbreeding depression in upland cotton. *Acta Agronomica Sinica.,* **17** : 18-23.

Wankhade, S. N., Patil, S. P., Kayande, N. V. and Burghate, S. K., 2008, Diallel analysis for estimating combining ability of quantitatively inherited traits in upland cotton. *J. Cotton Res. Dev.,* **22** (2) : 147-149.

Weber, C. R. and Moorthy, B. R., 1952, Heritable and non-heritable relationship and variabilities of oil content and organic character in F2 generation of soybean crosses. *Agron. J.,* **44** : 202-209.

Weir, B., Xu GU, Mingbo Wang, Narayana Updhyaya, Adri, R., Ellion and Richard Bretell, 2001, *Agrobacterium tumefaciens* mediated transformation of wheat using suspension cells as a model system and green fluorescent protein as a visual marker. *Australian J. Plant Physiol.,* **28** : 307-318.

Wendel, J. F., Brubaker, C. L. and Percival, A. E., 1992, Genetic diversity in *Gossypium hirsutum* and the origin of upland cotton. *American. J. Bot.,* **79** : 1291-1310.

Wendel, J. F., Rowley R, Stewart, J. and Mcd, 1994, Genetic diversity in and phylogenetic relationships of the Brazilian endemic cotton, *Gossypium mustelinum* (*Malvaceae*). *Plant Systematics and Evolution.,* **192** : 49-59.

White, T. G. and Richmond, T. R., 1963, Heterosis and combining ability in top and diallel crosses among primitive, foreign and cultivated upland cottons. *Crop Sci.,* **3** : 58-63.

Williams, J. G. K., Kubelik, A. R., Livak, K. J., Rafalski, J. A. and Tingey, S. V., 1990, DNA polymorphism amplified by arbitrary primers are useful as genetic markers. *Nucleic Acids. Res.,* **18** : 6531-6535.

Wilson, F. D. and Wilson, R. L., 1975, Breeding potential of non-cultivated cotton. I. Some agronomic and fibre properties of selected parents and their F_1 hybrids. *Crop Sci.,* **15** : 594-596.

Wong, S. C., Cowan, I. R. and Farquhar, G. D., 1979, Stomatal conductance correlates with photo synthesis capacity. *Nature.,* **282** : 424-426.

Wright, S., 1921, Correlation and causation. *J. Agric. Res.,* **20** : 557-585.

Wu, J., Zhang, X., Nie, Y. and Luo, X., 2005, High-efficiency transformation of *Gossypium hirsutum* embryogenic calli mediated by *Agrobacterium tumefaciens* and regeneration of insect-resistant plants. *Plant Breed.,* **124** : 142-146.

Wu, Y. T., T. Z. Zhang, X. F. Zhu, and G. M. Wang, 2002, Relationship between F1, F2 hybrid yield, heterosis and genetic distance measured by molecular markers and parent performance in cotton. *Sci. Agric. Sin.,* **1 :** 498-507.

Xiao, J. H., J. M. Li, L. P. Yung, and S. D. Tanksley, 1995, Dominance is the major genetic basis of heterosis in rice as released by QTL analysis using molecular markers. *Genetics.,* **140** : 745-754.

Xu-Xian, Wang, Xiaoshuan, Yin Zhimin and Xie Lingqin, 1995, Analysis of combining ability and heterosis for parental varieties in upland cotton. *J. Hebei Agric. Univ.,* **18** : 34-40.

Zambezi, B. T., Horner, E. S. And Martin, F. G., 1986, Inbred lines as testers for general combining ability of maize. *Crop Sci.,* **26** : 908-910.

Zapata, C., Park, S., El-Zik, K. M. and Smith, R. H., 1999, Transformation of Texas cotton cultivar by using *Agrobacterium* and the shoot apex. *Theor. Appl. Gene.,* **98** : 252-256.

Zhang Jinfa, Deng, Zhong and Sunhizhong, 1994, Heterosis and combining ability in inter specific crosses between *Gossypium hirsutum* L. × *Gossypium barbadense* L. *J. Huazhong Agric. Univ*, **13** : 9-14.

Zhang, Q., Saghai, M. A., Yang, G. P., Liu, K. D., Zhou, K. A., Gravois, C. G., Xu and Gao, Y. G., 1995, Correlatoons between molecular marker polymorphism and hybrid performance in rice. *Plant Genome IV Conference*, San Diego, CA, p. 307.

Zhang, Q., Z. Q. Zhou, G. P. Yang, C. G. Xu, K. D. Liu, and M. A. Saghai Maroof, 1996. Molecular marker heterozygosity and hybridperformance in indica and japonica rice. *Theor. Appl. Genet.,* **93** : 1218–1224.

Zhang, W., Ni zhang, B., Xu, Y. and Guo, S., 1998, Development of transgenic insect protected cotton plants. *Proc. of World Cotton Res. Conf. -2.*

Zhang, X. Q., Wang, X. D., Jiang, P. D., Hua, S. J., Zhang, H. P. and Dutt, Y., 2007, Relationship between molecular marker heterozygosity and hybrid performance in intra- and inter specific hybrids of cotton. *J. Plant Breed.,* **126 :** 385-391.

Zhao, M. F., X. H. Li, J. B. Yang, C. J. Xu, R. Y. Hu, D. J. Liu, and Q. F. Zhang, 1999, Relationship between molecular marker heterozygosity and hybrid performance in intra – and inter-subspecific cross of rice. *J. Plant Breed.,* **118** : 139-144.

Zhou, G. Y., Weng, J., Zeng, Y., Huang, J., Qian, S. and Liu, G., 1983, Introduction of exogenous DNA into cotton embryos. *Meth. Enzymol.,* **101** : 433-481.

Appendix 1. *Per se* performance of line x tester inter specific crosses (YHB) for different quantitative characters

Sl. No.	Crosses	Seed cotton yield (kg/ha)			Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympodia at 50% height (cm)	Inter branch distance (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	2.5% SL (mm)	UR %	Micronaire value (µg/inch)	Maturity ratio (%)	Tenacity (g/t)	Elongation %
		Value	Rank	BMC	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	**DH 18-31 x DB 533**	3128.72	1	**BMC**	263.84	2.00	28.84	24.20	4.60	6.33	64.92	32.83	12.19	27.66	4.73	37.30	45.20	3.11	0.61	24.83	6.57
2	**DH 13-7 x DB 533**	3047.62	2	**BMC**	257.67	1.84	27.34	40.25	3.54	7.59	71.33	31.83	12.17	30.73	5.44	31.90	41.70	3.26	0.62	23.57	6.57
3	**ZCH 8 x DB 533**	2868.23	3	**BMC**	275.17	1.84	28.50	30.67	4.08	6.67	66.67	35.50	10.01	31.30	4.54	35.43	44.43	3.44	0.65	23.91	6.73
4	DH46-1 x DB 533	2808.03	4		241.83	2.50	28.17	35.00	3.95	5.17	58.50	30.17	11.95	22.87	3.60	36.17	43.67	2.88	0.59	25.80	6.73
5	DH 23-4 x DB 534	2753.58	5		255.50	2.00	31.50	31.17	4.05	6.75	68.08	30.00	12.50	26.40	4.50	35.23	46.80	3.28	0.63	25.80	6.70
6	DH 98-27 x DB 532	2709.09	6		227.33	1.84	28.67	29.59	3.70	5.00	60.75	31.50	11.44	31.47	5.25	37.17	43.37	3.13	0.62	23.29	6.47
7	DH 37-4 x DB 533	2641.42	7		250.17	1.84	26.17	27.00	3.44	6.00	65.34	36.00	11.23	32.30	5.34	34.47	44.83	3.08	0.61	25.99	6.77
8	DH 11-8 x DB 534	2635.81	8		203.00	2.17	27.17	38.59	3.75	7.34	60.50	28.83	14.40	27.21	5.41	39.23	44.37	2.83	0.59	25.23	6.27
9	**RAHB 87**	2632.14			239.17	2.17	31.50	45.84	3.90	5.75	59.09	29.00	13.72	34.80	7.32	34.10	46.00	3.70	0.66	26.40	7.20
10	DH 49-1 x DB 533	2615.40	9		242.34	2.00	27.84	32.92	4.20	6.09	62.09	28.84	11.33	24.10	3.62	33.63	44.47	2.83	0.59	25.83	6.67
11	ZCH 8 x DB 532	2550.55	10		256.67	2.84	27.50	31.84	3.30	5.42	58.75	30.84	11.54	28.67	4.64	37.17	44.97	2.78	0.58	26.17	6.77
12	DH 98-27 x DB 533	2525.42	11		251.34	2.50	32.50	39.75	3.45	4.83	64.17	28.67	13.00	29.72	5.48	38.53	45.00	3.31	0.65	23.45	6.50
13	DH 35-17 x DB 531	2524.83	12		247.67	2.34	32.33	46.09	2.88	8.00	74.00	31.50	10.82	29.07	4.42	34.80	47.87	3.28	0.64	24.48	6.53
14	**178-24 x DB 533**	2487.64	13	**BMC**	244.83	1.84	32.00	31.59	4.23	5.25	56.42	27.84	12.55	34.46	6.64	38.27	42.50	2.87	0.59	23.88	6.57
15	178-24 x DB 531	2479.11	14		248.33	3.17	26.33	24.34	3.60	6.50	59.34	32.50	11.70	22.67	3.43	34.13	40.80	3.21	0.63	24.03	6.80
16	DH 53-2 x DB 533	2477.78	15		248.50	2.00	31.17	28.42	4.03	5.67	60.50	29.50	12.11	29.85	5.13	35.40	41.33	2.95	0.60	24.22	6.50
17	DH 24-4 x DB 531	2447.45	16		245.84	2.84	26.33	32.25	3.65	5.75	62.25	31.50	12.34	27.54	4.71	34.80	41.90	3.03	0.61	25.82	6.73
18	DH 24-4 x DB 532	2435.81	17		243.67	1.84	27.00	31.09	3.54	6.25	71.25	27.34	11.30	28.16	4.42	35.37	42.43	3.08	0.60	25.00	6.63
19	DH 53-2 x DB 532	2401.52	18		236.33	2.17	24.84	32.42	3.65	5.67	58.25	30.50	11.38	29.98	4.86	34.47	46.20	3.28	0.63	25.73	6.77
20	DH 82-3 x DB 533	2392.87	19		245.00	1.84	28.33	34.34	3.45	5.83	66.34	32.00	12.00	31.34	5.46	35.93	43.53	2.96	0.59	24.97	6.70
21	DH 35-17 x DB 532	2366.17	20		264.84	1.17	32.17	37.00	3.36	6.92	72.17	30.50	11.06	30.95	4.94	36.20	44.80	3.40	0.63	23.60	6.77
22	**MRC 6918 *Bt* check**	2358.05			247.83	2.17	29.17	30.84	3.90	5.84	60.67	30.34	13.33	30.06	5.72	36.10	46.00	2.90	0.60	28.60	6.60
23	DH 35-17 x DB 534	2345.45	21		238.17	1.84	29.00	31.50	3.51	5.25	62.34	31.50	11.45	26.09	4.07	36.83	44.13	2.93	0.61	25.05	6.57
24	DH 82-3 x DB 534	2314.31	22		240.50	1.84	25.50	29.59	3.57	6.67	66.67	30.33	10.80	30.43	4.73	34.63	46.90	3.42	0.63	25.93	6.70
25	DH 45-23 x DB 533	2305.34	23		243.00	3.00	31.17	30.25	3.63	5.50	61.08	29.67	12.37	27.11	4.63	33.93	43.57	2.99	0.61	24.58	6.80

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Sl. No.	Crosses	Seed cotton yield (kg/ha)			Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympodia at 50% height (cm)	Inter branch distance (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	2.5% SL (mm)	UR %	Micronaire value (µg/inch)	Maturity ratio (%)	Tenacity (g/t)	Elongation %
		Value	Rank	BMC	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
26	DH 23-1 x DB 533	2283.36	24		239.50	2.50	32.84	29.84	3.98	8.67	69.42	31.17	11.12	29.59	4.69	35.10	44.90	3.24	0.63	26.39	6.53
27	DH 18-31 x DB 532	2282.92	25		304.33	1.50	30.17	29.34	3.60	8.59	81.92	30.67	14.73	23.47	4.52	37.80	41.97	2.95	0.58	24.11	6.43
28	DH 23-4 x DB 533	2252.76	26		206.84	2.17	22.33	21.59	3.28	6.75	54.42	27.67	13.00	25.43	4.46	38.73	44.10	3.15	0.63	22.68	6.73
29	DH 49-1 x DB 532	2246.47	27		238.67	2.00	31.84	35.84	4.25	6.25	66.34	30.33	11.97	25.96	4.17	35.87	39.27	2.86	0.59	23.67	6.17
30	DH 23-1 x DB 532	2233.65	28		236.83	3.17	30.67	42.25	3.57	8.17	76.09	29.33	12.77	27.53	4.80	39.07	45.60	3.20	0.61	23.10	6.73
31	DH 24-4 x DB 533	2226.85	29		251.84	2.17	27.17	28.25	3.63	6.42	67.25	31.84	11.01	28.74	4.47	33.50	44.60	3.15	0.61	24.18	6.70
32	DH 91-1 x DB 532	2226.37	30		256.50	2.00	27.17	27.75	3.60	5.58	61.42	33.17	12.27	23.76	3.85	37.00	42.90	2.71	0.58	26.81	6.50
33	DH46-1 x DB 532	2219.49	31		224.17	2.17	25.83	27.92	3.30	5.50	62.09	29.00	10.61	23.90	3.32	36.33	43.73	3.80	0.69	22.24	6.47
34	178-24 x DB 532	2191.86	32		262.33	1.84	25.00	29.17	4.01	5.59	68.50	33.34	11.80	25.05	3.95	37.50	44.43	3.23	0.63	24.28	6.67
35	DH 23-4 x DB 531	2168.42	33		282.17	1.84	29.84	29.84	3.08	8.58	78.75	34.50	12.67	28.58	5.08	35.43	45.77	3.16	0.62	24.36	6.83
36	DH 91-1 x DB 533	2162.55	34		246.00	2.00	26.34	29.34	3.30	6.09	61.09	31.00	13.12	26.60	4.74	38.90	41.13	2.97	0.60	23.38	6.27
37	DH 37-4 x DB 532	2161.08	35		263.17	2.84	26.17	39.00	3.60	5.09	56.50	31.67	11.45	24.56	3.72	36.03	44.77	3.29	0.63	24.34	6.70
38	DH 98-27 x DB 531	2156.37	36		226.50	1.84	28.33	29.42	3.35	6.09	63.59	27.67	12.30	30.24	5.32	37.33	41.37	3.29	0.64	23.36	6.40
39	DH46-1 x DB 531	2127.93	37		252.34	2.00	24.67	34.00	3.45	6.42	69.92	30.50	12.83	26.63	4.64	37.23	45.60	2.95	0.61	25.99	6.80
40	DH 13-7 x DB 534	2118.85	38		225.84	2.84	24.33	32.25	3.93	5.34	58.75	30.84	12.83	29.34	5.37	33.93	41.07	3.45	0.64	23.55	6.67
41	DH 35-17 x DB 533	2105.27	39		272.67	2.00	26.50	37.17	3.48	5.92	64.84	30.67	12.84	25.30	4.39	36.47	44.70	3.02	0.61	25.34	6.53
42	DH 91-1 x DB 534	2084.98	40		260.34	1.84	34.33	34.17	3.87	7.34	67.84	31.00	11.66	29.38	4.87	35.23	45.07	3.73	0.67	23.97	6.57
43	DH 11-8 x DB 533	2083.37	41		259.84	1.84	27.17	29.17	3.72	5.75	65.84	30.50	13.96	27.27	5.21	40.20	42.97	2.39	0.56	24.66	6.20
44	**DH 18-31 x DB 534**	2078.47	42	**BMC**	248.17	1.84	26.67	28.67	3.48	5.17	56.67	31.00	14.00	27.16	5.20	39.57	43.30	3.18	0.62	23.97	6.67
45	DH 49-1 x DB 531	2075.24	43		254.50	2.34	28.17	30.59	3.50	5.34	64.42	31.84	12.66	25.81	4.40	35.00	41.87	3.10	0.61	25.09	6.90
46	DH 23-1 x DB 531	2072.97	44		258.50	2.17	28.50	33.42	3.48	5.25	61.59	30.34	13.01	26.08	4.63	37.37	46.57	2.84	0.59	25.38	6.40
47	DH 82-3 x DB 532	2068.47	45		230.50	3.00	27.17	37.42	3.58	6.84	66.75	30.00	12.35	25.68	4.26	36.33	44.37	3.36	0.65	22.95	6.50
48	DH 13-7 x DB 531	2064.96	46		256.17	1.84	31.50	31.92	4.08	5.34	52.09	29.67	13.56	29.25	5.62	37.93	45.57	3.24	0.64	22.12	6.63
49	**DH 98-27 x DB 534**	2054.78	47	**BMC**	253.00	3.34	30.67	32.42	4.10	5.25	61.42	31.50	13.45	31.35	6.16	34.73	40.80	3.06	0.61	23.61	6.83
50	DH 24-4 x DB 534	2032.07	48		239.67	1.84	27.84	29.50	3.92	6.34	70.34	31.84	12.80	24.90	4.26	37.67	42.73	2.74	0.59	25.16	6.73
51	DH 11-8 x DB 531	2031.68	49		228.83	2.17	26.34	32.17	3.33	5.17	54.75	34.67	11.49	29.56	4.82	34.57	45.77	2.87	0.59	26.89	6.67
52	DH 23-4 x DB 532	2017.01	50		252.00	1.67	28.67	35.25	3.78	5.59	71.34	29.67	13.84	29.06	5.69	37.63	44.57	2.53	0.56	25.54	6.50

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Sl. No.	Crosses	Seed cotton yield (kg/ha)			Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympodia at 50% height (cm)	Inter branch distance (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	2.5% SL (mm)	UR %	Micronaire value (µg/inch)	Maturity ratio (%)	Tenacity (g/t)	Elongation %
		Value	Rank	BMC	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
53	DH 37-4 x DB 531	2015.66	51		234.34	1.50	26.00	33.25	3.56	5.17	65.34	33.00	11.71	27.81	4.50	34.90	42.63	3.55	0.65	24.31	6.70
54	DH 45-23 x DB 532	1980.97	52		256.00	3.17	31.50	30.84	3.50	5.50	63.08	30.50	14.09	30.62	6.22	37.90	42.93	3.26	0.63	22.59	6.53
55	DH 45-23 x DB 531	1966.90	53		266.50	2.17	30.34	31.42	4.05	5.42	58.59	31.67	14.77	26.99	5.49	37.23	43.53	3.43	0.64	23.11	6.50
56	DH 13-7 x DB 532	1966.43	54		226.84	2.17	29.17	32.17	3.52	6.08	58.84	29.50	15.55	27.87	6.03	37.73	43.57	3.05	0.60	22.59	6.47
57	DH 53-2 x DB 534	1964.32	55		250.17	2.00	29.84	37.34	3.82	7.00	66.25	29.50	11.66	29.17	4.80	35.93	43.90	3.08	0.60	25.96	6.43
58	DH 45-23 x DB 534	1961.32	56		259.33	1.84	29.17	33.17	4.22	7.08	70.09	33.00	12.83	25.32	4.36	35.23	45.93	2.53	0.57	27.11	6.57
59	DH 11-8 x DB 532	1957.12	57		217.50	1.50	26.67	26.59	3.70	6.25	58.25	31.17	12.22	31.20	5.53	36.50	43.23	3.32	0.63	23.12	6.57
60	DH 18-31 x DB 531	1940.49	58		186.00	2.34	21.67	35.42	4.11	4.59	53.09	28.34	12.50	29.27	5.16	36.90	46.03	3.53	0.65	25.01	6.20
61	ZCH 8 x DB 531	1914.83	59		231.67	3.50	27.84	38.92	3.43	5.75	61.00	30.00	11.50	27.61	4.38	37.97	43.67	2.94	0.60	24.04	6.63
62	DH 91-1 x DB 531	1907.15	60		252.00	2.00	32.00	29.84	3.43	6.67	73.50	34.84	11.56	27.81	4.47	36.30	44.60	3.19	0.63	24.64	6.17
63	DH 82-3 x DB 531	1905.13	61		259.17	2.17	31.50	29.09	3.08	6.25	62.84	33.67	12.94	28.74	5.22	39.70	44.17	3.14	0.61	22.89	6.63
64	**178-24 x DB 534**	1899.90	62	**BMC**	246.00	2.00	29.67	32.17	3.44	6.00	67.17	27.67	12.82	27.92	4.98	37.97	43.67	3.04	0.62	23.10	6.53
65	**DCH 32**	1898.53			212.67	2.33	28.00	38.84	4.40	7.00	63.59	28.34	13.78	27.20	5.15	35.80	42.00	2.90	0.60	23.30	6.30
66	DH 37-4 x DB 534	1871.66	63		263.34	2.84	27.84	37.84	3.78	6.17	63.67	31.00	11.17	30.05	4.79	34.57	43.63	3.42	0.63	24.18	6.67
67	DH 49-1 x DB 534	1833.49	64		235.33	2.34	27.00	34.92	4.20	7.25	68.33	30.33	13.16	26.77	4.80	38.57	44.70	3.35	0.65	22.56	6.53
68	DH 23-21 x DB 533	1757.80	65		235.50	1.84	28.17	37.92	3.45	8.25	68.00	27.84	12.50	27.09	4.61	40.17	42.73	2.86	0.58	23.20	6.37
69	DH46-1 x DB 534	1724.99	66		242.67	2.00	29.67	32.09	4.08	5.84	61.67	30.00	15.39	21.91	4.33	40.53	42.53	2.77	0.59	23.26	6.10
70	DH 31-2 x DB 533	1659.60	67		224.34	2.00	26.34	22.92	3.10	5.83	65.67	29.34	12.95	29.15	5.37	34.77	43.83	2.90	0.60	24.70	6.63
71	DH 29-1 x DB 533	1657.66	68		263.34	1.84	31.33	36.50	3.85	6.50	73.25	29.34	12.00	25.85	4.21	32.93	45.03	2.55	0.57	28.92	6.67
72	DH 23-1 x DB 534	1652.45	69		240.84	1.50	26.83	27.00	3.93	5.84	63.92	31.00	12.78	28.22	5.03	39.70	44.17	2.97	0.60	24.74	6.67
73	**ZCH 8 x DB 534**	1643.88	70	**BMC**	250.17	2.84	32.17	37.25	3.30	6.84	65.09	32.67	10.76	28.89	4.36	34.57	46.67	3.57	0.66	25.77	6.63
74	DH 8-7 x DB 533	1597.88	71		257.67	1.84	24.34	26.67	3.57	6.67	69.00	33.84	10.45	28.27	4.14	33.67	46.57	3.18	0.62	26.13	6.90
75	DH 14-2 x DB 534	1587.76	72		242.34	1.50	27.00	32.34	3.61	6.75	67.92	33.50	12.60	31.38	5.77	33.50	46.80	3.39	0.64	25.53	6.87
76	DH 14-2 x DB 533	1584.00	73		257.17	1.84	31.00	35.17	3.78	6.00	65.92	30.67	13.19	24.07	4.21	37.67	40.07	3.11	0.62	24.04	6.73
77	DH 75- 23 x DB 534	1580.75	74		196.17	1.17	26.34	29.00	4.45	6.17	55.50	28.84	11.50	25.96	4.03	35.80	44.63	3.56	0.65	24.67	6.40
78	DH 31-2 x DB 534	1578.68	75		214.83	2.17	22.67	34.67	4.30	5.42	59.17	33.33	12.08	29.74	5.10	37.63	43.20	2.73	0.58	25.41	6.60
79	DH 75- 23 x DB 533	1561.45	76		233.84	2.17	26.67	27.42	3.33	6.17	60.59	30.50	11.52	26.54	4.19	37.60	40.93	2.87	0.60	23.15	6.43

Contd...

Sl. No.	Crosses	Seed cotton yield (kg/ha)			Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympodia at 50% height (cm)	Inter branch distance (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	2.5% SL (mm)	UR %	Micronaire value (µg/inch)	Maturity ratio (%)	Tenacity (g/t)	Elongation %
		Value	Rank	BMC	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
80	DH 14-2 x DB 531	1560.21	77		245.17	1.67	31.00	38.34	3.40	6.75	67.50	34.00	12.61	30.37	5.49	37.17	43.33	3.31	0.64	25.72	6.30
81	DH 23-21 x DB 531	1544.88	78		262.50	1.84	30.00	31.09	3.88	6.34	69.09	31.17	11.61	28.90	4.74	36.50	44.23	3.23	0.63	23.59	6.70
82	DH 29-1 x DB 534	1509.06	79		247.67	2.17	29.17	40.42	4.23	7.17	67.42	30.84	13.83	26.12	4.90	39.53	44.77	3.24	0.63	23.18	6.40
83	DH 53-2 x DB 531	1496.96	80		241.17	2.17	27.17	30.25	3.98	6.75	68.67	31.83	11.46	25.63	3.96	37.90	44.43	3.11	0.61	25.02	6.23
84	DH 23-21 x DB 534	1493.24	81		231.67	2.00	27.34	37.00	3.18	5.67	55.42	32.17	11.88	31.87	5.59	35.43	44.70	3.83	0.68	23.97	6.90
85	DH 23-21 x DB 532	1483.86	82		263.34	2.00	32.50	45.34	3.07	6.00	66.59	30.33	15.45	29.22	6.37	40.00	46.47	2.54	0.56	24.74	6.53
86	DH 8-7 x DB 534	1473.71	83		254.50	1.50	30.67	42.42	4.08	5.17	59.17	31.00	13.72	29.65	5.78	37.97	42.63	3.13	0.62	23.90	6.13
87	DH 31-2 x DB 532	1472.10	84		281.84	2.84	34.00	33.67	4.03	6.33	68.00	32.00	11.50	26.70	4.19	36.07	43.10	2.71	0.58	25.05	6.37
88	DH 31-2 x DB 531	1454.68	85		302.67	1.84	32.00	36.09	4.05	7.58	71.50	32.00	12.78	27.78	4.92	36.70	44.17	3.02	0.59	23.89	6.80
89	DH 8-7 x DB 532	1453.87	86		239.17	2.17	29.50	34.75	3.61	5.17	65.83	26.84	12.07	25.95	4.25	37.63	43.73	2.98	0.60	24.98	6.43
90	DH 75- 23 x DB 532	1450.42	87		232.17	2.34	29.17	33.84	3.68	7.00	65.42	32.00	10.72	29.92	4.59	34.27	45.07	3.17	0.62	25.29	6.43
91	DH 29-1 x DB 532	1429.57	88		223.34	1.84	26.67	31.34	3.70	7.75	60.08	29.34	12.45	20.11	3.17	38.07	44.63	3.04	0.60	23.03	6.70
92	DH 75- 23 x DB 531	1291.15	89		238.83	2.84	25.50	29.84	4.00	6.67	62.25	28.84	11.45	32.36	5.47	34.23	43.23	3.86	0.67	24.40	6.40
93	DH 8-7 x DB 531	1268.39	90		261.67	2.84	29.83	34.17	4.10	6.50	68.33	33.50	13.34	29.94	5.69	34.83	43.30	3.15	0.62	23.96	6.80
94	DH 14-2 x DB 532	1226.05	91		260.84	1.50	27.34	28.50	3.65	7.09	72.25	33.33	11.07	26.02	3.92	36.77	45.20	3.15	0.63	23.92	6.83
95	DH 29-1 x DB 531	1204.95	92		255.67	1.84	28.50	27.67	3.56	5.34	59.83	30.34	12.00	24.64	3.93	37.10	43.87	2.75	0.57	25.42	6.53
	Max	**3128.72**			**304.33**	**3.50**	**34.33**	**46.09**	**4.60**	**8.67**	**81.92**	**36.00**	**15.55**	**34.80**	**7.32**	**40.53**	**47.87**	**3.86**	**0.69**	**28.92**	**7.20**
	Min	**1204.95**			**186.00**	**1.17**	**21.67**	**21.59**	**2.88**	**4.59**	**52.09**	**26.84**	**10.01**	**20.11**	**3.17**	**31.90**	**39.27**	**2.39**	**0.56**	**22.12**	**6.10**
	CV %	**11.03**			**11.64**	**16.44**	**12.14**	**8.32**	**11.84**	**15.27**	**12.87**	**9.17**	**9.11**	**9.53**	**12.36**						
	S.E m	**159.37**			**20.26**	**0.25**	**2.45**	**1.93**	**0.45**	**0.67**	**5.86**	**2.84**	**0.62**	**1.30**	**0.42**						
	CD@ 5%	**447.51**			**57.10**	**0.69**	**6.93**	**5.42**	**0.89**	**1.89**	**16.52**	**5.63**	**1.74**	**3.65**	**1.18**						
	C.D. 1%	**592.58**			**75.84**	**0.92**	**9.21**	**7.18**	**1.18**	**2.50**	**21.95**	**7.47**	**2.31**	**4.83**	**1.57**						
	Mean of lxt crosses	**2036.47**			**246.61**	**2.12**	**28.47**	**32.65**	**3.70**	**6.23**	**64.55**	**30.97**	**12.34**	**27.82**	**4.78**	**36.52**	**43.96**	**3.11**	**0.61**	**24.49**	**6.58**
	Mean of bench mark crosses	**2335.88**			**254.06**	**2.27**	**30.13**	**32.09**	**3.83**	**5.79**	**62.81**	**30.96**	**12.35**	**29.81**	**5.26**	**37.05**	**43.95**	**3.20**	**0.63**	**24.07**	**6.63**

BMC: Bench Mark Crosses

Appendix 2. *Per se* performance of inter specific hybrids (Best HB) involved in heterotic box for different quantitative characters

Sl. No.	Hybrids	Seed cotton yield (kg/ha)			Plant height (cm)	No. of mono podia	No. of sym podia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympo dia at 50% height (cm)	Inter branch distance (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	2.5% SL (mm)	UR %	Micronaire value (µg/inch)	Tenacity (g/tex)	Elongation %
		Value	Rank	BMC	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
1	ZCH 8 x DB 533	2277.81	**1**	**BMC**	227.00	2.00	29.33	30.00	4.70	4.50	53.33	28.33	11.00	34.64	3.81	35.60	44.00	3.20	26.50	6.40
2	DH 98-27 x DB 534	2239.26	2	**BMC**	236.00	1.67	28.00	21.67	5.10	6.50	66.83	29.33	13.00	36.12	4.70	35.40	47.00	3.00	27.30	6.30
3	177-24 x DB 531	2223.63	3		237.67	2.67	30.33	28.00	3.50	6.67	72.17	28.67	12.00	29.19	3.50	40.40	44.00	2.60	24.00	5.60
4	DH 18-31 x DB 533	2216.33	4	**BMC**	204.00	0.67	31.00	31.67	3.60	4.67	52.00	27.67	12.00	38.11	4.57	33.90	45.00	3.10	25.40	6.20
5	DH 84-7 x DB 533	2211.12	**5**		199.67	1.67	31.00	39.00	5.20	6.00	64.33	25.33	12.00	32.92	3.95	38.00	45.00	2.90	25.70	5.70
6	ZCH 8 x DB 534	2182.99	6	**BMC**	256.00	2.67	30.33	34.00	3.70	7.17	75.33	30.33	13.00	34.23	4.45	39.70	43.00	3.00	24.50	5.90
7	DH 10-2 x DB 531	2153.81	7		247.67	1.00	28.67	28.33	5.00	5.67	72.00	31.00	12.00	32.62	3.91	38.80	44.00	3.30	23.80	5.90
8	178-24 x DB 533	2151.73	8	**BMC**	258.67	1.33	34.00	34.00	4.30	6.50	63.67	30.00	12.00	34.54	4.14	36.40	45.00	3.00	24.90	5.90
9	DH 11-10 x DB 534	2136.1	**9**		234.00	3.00	37.33	31.67	4.70	6.17	61.67	29.33	13.00	34.17	4.44	37.30	46.00	3.30	24.20	6.10
10	DH 98-27 x DB 533	2130.89	10	**BMC**	201.33	2.00	27.00	31.00	4.60	4.83	57.50	27.67	13.00	35.29	4.59	35.30	47.00	3.30	25.40	6.30
11	DH 18-31 x DB 534	2101.71	11	**BMC**	239.67	2.33	25.33	32.67	4.90	6.00	68.17	28.33	13.00	31.25	4.06	37.50	45.00	3.20	23.70	5.90
12	DH 25-3 x DB 533	2098.59	12		299.67	2.00	38.33	44.33	3.60	7.33	84.50	31.00	11.00	34.89	3.84	35.40	45.00	3.10	25.50	6.00
13	DH 44-14 x DB 534	2093.38	**13**		232.00	2.33	30.67	32.33	4.70	4.83	66.83	31.67	11.00	35.48	3.90	37.60	45.00	3.00	26.00	6.10
14	178-24 x DB 534	2092.34	14	**BMC**	243.00	2.67	31.00	35.33	4.10	5.50	70.33	32.33	13.00	36.39	4.73	36.20	46.00	3.20	26.30	6.20
15	**RAHB87**	2087.13			210.67	2.00	31.33	33.00	4.60	4.33	50.00	27.67	11.00	39.74	4.37	35.40	46.00	3.50	24.90	6.40
16	DH 91-1 x DB 531	2078.79	15		269.00	1.67	30.33	34.00	3.50	5.17	69.83	25.67	15.00	33.61	5.04	36.60	46.00	2.70	25.10	5.90
17	DH 31-27 x DB 532	2071.5	16		263.00	2.33	28.67	36.00	4.10	6.17	66.33	27.33	12.00	37.30	4.48	38.00	45.00	3.40	23.30	6.00
18	**MRC6918 *Bt* check**	2070.00			199.00	1.00	28.67	32.67	4.40	5.17	60.67	29.33	12.00	32.44	3.89	34.90	46.00	2.60	27.40	5.80
19	DH 11-8 x DB 534	2064.2	**17**		238.33	2.33	28.00	23.67	3.50	6.33	74.17	29.33	12.00	33.88	4.07	38.00	45.00	3.10	23.80	6.00
20	179-20x DB 532	2054.82	18		217.00	2.00	33.00	34.33	4.10	6.83	67.33	28.67	11.00	35.71	3.93	34.60	46.00	3.10	25.70	6.10
21	DH 40-29 x DB 532	2052.74	19		257.67	2.67	39.33	38.00	3.80	5.50	66.83	26.67	12.00	35.10	4.21	34.00	46.00	3.30	25.50	6.30
22	DH 95- 18 x DB 533	2005.85	20		201.33	2.33	24.00	29.67	5.10	4.67	59.00	30.00	14.00	31.93	4.47	40.00	44.00	2.90	23.50	5.90
23	DH 33-27 x DB 531	2000.64	**21**		289.00	1.33	30.00	36.00	4.00	6.50	78.00	30.00	13.00	34.73	4.52	37.30	46.00	3.50	25.50	6.40
24	DH 56-2 x DB 532	1994.39	22		293.67	3.00	31.67	35.33	4.50	5.50	72.50	31.67	12.00	31.88	3.83	36.70	45.00	2.70	25.50	5.90
25	DH 29-32 x DB 531	1990.22	23		263.33	2.67	30.67	22.67	4.80	6.17	68.83	33.00	13.00	33.43	4.35	37.90	44.00	3.30	23.10	5.90
26	DH 31-37 x DB 532	1985.01	24		244.67	1.67	33.00	35.67	3.60	5.50	61.83	26.00	12.00	32.85	3.94	35.30	45.00	3.20	25.90	6.10
27	DH 28-36 x DB 531	1963.13	**25**		252.33	2.33	31.00	33.33	4.60	5.33	72.67	30.00	15.00	34.38	5.16	38.90	43.00	2.90	25.70	6.10
28	DH 102-23 x DB 534	1956.88	26		301.00	1.33	30.67	21.00	4.90	7.00	89.50	37.00	13.00	34.33	4.46	36.60	44.00	2.70	24.90	6.10

Contd...

Sl. No.	Hybrids	Seed cotton yield (kg/ha)			Plant height (cm)	No. of mono podia	No. of sym podia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympo dia at 50% height (cm)	Inter branch distance (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	2.5% SL (mm)	UR %	Micronaire value (µg/inch)	Tenacity (g/tex)	Elongation %
		Value	Rank	BMC	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
29	DH 56-93 x DB 532	1945.41	27		233.33	3.00	31.00	29.00	3.90	6.50	70.17	23.67	14.00	34.78	4.87	36.10	45.00	3.20	25.90	6.40
30	DH 8-7 x DB 532	1940.2	28		254.00	1.33	27.33	26.67	5.20	4.83	63.67	28.00	12.00	31.56	3.79	39.30	44.00	3.10	25.50	5.90
31	DH 11-8 x DB 533	1915.2	**29**		221.33	1.33	32.33	31.33	4.10	5.67	59.67	20.67	13.00	36.25	4.71	35.40	49.00	3.30	25.00	6.00
32	ZCH 8 x DB 532	1886.02	30		229.67	1.67	32.67	27.33	4.30	5.33	78.83	27.67	12.00	33.50	4.02	36.40	46.00	3.20	25.50	6.30
33	DH 53-2 x DB 534	1874.56	31		234.33	2.00	33.00	33.00	5.20	5.33	67.67	27.00	14.00	31.25	4.38	40.20	43.00	2.80	24.00	5.90
34	DH 18-31 x DB 532	1859.97	32		178.00	2.00	23.00	27.00	4.50	4.83	55.50	28.67	12.00	37.46	4.50	34.20	46.00	3.20	25.40	6.20
35	DH 35-17 x DB 533	1859.97	**33**		249.33	1.67	25.00	35.67	4.40	6.00	68.00	30.00	12.00	35.53	4.26	34.30	46.00	3.20	25.20	6.20
36	DH 11-8 x DB 532	1797.45	34		209.67	3.67	29.00	27.00	5.20	5.17	70.67	27.33	13.00	31.07	4.04	36.50	46.00	3.30	25.20	6.40
37	DH 55-2 x DB 531	1795.37	35		223.33	1.33	29.00	35.33	4.20	6.67	70.67	34.67	14.00	36.04	5.05	36.20	46.00	2.60	25.60	6.00
38	DH 66 x DB 534	1793.28	36		233.00	3.00	28.00	32.00	3.90	6.00	68.17	31.00	13.00	30.20	3.93	40.20	45.00	2.80	24.30	5.80
39	DH 57-95 x DB 533	1787.03	**37**		234.67	1.00	33.33	32.00	4.70	7.00	70.33	29.33	11.00	37.66	4.14	35.10	45.00	3.20	25.60	6.40
40	DH 39-84 x DB 531	1781.82	38		231.33	1.67	33.67	27.00	5.20	5.00	57.50	29.33	13.00	27.76	3.61	35.50	44.00	3.40	24.20	6.20
41	DH 21-29 x DB 532	1775.57	39		230.00	2.33	26.67	31.00	4.60	4.33	60.50	34.00	12.00	32.54	3.90	38.10	45.00	3.30	23.20	5.80
42	**DCH32**	1767.23			256.67	1.33	34.67	30.67	5.00	5.17	62.33	30.33	15.00	34.38	5.16	39.60	45.00	3.50	22.70	6.10
43	DH 8-7 x DB 531	1750.56	40		201.00	2.67	28.00	29.33	5.00	4.83	59.00	30.00	12.00	36.78	4.41	32.40	46.00	3.60	23.60	6.30
44	DH 25-22 x DB 533	1718.26	**41**		276.00	3.00	27.33	23.33	4.30	7.33	87.17	32.00	12.00	31.52	3.78	40.30	43.00	2.50	24.30	5.80
45	DH 22-76 x DB 534	1687.00	42		234.00	2.33	29.67	47.33	4.30	7.00	71.17	29.67	11.00	38.25	4.21	35.20	47.00	3.10	26.40	6.70
46	DH 11-8 x DB 531	1673.45	43		235.00	2.33	31.67	31.67	3.50	5.33	61.17	34.67	11.00	33.14	3.65	33.40	48.00	2.80	30.60	6.40
47	DH 43-44 x DB 532	1648.44	44		227.67	4.00	31.67	32.00	3.70	6.33	67.17	30.67	13.00	31.69	4.12	38.10	44.00	2.60	25.50	6.00
48	DH 47-67 x DB 532	1640.11	**45**		229.67	3.67	28.00	29.33	4.40	4.83	58.83	29.33	11.00	34.73	3.82	38.20	44.00	3.00	24.20	5.90
49	DH 53-2 x DB 533	1564.04	46		239.67	3.00	27.00	30.67	3.80	4.83	58.17	32.33	14.00	32.81	4.59	36.90	46.00	2.90	25.50	6.00
50	DH 49-50 x DB 534	1359.81	47		192.33	1.67	23.33	27.00	4.90	5.83	64.33	29.67	13.00	31.88	4.14	39.20	45.00	2.80	25.50	6.10
51	DH 18-19 x DB 533	1333.76	48		253.33	3.33	31.67	35.67	4.60	5.00	60.00	32.00	14.00	29.45	4.12	39.20	43.00	2.80	25.10	5.90
52	DH 11-20 x DB 534	1232.69	**49**		202.67	2.67	30.33	27.33	4.30	6.17	62.00	27.67	12.00	34.31	4.12	38.90	44.00	2.80	25.70	6.00
	Mean of HB crosses	**1921.38**			**237.96**	**2.21**	**30.11**	**31.46**	**4.38**	**5.78**	**67.06**	**29.50**	**12.51**	**33.86**	**4.23**	**36.95**	**45.10**	**3.05**	**25.14**	**6.08**
	Mean of bench mark crosses	**2174.13**			**233.21**	**1.92**	**29.50**	**31.29**	**4.38**	**5.71**	**63.40**	**29.25**	**12.50**	**35.07**	**4.38**	**36.25**	**45.25**	**3.13**	**25.50**	**6.14**
	Mean	**1924.47**			**237.04**	**2.17**	**30.19**	**31.50**	**4.39**	**5.73**	**66.52**	**29.48**	**12.52**	**33.96**	**4.24**	**36.93**	**45.13**	**3.06**	**25.13**	**6.08**
	Max	**2277.81**			**301.00**	**4.00**	**39.33**	**47.33**	**5.20**	**7.33**	**89.50**	**37.00**	**15.00**	**39.74**	**5.16**	**40.40**	**49.00**	**3.60**	**30.60**	**6.70**
	Min	**1232.69**			**178.00**	**0.67**	**23.00**	**21.00**	**3.50**	**4.33**	**50.00**	**20.67**	**11.00**	**27.76**	**3.50**	**32.40**	**43.00**	**2.50**	**22.70**	**5.60**

BMC: Bench Mark Crosses

Appendix 3. *Per se* performance of 53 barbadense lines and 4 hirsutum testers for different quantitative characters

Sl. No.	Parents	Seed cotton yield (kg/ha)	Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympodia at 50% height (cm)	Inter branch distance (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Photosynthetic rate (µmol CO_2 m^{-2} s^{-1})	Stomatal conductance (µmol m^{-2} s^{-1})	Transpiration rate (mmol H_2O m^{-2} s^{-1})	2.5% SL (mm)	UR %	Micronaire value (µg/inch)	Maturity ratio	Tenacity (g/tex)	S/L ratio	Elongation %
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
1	DB 533 x DB 534 F5 IPS 44	893.52	96.50	1.90	19.17	37.50	2.27	3.67	34.33	8.33	6.49	29.58	3.21	21.36	1.05	9.58	33.16	44.47	2.42	0.55	30.37	0.92	6.40
2	DB 533 x DB 534 F5 IPS 62	697.10	100.33	1.33	21.17	39.33	2.03	5.25	39.75	9.00	6.41	27.25	2.03	24.76	0.92	9.56	32.83	46.39	2.70	0.58	30.32	0.92	6.27
3	DB 533 x DB 534 F5 IPS 105	1052.42	97.83	1.50	18.83	34.50	2.20	4.47	35.83	8.17	9.57	31.13	4.43	21.89	0.73	16.66	33.94	45.27	2.90	0.58	29.76	0.88	6.84
4	DB 533 x DB 534 F5 IPS 26	766.91	82.00	0.67	15.83	25.33	2.37	4.08	28.42	7.17	8.53	29.19	3.58	24.45	0.74	9.14	31.94	45.60	2.73	0.57	28.11	0.88	6.44
5	DB 533 x DB 534 F5 IPS 71	783.06	88.50	1.51	18.17	28.33	2.13	4.93	35.92	7.50	9.56	30.85	3.37	18.66	0.59	8.00	31.59	44.87	3.22	0.62	28.56	0.90	6.61
6	DB 533 x DB 534 F5 IPS 30	669.49	89.83	1.17	18.33	29.67	3.23	3.89	33.25	7.83	7.72	29.05	3.24	24.38	0.68	8.62	33.09	44.57	3.02	0.59	28.26	0.85	6.84
7	DB 533 x DB 534 F5 IPS 25	959.68	83.50	1.90	18.33	30.67	2.27	4.08	30.17	6.67	9.55	32.45	4.72	24.12	0.71	9.68	30.54	46.27	3.43	0.63	27.75	0.91	6.77
8	DB 533 x DB 534 F5 IPS 49	1368.15	83.00	1.00	16.17	25.67	2.73	3.67	34.50	8.67	9.50	24.77	3.35	26.80	0.87	9.65	33.69	45.64	3.03	0.59	28.05	0.83	6.49
9	DB 533 x DB 534 F5 IPS 23	710.64	80.33	0.39	14.83	28.00	1.90	4.00	28.83	7.33	8.45	30.63	3.59	22.25	0.84	9.35	34.21	42.69	2.72	0.59	29.36	0.86	6.52
10	DB 533 x DB 534 F5 IPS 36	670.01	82.33	0.73	17.83	29.50	1.93	4.08	29.25	7.83	7.55	27.73	2.86	20.17	0.62	8.26	35.49	44.70	2.86	0.58	28.89	0.81	6.45
11	DB 533 x DB 534 F5 IPS 15	828.91	80.00	0.83	17.50	25.83	2.67	3.83	35.33	8.33	7.39	31.33	3.27	18.04	0.55	8.28	35.53	44.49	2.86	0.57	29.07	0.82	6.29
12	DB 533 x DB 534 F5 IPS 1	858.09	67.67	0.50	13.83	26.83	2.37	3.08	26.08	6.50	9.61	30.94	3.96	22.19	0.71	8.87	34.52	46.14	3.27	0.62	28.02	0.81	6.69
13	DB 533 x DB 534 F5 IPS 33	441.81	77.33	1.28	17.00	31.17	1.67	4.25	30.75	9.00	7.55	27.85	3.32	22.43	0.89	9.59	35.31	44.85	2.78	0.57	29.51	0.84	6.35
14	DB 533 x DB 534 F5 IPS 24	585.08	74.67	0.95	18.17	31.50	2.27	3.91	29.17	8.67	8.59	27.86	2.93	22.73	0.76	8.48	34.78	43.99	2.78	0.57	29.08	0.84	6.40
15	DB 533 x DB 534 F5 IPS 16	1012.82	76.17	0.53	15.33	25.67	2.27	4.08	28.33	6.17	8.83	32.42	4.31	26.69	1.29	9.43	33.61	43.91	3.18	0.61	27.93	0.83	6.64
16	DB 533 x DB 534 F5 IPS 52	1092.54	72.67	0.89	15.67	27.00	2.50	3.50	26.25	6.83	10.06	31.86	3.56	25.84	0.82	8.85	35.24	43.92	3.15	0.59	26.52	0.75	6.41
17	DB 533 x DB 534 F5 IPS 12	764.31	79.50	0.33	15.83	27.83	2.17	4.42	30.08	8.00	9.78	28.62	4.23	23.85	0.72	8.67	34.06	46.04	3.03	0.59	28.26	0.83	6.50
18	DB 534 x DB 533 F5 IPS 22	1250.40	72.67	0.90	16.50	37.33	2.57	4.98	33.50	8.50	9.89	34.00	4.67	25.43	0.77	8.79	32.91	45.85	3.28	0.60	29.07	0.88	6.70
19	DB 533 x DB 534 F5 IPS 14	848.71	80.17	1.06	16.00	28.50	2.20	4.25	35.42	7.67	8.75	26.32	3.44	18.51	0.56	7.92	33.56	45.49	3.23	0.60	29.35	0.87	6.71

Contd....

Sl. No.	Parents	Seed cotton yield (kg/ha)	Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympodia at 50% height (cm)	Inter branch distance (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Photosynthetic rate (µmol $CO_2 m^{-2} s^{-1}$)	Stomatal conductance ((µmol $m^{-2} s^{-1}$)	Transpiration rate (mmol $H_2O m^{-2} s^{-1}$)	2.5% SL (mm)	UR %	Micronaire value (µg/inch)	Maturity ratio	Tenacity (g/tex)	S/L ratio	Elongation %
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
20	DB 533 x DB 534 F5 IPS 34	947.18	65.33	0.37	16.00	24.67	2.40	3.35	25.50	7.33	10.94	28.61	4.16	23.75	0.63	8.09	38.16	42.64	2.72	0.56	28.86	0.76	6.34
21	DB 533 x DB 534 F5 IPS 55	945.62	76.67	0.42	15.83	30.50	2.23	3.75	27.33	7.33	8.95	31.94	3.68	18.00	2.38	8.63	35.59	45.15	3.17	0.60	28.21	0.79	6.51
22	DB 533 x DB 534 F5 IPS 17	1037.31	67.83	0.58	15.00	28.33	2.33	3.42	26.08	8.17	8.44	30.23	4.45	19.63	0.57	8.17	33.66	44.22	2.95	0.58	27.90	0.83	6.57
23	DB 533 x DB 534 F5 IPS 32	606.97	74.17	1.17	13.83	27.83	1.77	3.92	31.50	8.17	7.62	26.20	2.95	23.70	0.74	9.58	35.23	43.21	2.67	0.55	29.11	0.83	6.47
24	DB 533 x DB 534 F5 IPS 38	754.93	87.00	1.28	14.17	30.00	1.73	4.08	31.75	7.83	8.88	28.57	4.11	26.54	0.73	8.93	32.97	45.69	2.49	0.55	29.68	0.90	6.44
25	DB 533 x DB 534 F5 IPS 48	993.55	73.50	1.90	16.67	38.17	2.47	5.08	29.42	8.50	8.47	30.09	4.01	24.91	0.66	9.85	35.13	44.04	3.11	0.60	27.28	0.78	6.52
26	DB 533 x DB 534 F5 IPS 13	881.01	68.83	1.33	19.33	32.17	2.17	3.42	31.50	7.33	8.78	29.33	4.25	27.15	1.00	10.20	32.92	44.56	3.16	0.60	28.78	0.87	6.57
27	DB 533 x DB 534 F5 IPS 6	844.54	70.33	2.50	20.00	29.83	1.97	3.98	25.75	9.33	9.12	28.85	3.75	20.60	0.77	9.34	33.64	44.22	2.85	0.56	28.92	0.86	6.64
28	DB 533 x DB 534 F5 IPS 8	866.42	77.33	1.00	21.00	32.17	2.07	3.28	24.17	9.00	9.00	32.42	4.20	16.49	0.67	9.25	34.34	45.14	2.84	0.59	28.71	0.84	6.37
29	DB 533 x DB 534 F5 IPS 61	1328.03	74.33	1.00	20.50	30.00	2.50	2.83	30.33	8.67	9.00	29.78	3.82	17.06	0.57	8.47	32.12	45.61	3.60	0.62	28.39	0.88	6.88
30	DB 533 x DB 534 F5 IPS 27	1157.66	68.83	1.50	20.00	34.83	2.47	3.00	21.67	9.83	9.00	28.72	3.63	19.00	0.68	8.72	34.82	45.48	3.41	0.58	30.42	0.87	6.24
31	**Suvin**	1421.81	83.00	0.83	19.00	31.17	2.57	3.08	29.25	8.33	9.00	31.94	4.22	25.88	0.90	10.06	33.58	45.41	3.77	0.64	29.02	0.86	6.54
32	DB 533 x DB 534 F5 IPS 96	1296.77	71.33	1.00	16.67	22.50	2.57	2.92	24.33	8.83	7.00	32.14	3.32	14.04	0.54	8.38	31.52	46.78	3.75	0.63	30.32	0.96	6.74
33	DB 533 x DB 534 F5 IPS 88	1566.65	90.17	1.33	20.00	35.33	2.50	3.17	33.58	8.50	8.00	30.50	3.51	17.02	0.52	7.77	33.15	46.38	3.52	0.62	31.67	0.96	6.68
34	DB 533 x DB 534 F5 IPS 4	1336.37	86.33	1.17	21.67	31.50	2.13	3.00	32.08	7.33	7.00	29.22	2.89	14.60	0.56	8.26	28.78	47.48	3.40	0.60	29.02	1.01	6.51
35	DB 533 x DB 534 F5 IPS 68	976.88	88.83	1.00	20.83	29.50	2.53	2.67	24.00	8.33	9.00	26.67	3.27	18.29	1.15	11.15	37.35	44.64	3.01	0.58	30.45	0.82	6.38
36	DB 533 x DB 534 F5 IPS 11	1791.72	74.33	1.33	15.33	30.00	2.50	3.08	22.42	8.50	9.00	30.05	3.87	19.64	0.64	9.13	31.98	46.91	3.65	0.62	28.78	0.90	6.91
37	DB 533 x DB 534 F5 IPS 20	1290.52	87.67	1.00	21.83	25.83	2.73	2.67	26.42	9.00	10.00	27.04	3.71	21.10	0.69	8.17	34.18	45.84	3.40	0.60	29.85	0.87	6.64
38	DB 533 x DB 534 F5 IPS 112	1266.03	90.83	1.00	20.33	26.83	2.50	3.17	29.75	9.17	10.00	26.47	3.60	16.95	0.94	11.72	38.08	43.88	3.74	0.63	29.51	0.77	6.64
39	DB 533 x DB 534 F5 IPS 35	1184.75	89.50	0.83	20.50	24.33	2.67	3.17	27.83	8.83	9.00	28.99	3.67	21.99	0.92	10.25	33.28	46.01	3.94	0.64	28.86	0.87	6.84
40	DB 533 x DB 534 F5 IPS 2	1247.80	86.83	0.67	19.50	25.50	2.85	3.08	30.50	9.00	8.00	30.14	3.45	20.69	0.79	11.45	35.85	44.38	3.18	0.58	27.08	0.76	6.18
41	DB 533 x DB 534 F5 IPS 79	1559.35	80.33	1.17	20.67	28.17	2.63	3.00	27.08	8.50	8.00	33.61	4.05	14.52	0.70	8.56	32.42	46.14	3.87	0.64	30.64	0.95	6.91

Sl. No.	Parents	Seed cotton yield (kg/ha)	Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	Length of sympodia at 50% height (cm)	Inter branch distance (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Photosynthetic rate (µmol $CO_2 m^{-2} s^{-1}$)	Stomatal conductance (µmol $m^{-2} s^{-1}$)	Transpiration rate (mmol $H_2O m^{-2} s^{-1}$)	2.5% SL (mm)	UR %	Micronaire value (µg/inch)	Maturity ratio	Tenacity (g/tex)	S/L ratio	Elongation %
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
42	DB 533 x DB 534 F5 IPS 10	1454.11	94.50	1.83	21.17	31.33	2.33	3.17	31.33	8.83	9.00	34.64	4.77	20.16	2.03	13.62	33.08	45.11	4.07	0.65	30.75	0.93	6.74
43	DB 533 x DB 534 F5 IPS 57	1564.56	90.00	1.33	19.17	26.67	2.87	2.92	29.50	8.00	8.00	35.23	4.35	21.73	0.70	9.12	32.65	45.44	4.03	0.64	30.80	0.94	6.94
44	DB 533 x DB 534 F 3 IPS 19	1383.78	71.83	0.17	18.17	28.33	2.80	3.00	25.00	7.17	9.00	33.63	4.56	12.59	0.42	7.23	32.75	47.54	4.39	0.70	29.98	0.92	6.91
45	DB 533 x DB 534 F5 IPS 101	1410.35	78.33	1.50	18.33	30.83	2.87	2.58	22.83	7.83	12.00	30.56	5.28	19.77	0.57	8.93	31.48	46.01	4.47	0.69	29.24	0.93	6.94
46	DB 533 x DB 534 F5 IPS 65	1541.12	83.83	1.17	20.00	31.50	2.80	2.67	24.50	8.00	9.00	34.76	4.79	22.29	0.85	10.51	33.08	46.74	4.02	0.65	30.39	0.92	6.64
47	DB 533 x DB 534 F5 IPS 39	1727.64	92.17	0.83	19.17	29.67	2.57	2.92	28.00	8.00	9.00	33.53	4.54	15.66	0.63	8.40	33.25	46.44	4.12	0.65	29.35	0.88	6.51
48	DB 533 x DB 534 F5 IPS 37	1728.68	89.83	1.00	24.83	33.17	2.93	3.08	28.58	7.50	10.00	30.97	4.49	20.60	0.74	10.14	35.75	45.78	3.72	0.63	29.17	0.82	6.74
49	DB 533 x DB 534 F5 IPS 109	1934.47	87.83	0.83	19.83	31.67	2.42	3.25	29.33	8.50	9.00	32.65	4.36	11.96	0.45	7.70	33.32	45.41	3.92	0.64	30.05	0.90	6.74
50	DB 533 x DB 534 F5 IPS 80	1994.39	79.83	1.33	21.33	34.17	2.30	3.42	28.58	9.00	10.00	29.94	4.27	13.08	0.42	8.34	37.42	45.98	3.46	0.59	30.23	0.81	6.71
51	DB 533 x DB 534 F5 IPS 132	2175.70	87.50	1.67	19.83	29.67	3.17	2.92	32.08	8.00	11.00	31.09	4.96	9.52	0.30	7.13	35.58	46.64	3.72	0.64	28.63	0.80	6.41
52	DB 533 x DB 534 F5 IPS 18	2151.21	91.83	2.17	21.50	27.67	2.93	3.00	30.83	8.83	10.00	35.13	5.41	19.10	0.61	9.51	32.12	45.78	4.14	0.65	29.15	0.91	6.88
53	DB 533 x DB 534 F5 IPS 21	1855.80	96.17	1.17	22.50	32.33	2.87	2.92	26.33	9.00	10.00	29.24	4.13	23.62	0.79	10.06	37.42	44.84	3.38	0.58	29.05	0.78	6.28
	Mean	**1178.82**	**81.92**	**1.11**	**18.47**	**29.93**	**2.43**	**3.54**	**29.33**	**8.16**	**8.90**	**30.32**	**3.90**	**20.49**	**0.77**	**9.28**	**33.90**	**45.30**	**3.32**	**0.61**	**29.14**	**0.86**	**6.59**
	Max	**2175.70**	**100.33**	**2.50**	**24.83**	**39.33**	**3.23**	**5.25**	**39.75**	**9.83**	**12.00**	**35.23**	**5.41**	**27.15**	**2.38**	**16.66**	**38.16**	**47.54**	**4.47**	**0.70**	**31.67**	**1.01**	**6.94**
	Min	**441.81**	**65.33**	**0.17**	**13.83**	**22.50**	**1.67**	**2.58**	**21.67**	**6.17**	**6.41**	**24.77**	**2.03**	**9.52**	**0.30**	**7.13**	**28.78**	**42.64**	**2.42**	**0.55**	**26.52**	**0.75**	**6.18**
	Females																						
1	DH 98-27	2503.93	94.00	1.42	20.67	34.67	4.30	3.12	28.50	8.67	9.72	35.20	6.14	23.64	0.96	10.09	29.12	49.11	4.37	0.69	22.90	0.79	5.81
2	ZCH8	2368.99	97.33	1.90	19.83	28.17	3.95	3.50	35.08	8.67	10.44	37.84	6.18	22.35	0.81	10.68	28.65	48.11	4.45	0.69	21.70	0.76	5.88
3	178-24	1870.91	93.50	1.00	18.33	24.50	4.45	3.08	30.17	9.17	11.67	34.25	6.40	29.62	1.22	11.77	32.52	44.31	4.19	0.68	22.72	0.70	5.71
4	DH18-31	2074.10	100.67	0.50	22.83	25.67	4.45	3.89	38.92	9.17	9.83	39.14	6.56	21.20	0.78	10.55	27.85	47.88	4.87	0.72	20.01	0.72	5.41
	Mean	**2204.48**	**96.38**	**1.20**	**20.42**	**28.25**	**4.29**	**3.40**	**33.17**	**8.92**	**10.42**	**36.61**	**6.32**	**24.20**	**0.94**	**10.77**	**29.53**	**47.35**	**4.47**	**0.69**	**21.83**	**0.74**	**5.70**
	Max	**2503.93**	**100.67**	**1.90**	**22.83**	**34.67**	**4.45**	**3.89**	**38.92**	**9.17**	**11.67**	**39.14**	**6.56**	**29.62**	**1.22**	**11.77**	**32.52**	**49.11**	**4.87**	**0.72**	**22.90**	**0.79**	**5.88**
	Min	**1870.91**	**93.50**	**0.50**	**18.33**	**24.50**	**3.95**	**3.08**	**28.50**	**8.67**	**9.72**	**34.25**	**6.14**	**21.20**	**0.78**	**10.09**	**27.85**	**44.31**	**4.19**	**0.68**	**20.01**	**0.70**	**5.41**

Appendix 4. *Per se* performance of derived F_1 crosses for different quantitative characters

Sl.No	Crosses	Seed cotton yield (kg/ha)	Plant height (cm)	No. of monopodia	No. of sympodia	No. of bolls	Mean boll weight (g)	Reproductive points on sympodia	sympodia at 50% Length of height (cm)	Inter branch distant (cm)	Seed index (g)	Ginning outturn (%)	Lint index (g)	Photosynthetic rate (µmol CO_2 m^{-2} s^{-1})	Stomatal conductance ((µmol m^{-2} s^{-1})	Transpiration rate (mmol H_2O m^{-2} s^{-1})	2.5% SL (mm)	UR %	Micronaire value (µg/inch)	Maturity ratio	Tenacity (g/t)	Elongation %
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
1	[[DH 98-27 x (DB 533 x DB 534 F4 IPS 44)]	2029.82	115.17	2.05	21.00	41.17	2.50	4.17	54.92	7.50	8.34	30.67	3.13	13.01	0.30	2.26	33.08	45.88	2.74	0.58	28.08	6.58
2	[DH 98-27 x (DB 533 x DB 534 F4 IPS 62)]	1819.33	141.33	1.83	22.50	55.67	3.35	4.42	53.33	6.33	10.28	31.83	5.15	30.74	0.93	4.75	35.73	44.88	3.00	0.61	27.15	6.43
3	[DH 98-27 x (DB 533 x DB 534 F4 IPS 105)]	2606.56	127.67	1.97	19.50	47.17	2.95	4.50	49.58	6.17	8.83	29.11	3.37	27.38	0.70	5.85	31.13	45.67	3.61	0.64	22.91	5.88
4	[DH 98-27 x (DB 533 x DB 534 F4 IPS 26)]	1878.73	118.33	2.33	20.83	39.17	2.65	4.42	46.67	7.83	10.34	34.25	5.03	30.55	0.69	7.32	32.33	43.63	3.23	0.62	24.76	6.13
5	[DH 98-27 x (DB 533 x DB 534 F4 IPS 71)]	1894.36	126.00	2.33	22.50	48.83	3.15	3.42	44.58	7.17	10.45	27.54	5.26	25.15	0.47	6.09	31.88	45.55	3.50	0.65	23.25	6.15
6	[DH 98-27 x (DB 533 x DB 534 F4 IPS 30)]	1785.99	130.00	1.83	18.00	40.83	3.05	4.92	43.58	7.50	10.06	30.16	3.83	25.33	0.62	5.31	31.42	46.12	3.21	0.63	24.94	6.20
7	[DH 98-27 x (DB 533 x DB 534 F4 IPS 25)]	2152.77	133.67	1.57	21.50	38.83	3.10	5.28	43.00	8.17	12.83	30.91	5.84	23.18	0.62	4.69	33.91	45.22	2.95	0.60	28.71	6.29
8	[DH 98-27 x (DB 533 x DB 534 F4 IPS 49)]	2884.26	119.50	1.33	22.83	49.17	3.45	4.11	42.58	6.50	10.22	27.59	5.44	30.37	0.80	6.27	34.86	44.45	3.16	0.61	28.29	6.46
9	[DH 98-27 x (DB 533 x DB 534 F4 IPS 23)]	1855.28	115.33	1.15	23.67	55.50	3.85	4.92	42.42	7.17	10.78	30.97	6.01	24.17	0.47	5.56	33.66	45.12	3.22	0.60	29.60	6.67
10	[DH 98-27 x (DB 533 x DB 534 F4 IPS 36)]	1812.04	122.67	2.00	21.50	66.17	3.30	3.00	41.50	7.00	10.50	29.11	3.67	8.08	0.09	4.04	33.34	44.45	2.94	0.58	28.70	6.62
11	[DH 98-27 x (DB 533 x DB 534 F4 IPS 15)]	1902.69	119.67	1.67	24.00	46.00	2.65	4.67	41.50	7.33	10.95	27.80	4.86	14.67	0.29	4.03	33.44	45.76	2.76	0.57	29.04	6.45
12	[DH 98-27 x (DB 533 x DB 534 F4 IPS 1)]	1980.32	134.17	1.33	22.50	40.33	3.30	4.00	41.06	7.00	9.97	27.32	3.47	20.84	0.44	10.04	35.06	44.01	2.86	0.58	28.16	6.47
13	[DH 98-27 x (DB 533 x DB 534 F4 IPS 33)]	1642.19	124.83	1.73	22.00	39.50	4.20	3.58	40.67	7.33	10.88	31.44	4.91	32.01	1.06	7.35	34.63	44.97	3.02	0.58	28.74	6.70
14	[DH 98-27 x (DB 533 x DB 534 F4 IPS 24)]	1703.15	143.83	1.72	20.17	48.17	2.50	3.64	40.33	6.33	9.06	32.18	4.35	31.40	0.83	4.58	33.66	45.22	2.76	0.57	29.48	6.52
15	[DH 98-27 x (DB 533 x DB 534 F4 IPS 16)]	2384.62	102.17	1.94	24.83	50.67	2.75	4.67	39.83	7.00	10.70	30.42	5.20	32.53	1.03	8.40	36.79	43.16	3.04	0.58	28.74	6.56
16	[DH 98-27 x (DB 533 x DB 534 F4 IPS 52)]	2636.78	137.50	2.00	24.50	43.67	3.05	4.50	39.75	7.00	12.89	33.36	6.17	31.27	0.82	5.79	34.89	44.31	3.47	0.61	27.99	6.47
17	[DH 98-27 x (DB 533 x DB 534 F4 IPS 12)]	1861.53	118.00	1.83	23.50	49.00	2.85	4.83	39.58	6.50	10.45	31.78	5.16	26.87	0.67	5.15	33.34	44.57	3.17	0.60	28.46	6.69
18	[DH 98-27 x (DB 534 x DB 533 F4 IPS 22)]	2800.90	102.67	2.22	23.67	52.67	2.55	3.67	39.33	7.67	9.95	30.20	4.69	6.40	0.25	5.57	36.66	43.97	3.12	0.61	26.42	6.42
19	[DH 98-27 x (DB 533 x DB 534 F4 IPS 14)]	1955.83	131.17	1.47	24.50	58.50	3.60	3.83	39.25	6.50	10.52	29.42	3.98	31.78	1.00	7.03	34.39	45.15	3.12	0.60	27.88	6.60
20	[DH 98-27 x (DB 533 x DB 534 F4 IPS 34)]	2074.62	109.83	1.42	21.50	53.50	3.35	4.67	39.17	6.67	8.45	28.45	4.83	25.72	0.64	5.80	35.22	44.52	3.28	0.62	27.90	6.72
21	[DH 98-27 x (DB 533 x DB 534 F4 IPS 55)]	2074.10	103.17	1.42	19.33	34.83	3.25	3.92	39.08	5.67	10.28	33.12	5.92	29.82	0.66	4.94	36.33	42.79	3.01	0.59	27.35	6.27

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		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
22	[DH 98-27 x (DB 533 x DB 534 F4 IPS 17)]	2433.59	123.83	1.56	20.00	35.00	2.85	3.75	38.67	7.50	9.47	26.13	3.97	32.13	0.81	6.36	36.01	42.92	2.80	0.56	28.66	6.35
23	[DH 98-27 x (DB 533 x DB 534 F4 IPS 32)]	1761.50	108.33	1.90	24.17	49.00	3.45	4.08	37.67	7.00	17.50	31.48	7.40	15.27	0.18	3.65	33.94	45.64	3.15	0.60	28.79	6.62
24	[DH 98-27 x (DB 533 x DB 534 F4 IPS 38)]	1859.97	137.00	1.33	22.17	53.00	2.95	4.08	37.58	6.50	8.20	31.89	3.56	17.37	0.32	5.54	35.21	43.95	2.62	0.56	29.06	6.42
25	[DH 98-27 x (DB 533 x DB 534 F4 IPS 48)]	2380.97	112.17	1.83	18.33	52.33	3.55	3.94	37.25	7.33	10.73	31.45	6.04	27.93	0.82	7.13	36.24	43.64	2.83	0.58	27.53	6.32
26	[DH 98-27 x (DB 533 x DB 534 F4 IPS 13)]	2009.50	117.67	1.55	20.17	53.00	2.55	4.17	37.17	6.50	7.00	29.18	3.81	30.97	1.02	7.33	34.48	43.64	2.90	0.59	28.09	6.40
27	[DH 98-27 x (DB 533 x DB 534 F4 IPS 6)]	1923.53	127.50	1.98	19.50	51.33	3.05	4.33	37.00	6.33	10.94	32.86	4.89	31.55	0.86	6.06	33.96	44.24	3.11	0.60	27.60	6.64
28	[DH 98-27 x (DB 533 x DB 534 F4 IPS 8)]	1999.08	135.83	2.00	23.67	57.50	3.85	2.85	36.83	7.67	9.50	28.17	5.34	22.98	0.61	4.73	33.69	43.77	2.79	0.58	28.42	6.59
29	[ZCH 8 x (DB 533 x DB 534 F4 IPS 44)]	1772.44	116.33	1.72	20.50	57.84	3.15	2.75	36.75	7.33	9.50	22.65	3.07	22.53	0.70	5.97	31.83	45.82	3.43	0.63	27.09	6.54
30	[ZCH 8 x (DB 533 x DB 534 F4 IPS 62)]	1575.50	104.83	2.00	22.67	44.17	2.65	3.17	36.75	7.17	9.83	29.82	4.14	17.80	0.43	6.08	33.42	45.07	2.80	0.57	28.68	6.60
31	[ZCH 8 x (DB 533 x DB 534 F4 IPS 105)]	2015.23	109.17	1.50	22.50	49.33	3.05	5.08	36.75	5.83	10.62	24.33	3.46	15.47	0.36	4.31	32.14	45.44	3.11	0.61	29.36	6.70
32	[ZCH 8 x (DB 533 x DB 534 F4 IPS 26)]	1645.32	103.33	1.11	22.50	43.67	2.95	3.58	36.67	9.17	10.39	32.63	5.87	28.09	0.65	6.39	32.09	45.05	2.96	0.60	28.71	6.54
33	[ZCH 8 x (DB 533 x DB 534 F4 IPS 71)]	1674.49	114.00	2.17	20.33	47.50	3.55	3.25	36.67	6.33	7.79	29.81	3.33	5.48	0.11	4.10	34.19	44.84	2.96	0.59	28.59	6.81
34	[ZCH 8 x (DB 533 x DB 534 F4 IPS 30)]	1514.03	120.50	2.17	22.17	45.00	3.15	4.75	36.58	6.33	8.72	23.15	2.71	7.64	0.10	3.98	33.09	45.66	2.50	0.55	31.22	6.37
35	[ZCH 8 x (DB 533 x DB 534 F4 IPS 25)]	1822.46	99.17	1.70	17.50	46.83	2.95	4.08	36.50	6.33	11.50	29.81	6.36	28.64	0.59	6.47	32.84	45.82	2.73	0.57	30.23	6.44
36	[ZCH 8 x (DB 533 x DB 534 F4 IPS 49)]	2250.72	123.17	2.17	24.00	53.00	2.95	2.58	35.83	8.50	10.72	27.14	4.33	25.64	0.55	5.90	33.68	45.48	2.64	0.57	28.22	6.47
37	[ZCH 8 x (DB 533 x DB 534 F4 IPS 23)]	1622.92	110.67	1.68	20.67	43.50	2.55	3.83	35.67	8.33	9.61	28.02	4.39	25.03	0.84	7.32	33.67	44.67	2.61	0.57	28.66	6.77
38	[ZCH 8 x (DB 533 x DB 534 F4 IPS 36)]	1520.28	119.83	1.67	24.67	46.17	2.95	3.53	35.67	7.17	10.84	27.49	4.69	25.85	0.93	8.64	34.80	44.68	2.69	0.59	27.80	6.68
39	[ZCH 8 x (DB 533 x DB 534 F4 IPS 15)]	1693.25	123.33	1.11	22.00	38.17	2.70	4.08	35.42	6.17	11.00	29.53	5.58	24.30	0.43	5.88	34.40	44.47	2.81	0.59	26.33	6.35
40	[ZCH 8 x (DB 533 x DB 534 F4 IPS 1)]	1734.41	113.17	1.83	22.33	54.50	2.90	3.67	35.17	5.67	9.52	24.86	3.09	8.48	0.12	4.04	34.55	44.78	2.87	0.59	26.37	6.48
41	[ZCH 8 x (DB 533 x DB 534 F4 IPS 33)]	1388.47	120.83	2.00	23.67	58.17	3.50	3.17	35.17	7.33	8.51	13.81	3.16	3.15	0.24	3.87	34.43	44.28	2.59	0.59	29.06	6.52
42	[ZCH 8 x (DB 533 x DB 534 F4 IPS 24)]	1474.43	124.00	1.73	19.67	50.83	3.25	3.83	35.08	6.33	10.06	29.94	3.33	23.42	0.36	6.47	33.05	43.00	2.72	0.59	23.74	6.22
43	[ZCH 8 x (DB 533 x DB 534 F4 IPS 16)]	1985.01	106.67	2.05	20.50	41.00	3.00	3.83	35.00	7.17	9.33	31.78	5.29	20.61	0.36	4.85	33.20	45.03	2.60	0.58	28.65	6.72
44	[ZCH 8 x (DB 533 x DB 534 F4 IPS 52)]	2040.76	116.33	2.33	20.00	45.00	3.80	4.58	34.92	6.83	9.02	28.81	3.50	34.25	1.17	8.33	32.77	44.43	2.61	0.58	27.66	6.43
45	[ZCH 8 x (DB 533 x DB 534 F4 IPS 12)]	1630.73	89.67	1.61	19.67	41.00	3.10	2.75	34.92	7.50	8.32	30.07	4.41	20.47	0.32	5.08	31.42	45.22	3.02	0.58	29.21	6.82
46	[ZCH 8 x (DB 534 x DB 533 F4 IPS 22)]	2112.13	105.33	1.17	18.83	47.33	3.00	2.83	34.92	6.17	9.75	31.28	4.30	24.97	0.82	7.02	35.63	44.33	2.93	0.61	27.19	6.62
47	[ZCH 8 x (DB 533 x DB 534 F4 IPS 14)]	1713.05	114.50	1.83	23.00	34.50	3.00	4.17	34.75	7.67	8.87	30.31	4.32	16.58	0.50	5.99	33.87	45.55	2.75	0.59	28.38	6.53
48	[ZCH 8 x (DB 533 x DB 534 F4 IPS 34)]	1815.69	110.50	2.17	21.67	53.00	2.65	3.92	34.67	5.83	9.95	27.17	3.97	24.10	0.71	7.70	34.17	43.93	2.69	0.59	27.69	6.48
49	[ZCH 8 x (DB 533 x DB 534 F4 IPS 55)]	1806.31	135.17	2.37	22.50	38.00	3.05	4.39	34.50	7.83	9.52	30.29	4.36	12.07	0.25	3.80	34.82	44.77	2.78	0.59	26.60	6.50
50	[ZCH 8 x (DB 533 x DB 534 F4 IPS 17)]	2001.68	128.17	1.74	24.17	49.50	3.70	3.25	34.33	5.33	8.61	29.37	3.39	23.55	0.52	5.81	31.80	46.15	2.66	0.57	28.83	6.73
51	[ZCH 8 x (DB 533 x DB 534 F4 IPS 32)]	1481.72	128.67	1.72	20.00	43.00	2.95	3.44	33.92	7.67	10.73	26.60	3.25	31.73	1.07	6.69	32.30	45.52	2.84	0.59	26.84	6.58
52	[ZCH 8 x (DB 533 x DB 534 F4 IPS 38)]	1625.52	120.33	2.10	21.83	40.17	3.50	2.69	33.89	7.17	10.78	28.06	5.36	30.76	0.70	7.00	34.22	43.45	2.90	0.60	26.94	6.55
53	[ZCH 8 x (DB 533 x DB 534 F4 IPS 48)]	1908.42	99.67	2.00	23.00	55.50	2.95	2.92	33.83	6.00	9.78	28.34	4.06	26.02	0.48	5.63	32.95	45.50	2.88	0.60	27.80	6.62

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		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
54	[ZCH 8 x (DB 533 x DB 534 F4 IPS 13)]	1758.90	116.50	1.50	20.00	46.00	3.10	2.83	33.83	6.83	9.00	27.70	3.54	32.85	1.16	8.14	34.45	45.12	2.64	0.58	28.04	6.67
55	[ZCH 8 x (DB 533 x DB 534 F4 IPS 6)]	1706.28	105.67	1.83	21.00	49.00	3.25	4.00	33.36	6.83	12.55	28.97	4.72	26.13	0.50	6.04	33.80	44.87	2.90	0.59	26.89	6.50
56	[ZCH 8 x (DB 533 x DB 534 F4 IPS 8)]	1750.04	120.17	1.83	19.67	44.67	3.15	3.42	33.33	7.67	8.78	29.80	4.33	22.95	0.74	5.42	34.03	43.97	2.73	0.60	27.81	6.62
57	[178-24 x (DB 533 x DB 534 F4 IPS 44)]	1878.73	107.17	1.35	23.00	43.33	3.05	3.17	33.33	7.00	11.11	35.31	6.31	31.82	0.53	7.00	36.17	44.43	2.92	0.60	26.50	6.53
58	[178-24 x (DB 533 x DB 534 F4 IPS 62)]	1565.08	115.83	1.68	22.50	35.50	2.40	3.25	33.25	7.00	9.52	32.60	3.46	29.17	0.58	7.25	36.40	44.72	3.09	0.62	25.61	6.25
59	[178-24 x (DB 533 x DB 534 F4 IPS 105)]	2026.17	98.17	1.83	18.83	37.17	2.95	4.25	33.17	6.17	10.52	31.39	5.70	21.48	0.48	4.33	34.57	44.42	2.96	0.61	26.81	6.58
60	[178-24 x (DB 533 x DB 534 F4 IPS 26)]	1651.57	112.00	1.67	19.83	38.67	3.65	3.58	33.17	7.00	9.61	31.97	4.67	23.50	0.41	6.10	34.30	45.43	2.97	0.61	27.40	6.47
61	[178-24 x (DB 533 x DB 534 F4 IPS 71)]	1701.59	112.50	2.44	20.00	52.67	2.90	3.17	33.00	8.33	9.89	29.44	4.91	26.09	0.77	8.59	34.28	44.78	2.85	0.59	27.47	6.47
62	[178-24 x (DB 533 x DB 534 F4 IPS 30)]	1486.41	92.67	2.17	18.17	47.67	3.15	4.00	32.92	6.33	10.39	31.88	5.73	24.05	0.59	4.89	34.65	44.65	2.90	0.59	26.45	6.45
63	[178-24 x (DB 533 x DB 534 F4 IPS 25)]	1930.83	112.00	1.35	21.33	38.17	3.05	3.75	32.83	6.67	8.50	33.35	4.89	26.13	0.52	6.17	32.25	45.70	2.63	0.57	29.10	6.73
64	[178-24 x (DB 533 x DB 534 F4 IPS 49)]	2207.48	100.17	2.06	21.00	39.83	2.90	4.11	32.67	8.33	9.82	31.47	4.75	27.95	0.94	8.59	31.97	45.20	2.75	0.58	28.70	6.85
65	[178-24 x (DB 533 x DB 534 F4 IPS 23)]	1565.08	108.83	1.95	23.17	40.33	2.70	3.33	32.58	5.83	9.07	33.16	4.89	21.90	0.34	4.38	35.35	43.38	2.60	0.57	27.76	6.43
66	[178-24 x (DB 533 x DB 534 F4 IPS 36)]	1512.98	89.17	1.33	22.83	40.33	3.10	2.25	32.50	8.00	11.72	30.82	5.28	30.51	0.65	6.14	35.40	43.50	3.04	0.62	25.86	6.55
67	[178-24 x (DB 533 x DB 534 F4 IPS 15)]	1768.27	118.50	1.83	23.00	44.00	2.50	3.75	32.25	7.00	9.52	31.04	4.83	8.12	0.09	3.67	34.00	43.43	2.60	0.58	26.15	6.32
68	[178-24 x (DB 533 x DB 534 F4 IPS 1)]	1828.71	113.17	1.61	22.67	56.33	3.10	3.22	32.17	7.83	8.83	31.14	4.38	23.25	0.65	7.78	34.47	43.95	2.50	0.56	27.38	6.55
69	[178-24 x (DB 533 x DB 534 F4 IPS 33)]	1146.20	92.67	1.67	21.17	46.17	2.90	3.17	32.17	8.50	12.00	29.53	4.74	22.56	0.84	6.18	32.55	45.40	2.49	0.57	28.31	6.58
70	[178-24 x (DB 533 x DB 534 F4 IPS 24)]	1298.85	118.17	2.00	19.67	37.00	2.90	3.83	31.92	6.33	11.33	28.56	4.11	27.02	0.57	6.97	36.28	42.98	2.78	0.59	26.04	6.50
71	[178-24 x (DB 533 x DB 534 F4 IPS 16)]	1983.45	96.83	1.50	17.83	43.17	3.70	3.33	31.83	7.00	9.34	28.58	3.64	8.67	0.10	3.34	34.37	43.45	2.80	0.58	26.11	6.60
72	[178-24 x (DB 533 x DB 534 F4 IPS 52)]	2027.73	106.50	2.09	23.50	43.67	3.25	2.92	31.67	7.50	7.90	30.75	5.70	25.25	0.95	8.16	34.18	44.63	2.72	0.57	26.80	6.77
73	[178-24 x (DB 533 x DB 534 F4 IPS 12)]	1580.71	136.83	1.67	22.00	41.33	2.35	3.15	31.67	8.17	9.94	26.83	4.56	25.74	0.39	4.95	32.90	46.45	2.52	0.57	28.60	6.67
74	[178-24 x (DB 534 x DB 533 F4 IPS 22)]	2099.11	107.00	1.53	20.83	45.33	2.75	3.08	31.58	8.00	8.78	33.50	4.90	21.08	0.88	8.31	33.85	46.53	2.95	0.61	28.88	6.60
75	[178-24 x (DB 533 x DB 534 F4 IPS 14)]	1815.16	107.83	1.33	25.17	37.83	3.45	3.17	31.42	7.67	8.52	31.17	4.48	14.83	0.58	7.56	35.15	44.13	2.82	0.58	26.78	6.73
76	[178-24 x (DB 533 x DB 534 F4 IPS 34)]	1902.69	125.00	1.79	23.67	50.83	3.45	2.92	31.33	6.50	9.56	25.45	3.07	25.02	0.80	7.31	35.12	43.50	2.70	0.58	27.23	6.58
77	[178-24 x (DB 533 x DB 534 F4 IPS 55)]	1899.05	103.50	1.83	19.50	41.33	3.20	3.33	31.33	8.33	10.94	28.80	3.81	20.01	0.36	5.46	33.55	45.12	2.69	0.58	27.46	6.62
78	[178-24 x (DB 533 x DB 534 F4 IPS 17)]	2025.13	132.00	2.22	24.83	47.67	2.80	3.28	31.17	7.83	10.61	29.58	4.67	22.79	0.70	7.58	33.72	44.47	2.84	0.60	26.89	6.53
79	[178-24 x (DB 533 x DB 534 F4 IPS 32)]	1391.07	90.00	1.83	16.83	50.50	3.50	2.17	31.00	7.67	8.85	29.42	3.64	17.66	0.23	2.07	35.62	44.52	2.58	0.57	27.07	6.67
80	[178-24 x (DB 533 x DB 534 F4 IPS 38)]	1568.73	91.83	2.15	19.83	44.67	3.55	3.42	31.00	7.67	11.39	24.98	4.34	24.28	0.91	8.78	32.42	44.83	2.54	0.57	27.14	6.35
81	[178-24 x (DB 533 x DB 534 F4 IPS 48)]	1980.84	99.83	1.50	20.67	36.50	2.80	3.42	31.00	6.50	9.78	29.51	4.92	28.75	0.91	8.77	34.72	42.60	3.00	0.61	26.52	6.68
82	[178-24 x (DB 533 x DB 534 F4 IPS 13)]	1859.97	127.33	1.15	21.83	58.33	2.65	2.67	30.92	9.50	10.96	30.60	5.12	24.72	0.77	8.65	34.38	43.60	3.00	0.59	27.25	6.52
83	[178-24 x (DB 533 x DB 534 F4 IPS 6)]	1814.64	104.00	2.10	16.83	44.00	2.85	4.42	30.92	6.17	8.56	29.73	4.60	22.35	0.78	6.96	32.68	44.52	2.62	0.57	27.96	6.67
84	[178-24 x (DB 533 x DB 534 F4 IPS 8)]	1840.69	100.17	1.75	23.50	53.67	3.45	2.94	30.75	7.83	8.56	28.90	4.20	23.92	0.74	8.15	34.85	43.63	2.72	0.59	28.76	6.65
85	[DH 18-31 x (DB 533 x DB 534 F4 IPS 44)]	2322.62	105.17	2.05	19.50	53.17	2.80	4.16	30.33	7.33	10.78	32.27	5.30	28.93	0.68	6.31	33.80	45.88	2.87	0.60	27.82	6.65

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		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
86	[DH 18-31 x (DB 533 x DB 534 F4 IPS 62)]	2024.61	120.83	1.49	20.67	51.67	2.95	3.58	30.17	6.50	10.55	31.18	6.57	29.45	0.96	6.71	35.47	44.03	2.90	0.60	26.52	6.48
87	[DH 18-31 x (DB 533 x DB 534 F4 IPS 105)]	2024.61	113.17	1.50	21.17	42.00	2.85	3.50	30.17	6.50	10.55	31.18	6.57	29.45	0.96	6.71	35.83	43.58	3.09	0.61	25.74	6.33
88	[DH 18-31 x (DB 533 x DB 534 F4 IPS 26)]	2255.93	110.67	1.33	20.17	41.67	2.70	4.00	30.00	6.67	10.56	31.22	6.18	29.98	0.64	5.87	34.97	42.78	2.97	0.59	26.69	6.53
89	[DH 18-31 x (DB 533 x DB 534 F4 IPS 71)]	2259.58	104.00	2.17	19.50	53.67	2.70	2.84	30.00	7.67	12.43	30.35	4.61	29.35	0.69	6.45	35.02	44.58	2.92	0.60	26.81	6.38
90	[DH 18-31 x (DB 533 x DB 534 F4 IPS 30)]	2003.25	114.50	1.83	21.00	37.83	3.40	3.50	29.83	6.67	11.44	29.45	5.01	19.42	0.53	4.53	36.08	43.77	2.77	0.60	25.65	6.43
91	[DH 18-31 x (DB 533 x DB 534 F4 IPS 25)]	2342.42	104.17	2.33	23.33	52.83	2.85	3.00	29.67	8.00	12.50	30.67	6.47	30.18	0.58	5.69	35.53	44.60	2.96	0.60	25.51	6.42
92	[DH 18-31 x (DB 533 x DB 534 F4 IPS 49)]	2515.91	104.17	1.83	20.00	36.67	2.65	4.67	29.58	6.83	8.55	31.73	4.95	29.90	0.66	6.26	33.42	44.10	2.69	0.57	27.70	6.57
93	[DH 18-31 x (DB 533 x DB 534 F4 IPS 23)]	2111.61	99.67	1.73	17.17	44.00	2.75	3.58	29.50	8.67	11.06	29.27	5.77	27.77	1.04	7.31	34.53	43.25	3.23	0.63	25.62	6.75
94	[DH 18-31 x (DB 533 x DB 534 F4 IPS 36)]	2007.93	105.33	1.83	21.00	50.83	3.10	3.33	29.50	7.50	11.55	32.14	5.26	30.39	0.60	6.90	35.77	43.68	2.67	0.58	26.63	6.48
95	[DH 18-31 x (DB 533 x DB 534 F4 IPS 15)]	2271.56	109.17	1.33	21.67	44.00	3.55	3.17	29.00	7.83	9.74	29.46	4.59	20.69	0.66	4.83	33.47	45.20	2.75	0.59	28.16	6.52
96	[DH 18-31 x (DB 533 x DB 534 F4 IPS 1)]	2297.61	91.67	1.33	18.67	38.00	3.45	2.75	28.75	6.33	9.50	27.90	5.25	25.35	0.51	4.42	33.78	44.10	2.61	0.57	27.83	6.38
97	[DH 18-31 x (DB 533 x DB 534 F4 IPS 33)]	1899.57	91.67	1.33	18.67	38.00	3.45	2.75	28.75	6.83	10.86	29.98	5.06	25.98	0.72	7.49	32.85	44.57	2.74	0.59	27.68	6.65
98	[DH 18-31 x (DB 533 x DB 534 F4 IPS 24)]	1928.22	84.67	2.21	22.83	52.67	3.00	2.58	28.67	6.50	10.12	30.71	4.80	28.73	0.59	6.56	32.08	45.72	2.91	0.61	28.02	6.62
99	[DH 18-31 x (DB 533 x DB 534 F4 IPS 16)]	2424.73	93.33	1.83	20.67	54.33	2.80	3.42	28.67	6.50	9.51	31.34	5.81	25.40	0.51	6.00	33.53	44.45	2.72	0.58	27.04	6.75
100	[DH 18-31 x (DB 533 x DB 534 F4 IPS 52)]	2490.38	93.83	2.05	20.17	39.67	3.25	3.50	28.33	7.00	9.00	31.41	6.11	32.00	0.68	6.92	35.32	43.47	2.77	0.58	27.32	6.58
101	[DH 18-31 x (DB 533 x DB 534 F4 IPS 12)]	2120.47	102.00	1.78	24.33	48.33	3.90	2.03	28.25	5.67	12.39	28.53	4.59	28.52	0.64	6.05	34.35	45.87	2.89	0.61	27.40	6.37
102	[DH 18-31 x (DB 534 x DB 533 F4 IPS 22)]	2502.36	96.50	1.63	21.67	53.00	3.05	3.58	27.83	7.50	10.00	27.83	3.87	28.67	0.63	6.96	34.53	44.87	2.84	0.59	27.36	6.40
103	[DH 18-31 x (DB 533 x DB 534 F4 IPS 14)]	2275.73	106.50	1.17	20.33	47.50	3.30	2.61	27.67	6.67	9.00	33.41	4.57	30.15	0.63	6.63	32.87	45.75	2.68	0.58	28.43	6.70
104	[DH 18-31 x (DB 533 x DB 534 F4 IPS 34)]	2340.33	99.67	1.69	22.67	42.17	2.65	1.92	27.58	7.17	10.50	32.64	5.10	27.18	0.58	5.70	33.95	45.05	2.56	0.58	28.24	6.63
105	[DH 18-31 x (DB 533 x DB 534 F4 IPS 55)]	2326.79	105.00	1.33	19.83	35.67	3.50	2.83	27.00	7.00	10.50	29.88	5.59	30.93	0.61	6.60	33.25	45.02	2.71	0.59	28.12	6.58
106	[DH 18-31 x (DB 533 x DB 534 F4 IPS 17)]	2455.99	91.17	1.50	16.00	38.17	3.70	2.42	26.83	8.00	9.56	33.83	4.02	26.62	0.67	6.20	33.65	43.67	2.72	0.59	25.34	6.38
107	[DH 18-31 x (DB 533 x DB 534 F4 IPS 32)]	1975.11	114.00	1.72	21.17	59.50	2.90	1.94	26.75	7.17	10.44	32.18	4.26	24.65	0.62	6.28	34.43	44.28	2.59	0.59	27.56	6.52
108	[DH 18-31 x (DB 533 x DB 534 F4 IPS 38)]	2118.39	96.83	1.50	23.00	49.50	2.85	2.67	26.42	8.17	8.62	29.31	4.48	27.83	0.56	5.94	33.95	44.12	2.87	0.59	24.77	6.32
109	[DH 18-31 x (DB 533 x DB 534 F4 IPS 48)]	2384.10	101.50	1.58	20.50	45.17	3.30	1.92	26.25	7.17	9.99	30.58	4.40	27.35	1.03	7.17	34.35	44.48	2.70	0.58	26.87	6.48
110	[DH 18-31 x (DB 533 x DB 534 F4 IPS 13)]	2321.06	108.00	1.58	25.17	42.50	3.35	3.08	25.17	6.67	10.61	30.84	5.50	30.67	0.69	6.08	33.62	44.07	2.74	0.59	27.22	6.48
111	[DH 18-31 x (DB 533 x DB 534 F4 IPS 6)]	2273.64	90.83	2.17	22.67	54.00	3.65	2.17	25.17	6.83	10.32	31.88	5.26	27.62	0.65	6.27	33.62	43.63	2.76	0.59	28.48	6.78
112	[DH 18-31 x (DB 533 x DB 534 F4 IPS 8)]	2314.80	92.17	2.33	20.17	40.67	2.65	2.50	24.42	8.00	8.50	31.71	4.61	26.53	0.92	7.42	33.12	46.55	2.54	0.58	29.75	6.63
	MRC6918 *Bt* check	2060.56	107.50	2.00	19.50	47.00	3.65	2.92	31.33	6.50	9.52	28.56	4.05	28.78	0.76	6.47	34.16	45.13	2.82	0.67	29.22	6.67
	DCH32	1998.67	116.50	1.67	21.50	41.50	3.30	3.50	40.25	7.33	9.50	33.62	5.10	24.15	0.35	5.18	32.07	44.37	2.83	0.54	27.96	6.45
	Mean	**1957.45**	**111.69**	**1.77**	**21.33**	**46.21**	**3.10**	**3.51**	**34.26**	**7.10**	**10.06**	**29.87**	**4.70**	**24.47**	**0.62**	**6.14**	**34.04**	**44.59**	**2.85**	**0.59**	**27.52**	**6.53**
	Max	**2884.26**	**143.83**	**2.44**	**25.17**	**66.17**	**4.20**	**5.28**	**54.92**	**9.50**	**17.50**	**35.31**	**7.40**	**34.25**	**1.17**	**10.04**	**36.79**	**46.55**	**3.61**	**0.67**	**31.22**	**6.85**
	Min	**1146.20**	**84.67**	**1.11**	**16.00**	**34.50**	**2.35**	**1.92**	**24.42**	**5.33**	**7.00**	**13.81**	**2.71**	**3.15**	**0.09**	**2.07**	**31.13**	**42.60**	**2.49**	**0.54**	**22.91**	**5.88**
	CV %	**19.70**	**13.81**	**13.71**	**13.71**	**19.51**	**17.07**	**13.98**	**19.16**	**16.89**	**9.40**	**10.41**	**17.25**	**9.50**	**11.04**	**12.69**						
	S.E	**273.03**	**10.91**	**0.17**	**2.07**	**6.39**	**0.37**	**0.35**	**4.64**	**0.85**	**0.67**	**2.20**	**0.57**	**1.64**	**0.05**	**0.55**						
	CD@ 5%	**765.14**	**30.58**	**0.48**	**6.93**	**12.54**	**0.89**	**0.98**	**13.00**	**5.63**	**1.87**	**6.17**	**1.60**	**4.60**	**0.14**	**1.55**						
	C.D. 1%	**1011.98**	**40.45**	**0.64**	**9.21**	**16.66**	**1.18**	**1.29**	**17.20**	**7.47**	**2.48**	**8.16**	**2.12**	**6.09**	**0.18**	**2.05**						

Appendix 5. Heterosis over mid parent and commercial checks for plant height, number of monopodia, number of sympodia, number of bolls and mean boll weight traits in derived F_1 crosses

Sl.No	Cross	Seed cotton yield (kg/ha)			Plant height (cm)			Number of monopodia			Number of sympodia			Number of bolls			Mean boll weight (g)		
		H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
1	[[DH 98-27 x (DB 533 x DB 534 F4 IPS 44)]	19.49	-1.49	1.56	34.03*	18.76	9.58	18.55	-1.75	18.02	-2.11	0.00	-9.30	30.71	0.35	13.66	-10.13	-19.18	-10.61
2	[DH 98-27 x (DB 533 x DB 534 F4 IPS 62)]	11.53	-11.71	-8.97	27.26*	14.73	5.87	-41.58**	-44.50**	-33.33*	12.82	12.82	2.33	16.24	-18.80	-8.03	-13.11	-26.03	-18.18
3	[DH 98-27 x (DB 533 x DB 534 F4 IPS 105)]	88.58**	26.50	30.41	-5.62	-16.59	-23.03	11.03	-19.50	-3.30	4.89	0.87	-8.51	32.26	-12.77	-1.19	-7.67	-15.07	-6.06
4	[DH 98-27 x (DB 533 x DB 534 F4 IPS 26)]	26.62	-8.82	-6.00	8.03	-0.93	-8.58	74.11**	4.25	25.23	11.89	20.51	9.30	38.25	-7.10	5.23	-3.20	-10.96	-1.52
5	[DH 98-27 x (DB 533 x DB 534 F4 IPS 71)]	18.36	-8.07	-5.22	2.57	-7.29	-14.45	26.18	-13.25	4.20	-17.95	-11.97	-20.16	18.92	-6.38	6.04	-13.18	-24.66	-16.67
6	[DH 98-27 x (DB 533 x DB 534 F4 IPS 30)]	16.50	-13.33	-10.64	9.28	0.47	-7.30	-2.01	-20.75	-4.80	22.78	29.08	17.07	25.93	-9.57	2.42	11.95	-8.22	1.52
7	[DH 98-27 x (DB 533 x DB 534 F4 IPS 25)]	67.66**	4.48	7.71	5.94	-4.49	-11.87	90.15**	11.00	33.33*	19.81	21.36	10.07	65.02**	12.06	26.93	-21.36	-30.14*	-22.73
8	[DH 98-27 x (DB 533 x DB 534 F4 IPS 49)]	108.16**	39.97*	44.31*	13.43	6.05	-2.15	87.98**	-14.00	3.30	-3.78	8.56	-1.53	83.06**	26.60	43.39*	-10.56	-20.55	-12.12
9	[DH 98-27 x (DB 533 x DB 534 F4 IPS 23)]	4.34	-9.96	-7.17	17.29	4.65	-3.43	67.41**	22.00	46.55**	1.27	2.56	-6.98	52.29*	12.05	26.92	-10.77	-20.55	-12.12
10	[DH 98-27 x (DB 533 x DB 534 F4 IPS 36)]	5.92	-12.06	-9.34	11.52	1.24	-6.58	14.71	-2.50	17.12	19.84	18.79	7.74	28.72	-14.19	-2.81	-12.20	-26.03	-18.18
11	[DH 98-27 x (DB 533 x DB 534 F4 IPS 15)]	30.17	-7.66	-4.80	7.84	-4.03	-11.45	13.20	-29.25*	-15.02	4.05	-0.85	-10.07	18.07	-25.89	-16.06	-2.26	-10.96	-1.52
12	[DH 98-27 x (DB 533 x DB 534 F4 IPS 1)]	26.68	-3.89	-0.92	5.96	-2.17	-9.73	105.51**	2.50	23.12	-6.40	0.00	-9.30	76.72**	13.12	28.12	-15.79	-23.29	-15.15
13	[DH 98-27 x (DB 533 x DB 534 F4 IPS 33)]	0.41	-20.30	-17.84	50.00**	22.79	13.30	112.47**	10.75	33.03*	36.04*	27.33	15.49	58.9*	1.41	14.87	-15.98	-23.29	-15.15
14	[DH 98-27 x (DB 533 x DB 534 F4 IPS 24)]	8.62	-17.35	-14.79	31.97*	10.07	1.57	81.32**	16.50	39.94**	16.84	6.85	-3.09	46.42	-16.67	-5.62	-16.07	-27.40	-19.70
15	[DH 98-27 x (DB 533 x DB 534 F4 IPS 16)]	80.8**	15.73	19.31	45.30**	18.60	9.44	136.53**	-1.25	18.62	14.14	0.00	-9.30	106.02**	9.21	23.70	-10.49	-16.44	-7.58
16	[DH 98-27 x (DB 533 x DB 534 F4 IPS 52)]	85.62**	27.96	31.93	-2.38	-17.06	-23.46	128.33**	-33.50**	-20.12	18.08	17.08	6.19	58.18	-14.18	-2.80	-9.02	-15.07	-6.06
17	[DH 98-27 x (DB 533 x DB 534 F4 IPS 12)]	13.27	-9.66	-6.86	41.00**	19.69	10.44	17.81	-14.00	3.30	3.00	2.56	-6.98	36.51	-8.51	3.63	-8.31	-19.18	-10.61
18	[DH 98-27 x (DB 534 x DB 533 F4 IPS 22)]	77.72**	35.93*	40.14*	-2.25	-15.51	-22.03	27.17*	8.25	30.03*	19.31	16.23	5.42	91.15**	14.89	30.14	19.97	0.00	10.61
19	[DH 98-27 x (DB 533 x DB 534 F4 IPS 14)]	47.39	-5.08	-2.14	-6.96	-21.24	-27.33*	76.45**	10.50	32.73*	25.12	17.10	6.21	99.38**	12.06	26.93	-8.88	-17.81	-9.09
20	[DH 98-27 x (DB 533 x DB 534 F4 IPS 34)]	45.22*	0.68	3.80	9.25	-3.87	-11.30	11.00	-44.50**	-33.33*	9.76	15.38	4.65	61.73*	-7.09	5.24	-10.40	-19.18	-10.61
21	[DH 98-27 x (DB 533 x DB 534 F4 IPS 55)]	30.72	0.66	3.77	31.46*	12.40	3.72	15.50	-25.50*	-10.51	5.96	5.97	-3.88	60.63*	9.94	24.52	-21.70	-19.18	-10.61
22	[DH 98-27 x (DB 533 x DB 534 F4 IPS 17)]	60.18**	18.10	21.76	53.69**	33.8*	23.46	12.56	-13.75	3.60	5.67	3.41	-6.21	66.56*	2.48	16.07	-30.41*	-31.51*	-24.24
23	[DH 98-27 x (DB 533 x DB 534 F4 IPS 32)]	38.68	-14.51	-11.87	20.72	2.94	-5.01	55.66**	-15.75	1.20	12.71	5.97	-3.88	60.61*	-7.45	4.83	-33.64**	-30.14*	-22.73
24	[DH 98-27 x (DB 533 x DB 534 F4 IPS 38)]	35.59	-9.73	-6.94	20.90	7.13	-1.15	146.99**	2.50	23.12	2.02	7.69	-2.33	48.79	-12.40	-0.78	-34.94**	-31.51*	-24.24
25	[DH 98-27 x (DB 533 x DB 534 F4 IPS 48)]	37.48*	15.55	19.13	31.08*	8.22	-0.14	4.07	-13.75	3.60	5.13	5.13	-4.65	77.04**	23.05	39.38	-4.11	-13.70	-4.55
26	[DH 98-27 x (DB 533 x DB 534 F4 IPS 13)]	20.74	-2.48	0.54	10.23	-7.28	-14.45	-10.79	-15.25	1.80	18.79	16.23	5.42	43.33	-10.29	1.61	-14.79	-27.40	-19.70
27	[DH 98-27 x (DB 533 x DB 534 F4 IPS 6)]	35.91	-6.65	-3.76	20.34	-0.93	-8.58	-19.66	-41.75**	-30.03*	10.90	4.26	-5.44	72.2**	1.06	14.47	-1.79	-9.59	0.00
28	[DH 98-27 x (DB 533 x DB 534 F4 IPS 8)]	31.79	-2.98	0.02	30.14*	11.47	2.86	39.46*	-16.50	0.30	19.83	26.49	14.72	63.88*	-1.78	11.25	-12.20	-19.18	-10.61
29	[ZCH 8 x (DB 533 x DB 534 F4 IPS 44)]	-8.45	-13.98	-11.32	30.32*	7.28	-1.00	-4.56	-42.50**	-30.93*	28.47	21.36	10.07	83.97**	18.09	33.75	9.53	5.48	16.67

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Sl. No.	Cross	Seed cotton yield (kg/ha)			Plant height (cm)			Number of monopodia			Number of sympodia			Number of bolls			Mean boll weight (g)		
		H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
30	[ZCH 8 x (DB 533 x DB 534 F4 IPS 62)]	-15.68	-23.54	-21.17	26.99	6.51	-1.72	26.77	-8.25	10.21	16.67	7.69	-2.33	40.54	-19.51	-8.83	1.80	-6.85	3.03
31	[ZCH 8 x (DB 533 x DB 534 F4 IPS 105)]	24.43	-2.20	0.83	40.32**	15.20	6.30	56.39**	-22.00	-6.31	15.93	2.56	-6.98	39.53	-25.53	-15.65	-20.61	-21.92	-13.64
32	[ZCH 8 x (DB 533 x DB 534 F4 IPS 26)]	-4.40	-20.15	-17.68	28.49*	9.77	1.29	146.31**	-8.25	10.21	20.50	20.51	9.30	90.88**	4.26	18.09	-20.61	-21.92	-13.64
33	[ZCH 8 x (DB 533 x DB 534 F4 IPS 71)]	4.18	-18.74	-16.22	10.71	-10.23	-17.17	80.61**	-18.50	-2.10	22.04	11.10	0.77	69.15**	12.77	27.73	-1.61	-16.44	-7.58
34	[ZCH 8 x (DB 533 x DB 534 F4 IPS 30)]	-1.68	-26.52	-24.25	38.09**	14.11	5.30	74.67**	0.00	20.12	24.04	10.26	0.00	135.61**	40.78*	59.45**	12.82	-9.59	0.00
35	[ZCH 8 x (DB 533 x DB 534 F4 IPS 25)]	41.19	-11.55	-8.82	19.84	-3.10	-10.59	164.03**	-8.25	10.21	20.59	2.56	-6.98	39.68	-21.99	-11.64	-16.54	-27.40	-19.70
36	[ZCH 8 x (DB 533 x DB 534 F4 IPS 49)]	61.65**	9.23	12.61	37.94**	16.13	7.15	292.09**	-13.25	4.20	16.80	12.82	2.33	47.20	-15.96	-4.81	32.28*	15.07	27.27
37	[ZCH 8 x (DB 533 x DB 534 F4 IPS 23)]	2.27	-21.24	-18.80	60.30**	31.47*	21.31	70.70**	-8.25	10.21	16.87	15.38	4.65	73.51**	18.44	34.15	7.54	-8.22	1.52
38	[ZCH 8 x (DB 533 x DB 534 F4 IPS 36)]	0.05	-26.22	-23.94	52.50**	27.44*	17.60	0.95	-33.50**	-20.12	17.72	13.69	3.12	83.82**	12.77	27.73	0.34	-19.18	-10.61
39	[ZCH 8 x (DB 533 x DB 534 F4 IPS 15)]	33.28	-17.83	-15.28	37.06*	12.09	3.43	149.57**	8.25	30.03*	22.59	13.69	3.12	66.67*	-4.26	8.45	-1.25	-13.70	-4.55
40	[ZCH 8 x (DB 533 x DB 534 F4 IPS 1)]	26.41	-15.83	-13.22	15.11	-2.02	-9.59	198.37**	-8.25	10.21	3.27	7.69	-2.33	84.27**	8.15	22.50	-2.82	-15.07	-6.06
41	[ZCH 8 x (DB 533 x DB 534 F4 IPS 33)]	-16.68	-32.62	-30.53	26.24	2.17	-5.73	25.78	-29.25*	-15.02	12.65	10.26	0.00	76.86**	13.83	28.93	-3.80	-8.22	1.52
42	[ZCH 8 x (DB 533 x DB 534 F4 IPS 24)]	-7.79	-28.45	-26.23	17.29	-3.26	-10.73	53.56**	5.00	26.13	-9.83	-13.69	-21.72	62.96*	-6.38	6.04	-13.83	-21.92	-13.64
43	[ZCH 8 x (DB 533 x DB 534 F4 IPS 16)]	47.05*	-3.67	-0.68	49.86**	20.93	11.59	100.00**	-8.25	10.21	0.46	-7.69	-16.28	62.25*	-13.12	-1.59	-14.27	-16.44	-7.58
44	[ZCH 8 x (DB 533 x DB 534 F4 IPS 52)]	40.60	-0.96	2.11	37.27**	15.35	6.44	160.90**	-13.25	4.20	-2.47	0.87	-8.51	97.4**	8.16	22.51	-8.64	-10.96	-1.52
45	[ZCH 8 x (DB 533 x DB 534 F4 IPS 12)]	-2.99	-20.86	-18.41	40.00*	5.27	-2.86	68.06**	-19.75	-3.60	31.37*	16.23	5.42	83.22**	19.86	35.76	-7.05	-15.07	-6.06
46	[ZCH 8 x (DB 534 x DB 533 F4 IPS 22)]	30.90	2.50	5.68	45.86**	11.94	3.29	75.37**	5.00	26.13	29.72	11.97	1.56	46.07	-14.54	-3.21	10.76	-4.11	6.06
47	[ZCH 8 x (DB 533 x DB 534 F4 IPS 14)]	25.54	-16.86	-14.29	68.57**	26.36	16.60	167.56**	0.00	20.12	47.16**	21.38	10.09	124.04**	22.34	38.57	12.90	5.48	16.67
48	[ZCH 8 x (DB 533 x DB 534 F4 IPS 34)]	23.84	-11.88	-9.16	42.77**	11.79	3.15	270.71**	-8.25	10.21	7.25	0.85	-8.53	70.15*	-4.97	7.64	-7.62	-13.70	-4.55
49	[ZCH 8 x (DB 533 x DB 534 F4 IPS 55)]	22.64	-12.34	-9.62	39.69**	11.32	2.72	23.79	-16.75	0.00	27.42	23.08	11.63	39.74	-2.13	10.86	-11.22	-27.40	-19.70
50	[ZCH 8 x (DB 533 x DB 534 F4 IPS 17)]	42.43	-2.86	0.15	13.55	-7.75	-14.88	7.09	-15.00	2.10	-4.97	-10.26	-18.60	57.87*	-0.35	12.87	4.98	-19.18	-10.61
51	[ZCH 8 x (DB 533 x DB 534 F4 IPS 32)]	28.14	-28.09	-25.86	26.83	0.78	-7.01	67.03**	-5.00	14.11	36.78*	23.92	12.40	76.04**	4.26	18.09	12.75	-5.48	4.55
52	[ZCH 8 x (DB 533 x DB 534 F4 IPS 38)]	29.22	-21.11	-18.67	30.70*	8.21	-0.15	163.84**	16.75	40.24**	0.41	2.56	-6.98	58.34*	-4.26	8.45	24.18	4.11	15.15
53	[ZCH 8 x (DB 533 x DB 534 F4 IPS 48)]	23.56	-7.38	-4.52	14.83	-9.92	-16.88	26.85	-25.00*	-9.91	18.45	17.95	6.98	49.63*	5.32	19.29	-13.18	-21.92	-13.64
54	[ZCH 8 x (DB 533 x DB 534 F4 IPS 13)]	19.08	-14.64	-12.00	52.52**	22.01	12.59	2.81	-26.75*	-12.01	28.96*	25.64	13.95	96.09**	24.47	40.98	15.85	-1.37	9.09
55	[ZCH 8 x (DB 533 x DB 534 F4 IPS 6)]	38.95	-17.19	-14.63	26.86	-0.77	-8.44	109.74**	2.25	22.82	12.33	5.13	-4.65	46.43	-12.77	-1.19	-10.65	-17.81	-9.09
56	[ZCH 8 x (DB 533 x DB 534 F4 IPS 8)]	31.62	-15.07	-12.44	45.25**	18.45	9.30	59.17*	-42.50**	-30.93*	6.51	11.97	1.56	104.06**	24.11	40.57	-21.07	-27.40	-19.70
57	[178-24 x (DB 533 x DB 534 F4 IPS 44)]	6.84	-8.82	-6.00	9.70	-13.18	-19.88	88.21**	-8.25	10.21	14.81	5.97	-3.88	80.11**	15.61	30.94	-14.70	-23.29	-15.15
58	[178-24 x (DB 533 x DB 534 F4 IPS 62)]	-7.44	-24.05	-21.69	30.45*	5.27	-2.86	23.20	-25.00*	-9.91	20.39	8.54	-1.56	56.03*	-10.64	1.22	-8.29	-21.92	-13.64
59	[178-24 x (DB 533 x DB 534 F4 IPS 105)]	40.52	-1.67	1.38	32.02*	4.19	-3.86	75.90**	-32.50**	-18.92	26.75	9.41	-0.77	52.16	-18.79	-8.01	-9.16	-16.44	-7.58
60	[178-24 x (DB 533 x DB 534 F4 IPS 26)]	7.00	-19.85	-17.37	27.99	5.27	-2.86	256.31**	-8.25	10.21	17.02	14.51	3.86	112.31**	15.96	31.34	-13.63	-20.55	-12.12
61	[178-24 x (DB 533 x DB 534 F4 IPS 71)]	-5.37	-17.42	-14.86	22.40	-5.12	-12.45	55.22**	-10.75	7.21	33.95*	24.79	13.19	56.77*	2.84	16.48	14.71	6.85	18.18
62	[178-24 x (DB 533 x DB 534 F4 IPS 30)]	-14.12	-27.86	-25.63	23.53	-2.33	-9.87	-4.49	-33.50**	-20.12	11.76	1.72	-7.74	29.30	-24.12	-14.05	8.53	-4.11	6.06
63	[178-24 x (DB 533 x DB 534 F4 IPS 25)]	30.31	-6.30	-3.39	65.50**	27.91	18.03	112.20**	0.00	20.12	44.12**	25.64	13.95	69.57*	-7.10	5.23	-12.23	-16.44	-7.58

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Sl. No.	Cross	Seed cotton yield (kg/ha)			Plant height (cm)			Number of monopodia			Number of sympodia			Number of bolls			Mean boll weight (g)		
		H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
64	[178-24 x (DB 533 x DB 534 F4 IPS 49)]	39.42	7.13	10.45	44.23**	16.28	7.30	159.42**	-10.50	7.51	22.94	21.36	10.07	93.03**	8.16	22.51	-0.72	-5.48	4.55
65	[178-24 x (DB 533 x DB 534 F4 IPS 23)]	-4.22	-24.05	-21.69	6.82	-13.80	-20.45	148.14**	8.25	30.03*	-0.45	-6.82	-15.49	52.54*	1.43	14.88	-2.63	-13.70	-4.55
66	[178-24 x (DB 533 x DB 534 F4 IPS 36)]	-3.43	-26.57	-24.30	14.80	-5.58	-12.88	41.26*	-21.25	-5.41	14.96	5.13	-4.65	61.3*	-3.90	8.84	7.84	-9.59	0.00
67	[178-24 x (DB 533 x DB 534 F4 IPS 15)]	34.20	-14.18	-11.53	5.40	-15.19	-21.74	125.56**	-25.00*	-9.91	-6.35	-17.95	-25.58	45.85	-18.80	-8.03	11.78	1.37	12.12
68	[178-24 x (DB 533 x DB 534 F4 IPS 1)]	28.85	-11.25	-8.50	10.63	-7.29	-14.45	384.85**	0.00	20.12	18.96	17.95	6.98	107.46**	18.09	33.75	-10.88	-19.18	-10.61
69	[178-24 x (DB 533 x DB 534 F4 IPS 33)]	-38.94*	-44.37*	-42.65*	64.20**	27.29	17.45	44.28*	-16.50	0.30	18.38	12.82	2.33	14.83	-12.05	-0.39	-31.54*	-35.62*	-28.79
70	[178-24 x (DB 533 x DB 534 F4 IPS 24)]	-28.23	-36.97*	-35.01	31.76*	4.19	-3.86	18.93	-16.75	0.00	9.17	1.69	-7.77	18.07	-17.73	-6.82	12.05	0.00	10.61
71	[178-24 x (DB 533 x DB 534 F4 IPS 16)]	27.09	-3.74	-0.76	25.17	-3.26	-10.73	127.89**	8.25	30.03*	11.96	0.00	-9.30	73.59**	14.18	29.33	-23.02	-26.03	-18.18
72	[178-24 x (DB 533 x DB 534 F4 IPS 52)]	21.99	-1.59	1.45	15.57	-6.82	-14.02	150.90**	-12.50	5.11	19.49	20.51	9.30	70.38**	14.19	29.34	-1.64	-5.48	4.55
73	[178-24 x (DB 533 x DB 534 F4 IPS 12)]	-5.70	-23.29	-20.91	53.49**	24.34	14.74	26.46	-21.75	-6.01	17.26	10.26	0.00	22.96	-17.37	-6.41	-4.62	-15.07	-6.06
74	[178-24 x (DB 534 x DB 533 F4 IPS 22)]	30.47	1.87	5.03	18.12	-2.48	-10.01	35.14*	0.00	20.12	26.51	16.23	5.42	55.88*	-6.03	6.43	-13.82	-27.40	-19.70
75	[178-24 x (DB 533 x DB 534 F4 IPS 14)]	33.49	-11.91	-9.18	34.16*	8.37	0.00	45.63*	-25.00*	-9.91	16.50	2.56	-6.98	73.58*	-2.13	10.86	-6.77	-15.07	-6.06
76	[178-24 x (DB 533 x DB 534 F4 IPS 34)]	30.20	-7.66	-4.80	41.74**	19.22	10.01	124.44**	-12.75	4.80	24.45	23.92	12.40	82.76**	5.32	19.29	11.28	1.37	12.12
77	[178-24 x (DB 533 x DB 534 F4 IPS 55)]	10.05	-7.84	-4.98	32.21*	-2.02	-9.59	30.53	-41.75**	-30.03*	2.73	-3.41	-12.40	59.53*	0.70	14.06	-10.45	-17.81	-9.09
78	[178-24 x (DB 533 x DB 534 F4 IPS 17)]	22.14	-1.72	1.32	48.56**	12.40	3.72	76.21**	0.00	20.12	32.12*	21.38	10.09	120.19**	23.77	40.19	10.24	-4.11	6.06
79	[178-24 x (DB 533 x DB 534 F4 IPS 32)]	-1.28	-32.49	-30.40	45.85**	7.75	-0.58	145.99**	-15.75	1.20	31.06*	15.38	4.65	44.40	-24.47	-14.45	-29.93*	-34.25*	-27.27
80	[178-24 x (DB 533 x DB 534 F4 IPS 38)]	3.85	-23.87	-21.51	62.84**	25.73	16.02	446.82**	18.25	42.04**	15.87	15.38	4.65	50.97	-19.15	-8.42	-10.95	-16.44	-7.58
81	[178-24 x (DB 533 x DB 534 F4 IPS 48)]	14.85	-3.87	-0.89	5.47	-16.28	-22.75	100.55**	-8.25	10.21	-7.77	-13.67	-21.70	54.99*	7.45	21.70	7.12	-4.11	6.06
82	[178-24 x (DB 533 x DB 534 F4 IPS 13)]	12.23	-9.73	-6.94	41.57**	14.57	5.72	87.04**	8.25	30.03*	34.59*	23.08	11.63	80.69**	12.77	27.73	-4.61	-19.18	-10.61
83	[178-24 x (DB 533 x DB 534 F4 IPS 6)]	28.86	-11.93	-9.21	28.30	1.55	-6.30	88.69**	-33.25**	-19.82	26.81	11.10	0.77	60.00*	-6.38	6.04	6.21	-2.74	7.58
84	[178-24 x (DB 533 x DB 534 F4 IPS 8)]	21.91	-10.67	-7.90	42.10**	17.21	8.15	413.19**	16.75	40.24**	16.37	15.38	4.65	73.87**	3.89	17.68	-5.76	-13.70	-4.55
85	[DH 18-31 x (DB 533 x DB 534 F4 IPS 44)]	31.18	12.72	16.21	46.45**	10.23	1.72	83.96**	-8.25	10.21	28.96	17.95	6.98	39.69	-6.38	6.04	-24.64	-31.51*	-24.24
86	[DH 18-31 x (DB 533 x DB 534 F4 IPS 62)]	18.87	-1.74	1.30	11.00	-14.73	-21.32	7.26	-33.50**	-20.12	7.18	-4.28	-13.19	34.53	-19.15	-8.42	9.79	-5.48	4.55
87	[DH 18-31 x (DB 533 x DB 534 F4 IPS 105)]	70.69**	20.46	24.18	22.73	-7.91	-15.02	132.28**	-8.25	10.21	22.00	4.28	-5.42	71.63*	-3.54	9.25	10.54	2.74	13.64
88	[DH 18-31 x (DB 533 x DB 534 F4 IPS 26)]	45.01*	9.48	12.87	9.99	-13.80	-20.46	209.77**	-16.75	0.00	11.91	8.56	-1.53	71*	-1.77	11.27	-14.52	-20.55	-12.12
89	[DH 18-31 x (DB 533 x DB 534 F4 IPS 71)]	45.27*	9.66	13.05	28.25	0.31	-7.44	3.49	-33.25**	-19.82	45.89**	29.08	17.07	21.07	-19.51	-8.83	13.77	-5.48	4.55
90	[DH 18-31 x (DB 533 x DB 534 F4 IPS 30)]	34.63	-2.78	0.23	12.92	-9.93	-16.88	-2.12	-25.00*	-9.91	5.96	-8.54	-17.05	54.19*	-8.15	4.04	29.48	1.37	12.12
91	[DH 18-31 x (DB 533 x DB 534 F4 IPS 25)]	89.07**	13.68	17.20	26.04	-1.71	-9.30	69.52**	-8.25	10.21	30.56	7.69	-2.33	87.27**	4.26	18.09	4.59	-10.96	-1.52
92	[DH 18-31 x (DB 533 x DB 534 F4 IPS 49)]	87.68**	22.10	25.88	26.59	2.94	-5.01	60.24*	-33.50**	-20.12	9.98	3.41	-6.21	55.76	-11.35	0.41	-13.11	-26.03	-18.18
93	[DH 18-31 x (DB 533 x DB 534 F4 IPS 23)]	29.59	2.48	5.65	10.68	-6.82	-14.02	53.16**	3.00	23.72	20.57	7.69	-2.33	23.20	-15.24	-4.00	-3.89	-20.55	-12.12
94	[DH 18-31 x (DB 533 x DB 534 F4 IPS 36)]	28.55	-2.55	0.46	45.57**	24.81	15.17	-16.22	-33.50**	-20.12	32.37*	15.38	4.65	38.67	-14.19	-2.81	16.09	-9.59	0.00
95	[DH 18-31 x (DB 533 x DB 534 F4 IPS 15)]	73.02**	10.24	13.65	13.20	-4.96	-12.30	70.55**	-3.00	16.52	52.83**	27.36	15.51	85.93**	7.80	22.10	-11.08	-24.66	-16.67
96	[DH 18-31 x (DB 533 x DB 534 F4 IPS 1)]	62.43**	11.50	14.96	4.62	-8.68	-15.73	107.34**	-8.25	10.21	1.81	-3.41	-12.40	33.52	-20.93	-10.43	-4.61	-19.18	-10.61
97	[DH 18-31 x (DB 533 x DB 534 F4 IPS 33)]	8.63	-7.81	-4.96	36.72*	6.51	-1.72	10.71	-8.25	10.21	23.21	17.95	6.98	-5.27	-26.60	-16.86	-11.31	-17.81	-9.09

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Sl. No.	Cross	Seed cotton yield (kg/ha)			Plant height (cm)			Number of monopodia			Number of sympodia			Number of bolls			Mean boll weight (g)		
		H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2
		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
98	[DH 18-31 x (DB 533 x DB 534 F4 IPS 24)]	14.69	-6.42	-3.52	29.36	2.79	-5.15	13.95	8.25	30.03*	18.76	11.13	0.79	59.79*	12.77	27.73	-17.38	-27.40	-19.70
99	[DH 18-31 x (DB 533 x DB 534 F4 IPS 16)]	69.3**	17.67	21.32	10.38	-14.27	-20.89	61.03**	16.75	40.24**	15.23	3.41	-6.21	29.78	-13.48	-2.00	-23.36	-27.40	-19.70
100	[DH 18-31 x (DB 533 x DB 534 F4 IPS 52)]	62.36**	20.86	24.60	19.62	-3.10	-10.58	94.57**	16.50	39.94**	18.13	19.64	8.51	65.52**	12.41	27.33	-17.57	-21.92	-13.64
101	[DH 18-31 x (DB 533 x DB 534 F4 IPS 12)]	25.29	2.91	6.09	12.79	-14.58	-21.18	56.65**	7.50	29.13*	-0.84	1.72	-7.74	33.67	-4.97	7.64	9.74	-2.74	7.58
102	[DH 18-31 x (DB 534 x DB 533 F4 IPS 22)]	53.99**	21.44	25.20	37.21*	6.05	-2.15	34.06**	8.25	30.03*	3.84	4.28	-5.42	57.47*	1.06	14.47	16.01	-2.74	7.58
103	[DH 18-31 x (DB 533 x DB 534 F4 IPS 14)]	65.39**	10.44	13.86	22.99	-7.13	-14.31	28.76	-25.00*	-9.91	9.72	5.97	-3.88	28.83	-22.34	-12.04	-15.41	-23.29	-15.15
104	[DH 18-31 x (DB 533 x DB 534 F4 IPS 34)]	58.39**	13.58	17.09	39.42**	9.92	1.43	119.18**	0.00	20.12	-6.73	0.85	-8.53	27.95	-21.28	-10.83	-12.39	-20.55	-12.12
105	[DH 18-31 x (DB 533 x DB 534 F4 IPS 55)]	38.98*	12.92	16.42	45.43**	11.16	2.58	-31.80**	-33.25**	-19.82	12.29	17.10	6.21	52.45*	4.61	18.48	10.14	-5.48	4.55
106	[DH 18-31 x (DB 533 x DB 534 F4 IPS 17)]	52.85**	19.19	22.88	40.35**	9.46	1.00	-29.55**	-22.50	-6.91	1.28	3.44	-6.19	82.76**	12.77	27.73	-13.78	-30.14*	-22.73
107	[DH 18-31 x (DB 533 x DB 534 F4 IPS 32)]	45.47	-4.15	-1.18	30.62	-0.47	-8.15	-12.86	-23.75	-8.41	8.70	6.85	-3.09	66.85*	-3.55	9.24	-14.26	-24.66	-16.67
108	[DH 18-31 x (DB 533 x DB 534 F4 IPS 38)]	45.16*	2.81	5.99	31.18*	4.34	-3.72	22.54	-8.25	10.21	-14.42	-6.00	-14.74	88.56**	11.34	26.11	10.68	-2.74	7.58
109	[DH 18-31 x (DB 533 x DB 534 F4 IPS 48)]	41.47*	15.70	19.28	25.10	-0.31	-8.01	11.80	-32.50**	-18.92	10.39	17.95	6.98	29.67	-7.81	4.42	-4.24	-16.44	-7.58
110	[DH 18-31 x (DB 533 x DB 534 F4 IPS 13)]	43.48*	12.64	16.13	18.51	-3.72	-11.16	26.55	-8.25	10.21	-4.48	0.00	-9.30	37.03	-12.05	-0.39	6.31	-12.33	-3.03
111	[DH 18-31 x (DB 533 x DB 534 F4 IPS 6)]	66.12**	10.34	13.76	27.81	1.55	-6.30	50.00*	-25.00*	-9.91	14.40	15.38	4.65	74.13**	4.97	18.89	-6.44	-16.44	-7.58
112	[DH 18-31 x (DB 533 x DB 534 F4 IPS 8)]	57.44**	12.34	15.82	5.43	-12.71	-19.45	174.25**	2.50	23.12	-8.00	3.41	-6.21	37.18	-15.60	-4.40	-0.31	-10.96	-1.52
	SEm+	**317.43**	**366.54**		**12.68**	**14.64**		**0.20**	**0.23**		**2.65**	**3.06**		**7.60**	**8.78**		**0.44**	**0.51**	
	CD at 5%	**629.01**	**726.32**		**25.13**	**29.02**		**0.40**	**0.46**		**5.25**	**6.07**		**15.06**	**17.39**		**0.87**	**1.00**	
	CD at 1%	**831.94**	**960.64**		**33.23**	**38.38**		**0.53**	**0.61**		**6.95**	**8.02**		**19.92**	**23.01**		**1.15**	**1.33**	

* Significant at P = 0.05 ** Significant at P = 0.01

Appendix 6. Heterosis over mid parent and commercial checks for reproductive points on sympodia, length of sympodia at 50% height, inter branch distance, seed index and ginning outturn in derived F_1 crosses

Sl.No	Cross	Reproductive points on sympodia			Length of sympodia at 50% height (cm)			Seed index (g)			Ginning outturn (%)		
		H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2
		1	2	3	4	5	6	7	8	9	10	11	12
1	[[DH 98-27 x (DB 533 x DB 534 F4 IPS 44)]	32.65**	54.37**	28.57*	57.83**	58.24**	23.19	2.84	-12.40	-12.26	-5.33	7.37	-8.79
2	[DH 98-27 x (DB 533 x DB 534 F4 IPS 62)]	13.95	40.14*	16.71	2.04	13.02	-12.01	21.38*	7.99	8.16	-5.56	11.45	-5.32
3	[DH 98-27 x (DB 533 x DB 534 F4 IPS 105)]	-18.58	-5.66	-21.43	8.26	11.42	-13.25	-2.75	-7.20	-7.05	-8.77	1.94	-13.4
4	[DH 98-27 x (DB 533 x DB 534 F4 IPS 26)]	-22.83*	0.00	-16.71	-13.53	1.07	-21.32	26.65**	8.62	8.79	-0.31	19.92	1.87
5	[DH 98-27 x (DB 533 x DB 534 F4 IPS 71)]	-14.29	22.98	2.43	-13.55	-5.86	-26.71	29.55**	9.77	9.95	-11.82	-3.59	-18.10*
6	[DH 98-27 x (DB 533 x DB 534 F4 IPS 30)]	-29.49**	5.83	-11.86	-32.74*	-19.69	-37.48*	19.44*	5.73	5.89	-7.32	5.60	-10.29
7	[DH 98-27 x (DB 533 x DB 534 F4 IPS 25)]	-12.06	25.73	4.71	12.52	25.53	-2.27	41.96**	34.84**	35.05**	0.51	8.23	-8.06
8	[DH 98-27 x (DB 533 x DB 534 F4 IPS 49)]	-57.53**	-33.45*	-44.57**	-31.99*	-14.63	-33.54*	25.9**	7.41	7.58	-16.87*	-3.38	-17.92*
9	[DH 98-27 x (DB 533 x DB 534 F4 IPS 23)]	-16.55	8.58	-9.57	2.60	5.31	-18.01	11.72	13.24	13.42	-6.63	8.44	-7.88
10	[DH 98-27 x (DB 533 x DB 534 F4 IPS 36)]	-16.31	14.41	-4.71	-8.09	3.99	-19.04	4.95	10.35	10.53	-15.58*	1.93	-13.41
11	[DH 98-27 x (DB 533 x DB 534 F4 IPS 15)]	3.64	34.31*	11.86	18.43	24.72	-2.91	3.06	15.03	15.21	-14.95	-2.64	-17.3
12	[DH 98-27 x (DB 533 x DB 534 F4 IPS 1)]	-0.42	42.71*	18.86	-18.83	-3.19	-24.63	2.78	4.78	4.95	-22.26**	-4.36	-18.75*
13	[DH 98-27 x (DB 533 x DB 534 F4 IPS 33)]	-8.69	12.69	-6.14	9.52	-0.53	-22.56	19.21*	14.29	14.47	-2.35	10.08	-6.48
14	[DH 98-27 x (DB 533 x DB 534 F4 IPS 24)]	16.62	51.63**	26.29	46.98**	48.92*	15.94	-4.46	-4.78	-4.63	-3.95	12.69	-4.27
15	[DH 98-27 x (DB 533 x DB 534 F4 IPS 16)]	21.00	48.71**	23.86	26.31	18.08	-8.07	5.92	12.40	12.58	-4.08	6.53	-9.5
16	[DH 98-27 x (DB 533 x DB 534 F4 IPS 52)]	-43.5**	-22.81	-35.71*	-3.47	3.72	-19.25	40.4**	35.42**	35.63**	-2.35	16.81	-0.77
17	[DH 98-27 x (DB 533 x DB 534 F4 IPS 12)]	-14.48	18.01	-1.71	5.29	8.23	-15.74	8.40	9.83	10	-3.78	11.27	-5.47
18	[DH 98-27 x (DB 534 x DB 533 F4 IPS 22)]	-48.64**	-25.73	-38.14**	-29.11	-19.69	-37.48*	-0.50	4.57	4.74	-12.05	5.76	-10.16
19	[DH 98-27 x (DB 533 x DB 534 F4 IPS 14)]	-35.62**	-11.49	-26.29	-13.25	-8.52	-28.78	-0.94	10.51	10.68	-9.61	3.03	-12.48
20	[DH 98-27 x (DB 533 x DB 534 F4 IPS 34)]	-18.66	22.98	2.43	-2.00	17.03	-8.89	-12.84	-11.19	-11.05	-18.7*	-0.39	-15.38
21	[DH 98-27 x (DB 533 x DB 534 F4 IPS 55)]	2.43	22.98	2.43	-2.30	-3.73	-25.06	17.83*	7.99	8.16	3.10	15.97	-1.49
22	[DH 98-27 x (DB 533 x DB 534 F4 IPS 17)]	-1.29	25.04	4.14	18.06	28.72	0.21	4.30	-0.47	-0.32	-21.85**	-8.49	-22.26*

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Sl. No.	Cross	Reproductive points on sympodia			Length of sympodia at 50% height (cm)			Seed index (g)			Ginning outturn (%)		
		H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2
		1	2	3	4	5	6	7	8	9	10	11	12
23	[DH 98-27 x (DB 533 x DB 534 F4 IPS 32)]	10.04	31.56	9.57	12.50	13.83	-11.38	80.45**	83.87**	84.16**	-0.54	10.22	-6.37
24	[DH 98-27 x (DB 533 x DB 534 F4 IPS 38)]	7.34	43.05*	19.14	52.19**	75.25**	36.43*	-6.55	-13.82	-13.68	-6.45	11.68	-5.13
25	[DH 98-27 x (DB 533 x DB 534 F4 IPS 48)]	-23.61*	-5.66	-21.43	25.29	17.28	-8.70	11.31	12.72	12.89	-7.04	10.10	-6.47
26	[DH 98-27 x (DB 533 x DB 534 F4 IPS 13)]	-49.51**	-34.31*	-45.29**	-15.46	-11.98	-31.48*	-29.96**	-26.43**	-26.32**	-16.98*	2.15	-13.22
27	[DH 98-27 x (DB 533 x DB 534 F4 IPS 6)]	-27.34*	-10.63	-25.57	-8.29	-11.71	-31.27*	3.11	14.98	15.16	-1.48	15.06	-2.26
28	[DH 98-27 x (DB 533 x DB 534 F4 IPS 8)]	-11.42	21.10	0.86	3.27	13.83	-11.38	-2.01	-0.21	-0.05	-21.32**	-1.38	-16.23
29	[ZCH 8 x (DB 533 x DB 534 F4 IPS 44)]	45.03**	68.78**	40.57**	34.65*	35.36	5.38	-1.12	-0.16	0	-24.47**	-20.69	-32.63**
30	[ZCH 8 x (DB 533 x DB 534 F4 IPS 62)]	-2.37	20.07	0.00	-14.26	-4.80	-25.89	-1.38	3.31	3.47	-4.75	4.39	-11.32
31	[ZCH 8 x (DB 533 x DB 534 F4 IPS 105)]	11.03	28.64	7.14	19.59	23.39	-3.94	0.31	11.56	11.74	-17.58*	-14.83	-27.65**
32	[ZCH 8 x (DB 533 x DB 534 F4 IPS 26)]	27.99*	65.87**	38.14**	7.84	26.33	-1.65	7.48	9.14	9.32	2.13	14.27	-2.93
33	[ZCH 8 x (DB 533 x DB 534 F4 IPS 71)]	0.77	22.98	2.43	-2.90	-11.17	-30.84*	-14.29	-18.18*	-18.05*	-9.44	4.38	-11.33
34	[ZCH 8 x (DB 533 x DB 534 F4 IPS 30)]	-20.00	2.92	-14.29	29.86	32.44	3.11	-7.65	-8.36	-8.21	-32.39**	-18.96	-31.16**
35	[ZCH 8 x (DB 533 x DB 534 F4 IPS 25)]	31.83**	60.21**	33.43*	0.29	-5.58	-26.50	14.34	20.86*	21.05*	-8.13	4.36	-11.35
36	[ZCH 8 x (DB 533 x DB 534 F4 IPS 49)]	-9.07	22.98	2.43	20.06	29.79	1.04	17.32*	12.66	12.84	-22.22**	-4.99	-19.29*
37	[ZCH 8 x (DB 533 x DB 534 F4 IPS 23)]	22.64	51.46**	26.14	84.71**	70.21**	32.51*	11.32	1.00	1.16	-10.95	-1.89	-16.66
38	[ZCH 8 x (DB 533 x DB 534 F4 IPS 36)]	7.71	40.14*	16.71	16.85	19.95	-6.62	20.49*	13.87	14.05	-16.14*	-3.75	-18.23*
39	[ZCH 8 x (DB 533 x DB 534 F4 IPS 15)]	32.5**	62.95**	35.71*	23.15	16.75	-9.11	14.44	15.55	15.74	-4.73	3.38	-12.18
40	[ZCH 8 x (DB 533 x DB 534 F4 IPS 1)]	-16.31	14.41	-4.71	-13.45	-5.86	-26.71	9.53	0.00	0.16	-25.64**	-12.96	-26.06**
41	[ZCH 8 x (DB 533 x DB 534 F4 IPS 33)]	34.24**	60.03**	33.29*	22.72	24.99	-2.70	-0.50	-10.56	-10.42	-58.48**	-51.63**	-58.91**
42	[ZCH 8 x (DB 533 x DB 534 F4 IPS 24)]	20.38	51.46**	26.14	-12.19	-1.34	-23.19	12.82	5.68	5.84	-13.42	4.85	-10.93
43	[ZCH 8 x (DB 533 x DB 534 F4 IPS 16)]	42.05**	68.61**	40.43**	33.09*	39.09	8.29	-2.07	-1.94	-1.79	-3.08	11.29	-5.46
44	[ZCH 8 x (DB 533 x DB 534 F4 IPS 52)]	-0.78	31.39	9.43	-5.49	11.97	-12.83	4.73	-5.25	-5.11	-18.24*	0.88	-14.31
45	[ZCH 8 x (DB 533 x DB 534 F4 IPS 12)]	3.71	10.29	-8.14	17.85	2.65	-20.09	-13.92	-12.56	-12.42	-9.09	5.29	-10.56
46	[ZCH 8 x (DB 534 x DB 533 F4 IPS 22)]	-18.15	-7.55	-23.00	10.80	8.14	-15.81	-2.79	2.42	2.58	-9.06	9.51	-6.98
47	[ZCH 8 x (DB 533 x DB 534 F4 IPS 14)]	-7.62	-2.23	-18.57	30.95	17.54	-8.50	-16.68*	-6.83	-6.68	-7.04	6.11	-9.86

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Sl. No.	Cross	Reproductive points on sympodia			Length of sympodia at 50% height (cm)			Seed index (g)			Ginning outturn (%)		
		H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2
		1	2	3	4	5	6	7	8	9	10	11	12
48	[ZCH 8 x (DB 533 x DB 534 F4 IPS 34)]	-1.87	17.32	-2.29	2.57	6.38	-17.18	2.37	4.57	4.74	-22.47**	-4.87	-19.19*
49	[ZCH 8 x (DB 533 x DB 534 F4 IPS 55)]	26.77*	60.03**	33.29*	40.08*	32.44	3.11	10.22	0.00	0.16	-3.92	6.07	-9.89
50	[ZCH 8 x (DB 533 x DB 534 F4 IPS 17)]	5.49	40.14*	16.71	10.89	16.48	-9.32	-4.25	-9.51	-9.37	-10.58	2.84	-12.64
51	[ZCH 8 x (DB 533 x DB 534 F4 IPS 32)]	11.32	39.97*	16.57	23.66	20.20	-6.42	11.68	12.77	12.95	-14.35	-6.86	-20.88*
52	[ZCH 8 x (DB 533 x DB 534 F4 IPS 38)]	12.67	57.12**	30.86*	0.24	11.42	-13.25	24.03**	13.24	13.42	-16.23*	-1.75	-16.54
53	[ZCH 8 x (DB 533 x DB 534 F4 IPS 48)]	-23.99*	-8.40	-23.71	-8.38	-15.70	-34.37*	6.83	2.79	2.95	-10.15	-0.79	-15.72
54	[ZCH 8 x (DB 533 x DB 534 F4 IPS 13)]	3.37	31.39	9.43	22.19	25.26	-2.48	-5.41	-5.41	-5.26	-15.66	-2.99	-17.59
55	[ZCH 8 x (DB 533 x DB 534 F4 IPS 6)]	9.65	31.56	9.57	17.98	11.70	-13.04	23.84**	31.84**	32.05**	-6.71	1.45	-13.82
56	[ZCH 8 x (DB 533 x DB 534 F4 IPS 8)]	-31.49**	-8.40	-23.71	-9.18	-1.34	-23.19	-4.67	-7.72	-7.58	-11.05	4.34	-11.36
57	[178-24 x (DB 533 x DB 534 F4 IPS 44)]	-5.14	17.15	-2.43	0.87	-8.52	-28.78	19.78*	16.76	16.95	4.44	23.63*	5.03
58	[178-24 x (DB 533 x DB 534 F4 IPS 62)]	-7.71	20.07	0.00	-4.86	-3.73	-25.06	-1.25	0.00	0.16	-7.20	14.13	-3.05
59	[178-24 x (DB 533 x DB 534 F4 IPS 105)]	4.60	28.64	7.14	12.26	4.79	-18.42	2.59	10.51	10.68	-5.83	9.91	-6.63
60	[178-24 x (DB 533 x DB 534 F4 IPS 26)]	-8.03	25.73	4.71	4.59	12.24	-12.62	3.00	1.00	1.16	-10.64	11.94	-4.91
61	[178-24 x (DB 533 x DB 534 F4 IPS 71)]	-38.78**	-30.53	-42.14**	3.20	-9.85	-29.81	-0.05	3.89	4.05	-12.22	3.06	-12.45
62	[178-24 x (DB 533 x DB 534 F4 IPS 30)]	-19.00	-2.74	-19.00	-11.95	-13.83	-32.92*	1.32	9.14	9.32	-8.50	11.64	-5.16
63	[178-24 x (DB 533 x DB 534 F4 IPS 25)]	36.67**	54.37**	28.57*	40.92*	26.85	-1.24	-21.77**	-10.67	-10.53	0.90	16.79	-0.79
64	[178-24 x (DB 533 x DB 534 F4 IPS 49)]	-20.92	0.17	-16.57	-3.83	0.00	-22.15	-1.31	3.15	3.32	-11.35	10.19	-6.4
65	[178-24 x (DB 533 x DB 534 F4 IPS 23)]	6.17	37.22*	14.29	12.38	5.04	-18.22	-7.00	-4.73	-4.58	3.93	16.12	-1.35
66	[178-24 x (DB 533 x DB 534 F4 IPS 36)]	-51.52**	-34.13*	-45.14**	-19.43	-16.23	-34.78*	15.95*	23.17*	23.37*	-7.24	7.91	-8.33
67	[178-24 x (DB 533 x DB 534 F4 IPS 15)]	-35.51**	-16.98	-30.86*	-10.91	-14.36	-33.33*	-11.26	0.00	0.16	-1.24	8.70	-7.66
68	[178-24 x (DB 533 x DB 534 F4 IPS 1)]	-29.68**	0.17	-16.57	-1.92	7.98	-15.94	-9.92	-7.20	-7.05	-8.08	9.03	-7.38
69	[178-24 x (DB 533 x DB 534 F4 IPS 33)]	-22.22*	8.06	-10.00	2.16	1.07	-21.32	22.34**	26.06**	26.26**	-14.67	3.40	-12.17
70	[178-24 x (DB 533 x DB 534 F4 IPS 24)]	-15.50	22.98	2.43	-3.28	5.84	-17.60	11.46	19.08*	19.26*	-20.48**	0.02	-15.04
71	[178-24 x (DB 533 x DB 534 F4 IPS 16)]	-29.74**	-2.74	-19.00	-5.76	-4.26	-25.47	-13.40	-1.89	-1.74	-16.25*	0.09	-14.98
72	[178-24 x (DB 533 x DB 534 F4 IPS 52)]	-33.71**	0.86	-16.00	-15.07	-1.87	-23.60	-19.93**	-17.03	-16.89	-15.92*	7.67	-8.54

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Sl. No.	Cross	Reproductive points on sympodia			Length of sympodia at 50% height (cm)			Seed index (g)			Ginning outturn (%)		
		H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2
		1	2	3	4	5	6	7	8	9	10	11	12
73	[178-24 x (DB 533 x DB 534 F4 IPS 12)]	43.52**	81.30**	51.00**	34.55*	37.23	6.83	7.58	4.41	4.58	-12.78	-6.06	-20.20*
74	[178-24 x (DB 534 x DB 533 F4 IPS 22)]	-18.32	8.58	-9.57	4.26	17.28	-8.70	-8.49	-7.72	-7.58	4.43	17.30	-0.36
75	[178-24 x (DB 533 x DB 534 F4 IPS 14)]	-22.70*	-2.74	-19.00	3.17	7.96	-15.95	-16.6*	-10.51	-10.37	2.90	9.12	-7.3
76	[178-24 x (DB 533 x DB 534 F4 IPS 34)]	-20.10	11.49	-7.14	-7.61	9.57	-14.70	2.91	0.47	0.63	-22.26**	-10.91	-24.32**
77	[178-24 x (DB 533 x DB 534 F4 IPS 55)]	-12.23	-2.74	-19.00	29.31	11.42	-13.25	5.91	14.98	15.16	-9.75	0.82	-14.35
78	[178-24 x (DB 533 x DB 534 F4 IPS 17)]	-7.38	8.75	-9.43	16.11	12.24	-12.62	-0.80	11.46	11.63	-10.96	3.57	-12.02
79	[178-24 x (DB 533 x DB 534 F4 IPS 32)]	1.09	11.49	-7.14	19.46	6.11	-17.39	-21.72**	-6.99	-6.84	-6.39	3.03	-12.48
80	[178-24 x (DB 533 x DB 534 F4 IPS 38)]	21.30	50.43**	25.29	7.12	10.10	-14.29	9.63	19.65*	19.84*	-26.26**	-12.54	-25.70**
81	[178-24 x (DB 533 x DB 534 F4 IPS 48)]	-36.93**	-25.73	-38.14**	11.04	-1.07	-22.98	4.77	2.79	2.95	-12.10	3.33	-12.22
82	[178-24 x (DB 533 x DB 534 F4 IPS 13)]	-28.69*	-11.32	-26.14	14.81	14.34	-10.98	13.05	15.19	15.37	-12.28	7.16	-8.97
83	[178-24 x (DB 533 x DB 534 F4 IPS 6)]	-7.24	8.75	-9.43	0.87	-7.45	-27.95	-17.02*	-10.09	-9.95	-10.19	4.08	-11.59
84	[178-24 x (DB 533 x DB 534 F4 IPS 8)]	-10.54	17.15	-2.43	34.58*	42.27*	10.76	-8.84	-10.04	-9.89	-18.68*	1.19	-14.04
85	[DH 18-31 x (DB 533 x DB 534 F4 IPS 44)]	14.85	28.64	7.14	18.16	2.92	-19.88	18.67*	13.24	13.42	-1.34	13.01	-4
86	[DH 18-31 x (DB 533 x DB 534 F4 IPS 62)]	-20.46	-5.66	-21.43	-5.99	-8.25	-28.57	11.71	10.83	11	-8.37	9.17	-7.26
87	[DH 18-31 x (DB 533 x DB 534 F4 IPS 105)]	6.00	18.18	-1.57	6.67	-4.26	-25.47	-10.00	-4.89	-4.74	11.31	25.65*	6.74
88	[DH 18-31 x (DB 533 x DB 534 F4 IPS 26)]	-13.29	8.58	-9.57	-1.03	2.65	-20.09	15.60	10.98	11.16	-9.98	9.31	-7.14
89	[DH 18-31 x (DB 533 x DB 534 F4 IPS 71)]	-9.96	8.58	-9.57	4.72	0.26	-21.95	43.37**	30.64**	30.84**	-1.15	6.27	-9.73
90	[DH 18-31 x (DB 533 x DB 534 F4 IPS 30)]	-10.05	14.41	-4.71	-4.39	1.58	-20.92	26.63**	20.18*	20.37*	-8.02	3.12	-12.4
91	[DH 18-31 x (DB 533 x DB 534 F4 IPS 25)]	14.29	37.22*	14.29	8.20	6.46	-17.12	29.55**	31.32**	31.53**	1.48	7.41	-8.76
92	[DH 18-31 x (DB 533 x DB 534 F4 IPS 49)]	2.56	37.22*	14.29	-14.79	-4.26	-25.47	-2.01	-10.14	-10	-2.88	11.10	-5.62
93	[DH 18-31 x (DB 533 x DB 534 F4 IPS 23)]	14.03	40.82*	17.29	8.45	4.26	-18.83	18.87*	16.18	16.37	-8.19	2.50	-12.92
94	[DH 18-31 x (DB 533 x DB 534 F4 IPS 36)]	5.47	37.22*	14.29	22.86	31.02	2.00	19.51*	21.33*	21.53*	-3.19	12.54	-4.4
95	[DH 18-31 x (DB 533 x DB 534 F4 IPS 15)]	30.13**	60.03**	33.29*	28.66	27.11	-1.04	-5.26	2.31	2.47	-6.22	3.13	-12.39
96	[DH 18-31 x (DB 533 x DB 534 F4 IPS 1)]	6.65	45.80**	21.43	-6.13	5.84	-17.60	1.55	-0.16	0	-17.58*	-2.31	-17.01
97	[DH 18-31 x (DB 533 x DB 534 F4 IPS 33)]	1.59	42.88*	19.00	20.00	10.90	-13.66	19.44*	14.14	14.32	-8.16	4.99	-10.81

Contd...

Sl. No.	Cross	Reproductive points on sympodia			Length of sympodia at 50% height (cm)			Seed index (g)			Ginning outturn (%)		
		H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2
		1	2	3	4	5	6	7	8	9	10	11	12
98	[DH 18-31 x (DB 533 x DB 534 F4 IPS 24)]	-8.79	34.31*	11.86	7.51	10.64	-13.86	7.01	6.31	6.47	-9.60	7.51	-8.67
99	[DH 18-31 x (DB 533 x DB 534 F4 IPS 16)]	-38.8**	-14.24	-28.57*	-18.04	-22.08	-39.34*	-5.59	-0.11	0.05	-2.60	9.73	-6.78
100	[DH 18-31 x (DB 533 x DB 534 F4 IPS 52)]	-33.11**	2.92	-14.29	-13.17	-5.33	-26.30	-1.61	-5.41	-5.26	-9.27	9.98	-6.57
101	[DH 18-31 x (DB 533 x DB 534 F4 IPS 12)]	4.51	17.15	-2.43	3.33	-1.07	-22.98	33.93**	30.16**	30.37**	-11.59	-0.11	-15.14
102	[DH 18-31 x (DB 534 x DB 533 F4 IPS 22)]	-6.07	11.49	-7.14	10.14	17.01	-8.91	4.09	5.10	5.26	-17.14*	-2.56	-17.22
103	[DH 18-31 x (DB 533 x DB 534 F4 IPS 14)]	5.00	17.15	-2.43	0.54	-1.07	-22.98	-12.01	-5.47	-5.32	5.06	16.96	-0.64
104	[DH 18-31 x (DB 533 x DB 534 F4 IPS 34)]	4.86	31.39	9.43	-9.35	1.85	-20.71	12.82	10.30	10.47	-4.68	14.27	-2.93
105	[DH 18-31 x (DB 533 x DB 534 F4 IPS 55)]	15.77	40.99*	17.43	56.98**	35.89	5.79	11.49	10.35	10.53	-6.72	4.60	-11.14
106	[DH 18-31 x (DB 533 x DB 534 F4 IPS 17)]	11.29	42.88*	19.00	22.19	18.61	-7.66	-2.22	0.47	0.63	1.48	18.47	0.64
107	[DH 18-31 x (DB 533 x DB 534 F4 IPS 32)]	-12.73	5.83	-11.86	12.96	0.78	-21.54	0.41	9.67	9.84	2.00	12.69	-4.27
108	[DH 18-31 x (DB 533 x DB 534 F4 IPS 38)]	0.13	35.16*	12.57	15.21	18.88	-7.45	-9.05	-9.46	-9.32	-13.77	2.64	-12.8
109	[DH 18-31 x (DB 533 x DB 534 F4 IPS 48)]	-0.94	8.58	-9.57	26.59	6.38	-17.18	6.71	4.94	5.11	-9.55	7.07	-9.04
110	[DH 18-31 x (DB 533 x DB 534 F4 IPS 13)]	-1.55	14.41	-4.71	5.78	0.00	-22.15	9.18	11.51	11.68	-12.20	7.98	-8.27
111	[DH 18-31 x (DB 533 x DB 534 F4 IPS 6)]	59.75**	74.27**	45.14**	35.28	17.28	-8.70	-0.17	8.41	8.58	-4.36	11.62	-5.18
112	[DH 18-31 x (DB 533 x DB 534 F4 IPS 8)]	-2.23	20.07	0.00	-10.16	-9.57	-29.60	-9.69	-10.67	-10.53	-11.37	11.03	-5.68
	SEm+	**0.42**	**0.48**		**5.41**	**6.24**		**0.74**	**0.85**		**2.61**	**3.01**	
	CD at 5%	**0.83**	**0.96**		**10.71**	**12.37**		**1.46**	**1.69**		**5.17**	**5.96**	
	CD at 1%	**1.10**	**1.27**		**14.17**	**16.36**		**1.93**	**2.23**		**6.83**	**7.89**	

* Significant at P = 0.05 ** Significant at P = 0.01

Appendix 7. Heterosis over mid parent and commercial checks for lint index, seed cotton yield, photosynthesis rate, stomatal conductance and transpiration rate in derived F_1 crosses

Sl.No	Crosses	Lint index (g)			Photosynthetic rate (µmol CO_2 m^{-2} s^{-1})			Stomatal conductance (µmol m^{-2} s^{-1})			Transpiration rate (mmol H_2O m^{-2} s^{-1})		
		H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2
		1	2	3	7	8	9	10	11	12	13	14	15
1	[[DH 98-27 x (DB 533 x DB 534 F4 IPS 44)]	-33.05*	-22.81	-38.57*	-42.14**	-54.79**	-46.10**	-70**	-60.53**	-14.29	-77.06**	-65.15 **	-56.47*
2	[DH 98-27 x (DB 533 x DB 534 F4 IPS 62)]	9.63	27.00	1.08	40.65**	6.77	27.29**	0.54	22.37	165.71**	-53.05**	-26.51*	-8.2
3	[DH 98-27 x (DB 533 x DB 534 F4 IPS 105)]	-29.83*	-16.89	-33.86*	7.44	-4.88	13.4	-38.05**	-7.89	100.00**	-45.17**	-9.58	12.93
4	[DH 98-27 x (DB 533 x DB 534 F4 IPS 26)]	3.07	24.17	-1.18	43.56**	6.11	26.51**	-24.38*	-9.21	97.14**	-27.25**	13.14	41.31
5	[DH 98-27 x (DB 533 x DB 534 F4 IPS 71)]	28.97	29.84	3.34	3.94	-12.63	4.16	-50.27**	-38.82**	32.86	-38**	-5.87	17.57
6	[DH 98-27 x (DB 533 x DB 534 F4 IPS 30)]	-6.58	-5.43	-24.73	7.54	-12.00	4.91	-27.91**	-18.42	77.14*	-47.53**	-17.93	2.51
7	[DH 98-27 x (DB 533 x DB 534 F4 IPS 25)]	38.72*	44.02*	14.62	-14.72	-19.45*	-3.98	-41.31**	-17.76	78.57**	-56.01**	-27.51	-9.46
8	[DH 98-27 x (DB 533 x DB 534 F4 IPS 49)]	26.73	34.16	6.77	32.18**	5.52	25.80**	-5.60	5.26	128.57**	-37.64**	-3.09	21.04
9	[DH 98-27 x (DB 533 x DB 534 F4 IPS 23)]	13.66	48.21*	17.96	6.17	-16.05	0.08	-44.64**	-38.82**	32.86	-58.45**	-14.14	7.24
10	[DH 98-27 x (DB 533 x DB 534 F4 IPS 36)]	-30.89*	-9.49	-27.97	-63.49**	-71.95**	-66.56**	-87.58**	-87.50**	-72.86*	-70.48**	-37.64*	-22.1
11	[DH 98-27 x (DB 533 x DB 534 F4 IPS 15)]	-10.25	19.85	-4.61	-43.03**	-49.04**	-39.24**	-69.59**	-61.18**	-15.71	-71.64**	-37.71*	-22.2
12	[DH 98-27 x (DB 533 x DB 534 F4 IPS 1)]	-36.79**	-14.30	-31.80*	-3.24	-27.58**	-13.67	-42.19**	-42.76**	24.29	-26.15**	**55.26****	93.92**
13	[DH 98-27 x (DB 533 x DB 534 F4 IPS 33)]	1.03	21.09	-3.63	33.14**	11.20	32.57**	25.07*	39.47**	202.86**	-23.54*	13.6	41.89
14	[DH 98-27 x (DB 533 x DB 534 F4 IPS 24)]	-11.01	7.15	-14.72	34.19**	9.08	30.05**	7.44	9.21	137.14**	-53.78**	-29.21	-11.58
15	[DH 98-27 x (DB 533 x DB 534 F4 IPS 16)]	4.16	28.11	1.96	20.34*	13.01	34.73**	4.86	34.87*	192.86**	-19.68*	29.75	62.07**
16	[DH 98-27 x (DB 533 x DB 534 F4 IPS 52)]	21.60	52.03**	21.00	36.98**	8.62	29.49**	8.55	8.55	135.71**	-41.19**	-10.51	11.78
17	[DH 98-27 x (DB 533 x DB 534 F4 IPS 12)]	8.57	27.37	1.37	27.08**	-6.64	11.31	-12.99	-11.84	91.43**	-43.05**	-20.4	-0.58
18	[DH 98-27 x (DB 534 x DB 533 F4 IPS 22)]	-1.78	15.78	-7.85	-68.81**	-77.78**	-73.51**	-64.03**	-67.11**	-28.57	-40.36**	-13.91	7.53
19	[DH 98-27 x (DB 533 x DB 534 F4 IPS 14)]	-18.42	-1.73	-21.79	31.66**	10.40	31.62**	10.56	30.92*	184.29**	-28.86**	8.66	35.71
20	[DH 98-27 x (DB 533 x DB 534 F4 IPS 34)]	-2.77	19.11	-5.20	29.038**	-10.67	6.5	-6.23	-15.79	82.86**	-37.52**	-10.43	11.87
21	[DH 98-27 x (DB 533 x DB 534 F4 IPS 55)]	26.12	45.87*	16.09	24.19**	3.58	23.48*	-19.27	-13.16	88.57**	-47.22**	-23.72	-4.73
22	[DH 98-27 x (DB 533 x DB 534 F4 IPS 17)]	-15.76	-2.10	-22.08	37.53**	11.64	33.09**	8.42	5.92	130.00**	-34.08**	-1.7	22.78
23	[DH 98-27 x (DB 533 x DB 534 F4 IPS 32)]	**53.71****	**82.61****	**45.34****	-43.44**	-46.95**	-36.76**	-81**	-76.32**	-48.57	-64.18**	-43.59*	-29.54
24	[DH 98-27 x (DB 533 x DB 534 F4 IPS 38)]	-27.35*	-12.21	-30.13*	-23.8*	-39.67**	-28.08**	-55.48**	-57.24**	-7.14	-42.19**	-14.37	6.95
25	[DH 98-27 x (DB 533 x DB 534 F4 IPS 48)]	11.19	48.83**	18.45	16.98	-2.97	15.68	-1.20	7.89	134.29**	-27.8**	10.28	37.74
26	[DH 98-27 x (DB 533 x DB 534 F4 IPS 13)]	-30.09*	-6.04	-25.22	33.28**	7.57	28.25**	34.44**	33.55*	190.00**	-28**	13.29	41.51
27	[DH 98-27 x (DB 533 x DB 534 F4 IPS 6)]	-11.97	20.59	-4.02	17.44*	9.61	30.67**	-10.94	12.5	144.29**	-43.48**	-6.34	16.99
28	[DH 98-27 x (DB 533 x DB 534 F4 IPS 8)]	-5.28	31.69	4.81	1.40	-20.18*	-4.85	-17.17	-19.08	75.71*	-53.24**	-26.89	-8.69
29	[ZCH 8 x (DB 533 x DB 534 F4 IPS 44)]	-35.44*	-24.41	-39.84**	-10.66	-21.73*	-6.69	-23.63*	-8.55	98.57**	-39.53**	-7.81	15.15

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Sl.No	Crosses	Lint index (g)			Photosynthetic rate (µmol $CO_2 m^{-2} s^{-1}$)			Stomatal conductance (µmol $m^{-2} s^{-1}$)			Transpiration rate (mmol $H_2O m^{-2} s^{-1}$)		
		H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2
		1	2	3	7	8	9	10	11	12	13	14	15
30	[ZCH 8 x (DB 533 x DB 534 F4 IPS 62)]	-13.21	2.10	-18.74	-27.57**	-38.16**	-26.28*	-47.9**	-42.76**	24.29	-40.22**	-6.11	17.28
31	[ZCH 8 x (DB 533 x DB 534 F4 IPS 105)]	-28.92*	-14.55	-31.99*	-45.16**	-46.26**	-35.93**	-65.38**	-52.63**	2.86	-59.74**	-33.38	-16.8
32	[ZCH 8 x (DB 533 x DB 534 F4 IPS 26)]	18.31	44.64*	15.11	17.04	-2.41	16.34	-20.36	-13.82	87.14**	-36.72**	-1.24	23.36
33	[ZCH 8 x (DB 533 x DB 534 F4 IPS 71)]	-31.65*	-18.00	-34.74*	-76.14**	-80.98**	-77.32**	-87.71**	-85.53**	-68.57*	-57.81**	-36.63*	-20.85
34	[ZCH 8 x (DB 533 x DB 534 F4 IPS 30)]	**-44.65****	**-33.29**	**-46.91****	-65.76**	-73.48**	-68.38**	-87.8**	-86.84**	-71.43*	-60.31**	-38.56*	-23.26
35	[ZCH 8 x (DB 533 x DB 534 F4 IPS 25)]	27.39*	56.84**	24.83	10.44	-0.50	18.62	-42.44**	-22.37	68.57*	-38.72**	0	24.9
36	[ZCH 8 x (DB 533 x DB 534 F4 IPS 49)]	-14.78	6.66	-15.11	18.04	-10.91	6.21	-32.51**	-28.29*	55.71	-40.7**	-8.81	13.9
37	[ZCH 8 x (DB 533 x DB 534 F4 IPS 23)]	-2.44	8.26	-13.84	14.28	-13.04	3.67	6.67	10.53	140.00**	-20.17	13.14	41.31
38	[ZCH 8 x (DB 533 x DB 534 F4 IPS 36)]	3.70	15.66	-7.95	21.57*	-10.21	7.04	29.82*	21.71	164.29**	-8.74	33.54	66.80**
39	[ZCH 8 x (DB 533 x DB 534 F4 IPS 15)]	20.69	37.73*	9.62	-2.40	-15.60	0.62	-53.13**	-43.42 **	22.86	-41.26**	-9.12	13.51
40	[ZCH 8 x (DB 533 x DB 534 F4 IPS 1)]	-34.29*	-23.67	-39.25**	-59.03**	-70.56**	-64.90**	-83.57**	-84.87 **	-67.14*	-57.09**	-37.64*	-22.1
41	[ZCH 8 x (DB 533 x DB 534 F4 IPS 33)]	-32.73*	-21.95	-37.88*	**-84.91****	**-89.07****	**-86.97****	-68.11**	-68.42 **	-31.43	-57.85**	-40.19*	-25.29
42	[ZCH 8 x (DB 533 x DB 534 F4 IPS 24)]	-29.56*	-17.88	-34.64*	15.98	-18.64*	-3	-46.13**	-51.97 **	4.29	-31.8**	-0.08	24.81
43	[ZCH 8 x (DB 533 x DB 534 F4 IPS 16)]	9.57	30.58	3.93	-13.52	-28.42**	-14.66	-59.21**	-52.63 **	2.86	-51.61**	-25.04	-6.37
44	[ZCH 8 x (DB 533 x DB 534 F4 IPS 52)]	-28.69*	-13.56	-31.21*	**74.56****	**18.97***	**41.83****	**75.94****	**53.95 ****	**234.29****	-11.52	28.75	60.81**
45	[ZCH 8 x (DB 533 x DB 534 F4 IPS 12)]	-12.77	8.63	-13.54	-10.66	-28.89**	-15.22	-61.56**	-57.89 **	-8.57	-46.45**	-21.56	-2.03
46	[ZCH 8 x (DB 534 x DB 533 F4 IPS 22)]	-15.23	6.04	-15.60	12.10	-13.27	3.4	8.25	7.89	134.29**	-28.13**	8.58	35.62
47	[ZCH 8 x (DB 533 x DB 534 F4 IPS 14)]	-16.47	6.66	-15.11	-35.97**	-42.38**	-31.31**	-48.05**	-34.21 *	42.86	-41.94**	-7.42	15.64
48	[ZCH 8 x (DB 533 x DB 534 F4 IPS 34)]	-24.62*	-2.22	-22.18	11.06	-16.29	-0.21	-4.70	-6.58	102.86**	-20.75*	18.93	48.55*
49	[ZCH 8 x (DB 533 x DB 534 F4 IPS 55)]	-7.88	7.40	-14.52	-47.61**	-58.09**	-50.03**	-73.44**	-67.76 **	-30	-61.37**	-41.27*	-26.64
50	[ZCH 8 x (DB 533 x DB 534 F4 IPS 17)]	-28.63*	-16.40	-33.46*	5.19	-18.19*	-2.46	-39.23**	-32.24 *	47.14	-42.67**	-10.2	12.16
51	[ZCH 8 x (DB 533 x DB 534 F4 IPS 32)]	-32.96*	-19.73	-36.11*	21.94**	10.23	31.41**	1.19	40.13 **	204.29**	-37.39**	3.32	29.05
52	[ZCH 8 x (DB 533 x DB 534 F4 IPS 38)]	8.46	32.06	5.10	41.02**	6.86	27.40**	-16.17	-7.89	100.00**	-30.54**	8.11	35.04
53	[ZCH 8 x (DB 533 x DB 534 F4 IPS 48)]	-10.47	0.12	-20.31	12.22	-9.62	7.74	-44.02**	-36.84 **	37.14	-39.35**	-12.98	8.69
54	[ZCH 8 x (DB 533 x DB 534 F4 IPS 13)]	-22.44	-12.82	-30.62*	45.72**	14.10	36.03**	47.6**	51.97 **	230.00**	-15.08	25.73	57.05*
55	[ZCH 8 x (DB 533 x DB 534 F4 IPS 6)]	1.34	16.52	-7.26	-0.16	-9.22	8.22	-49.37**	-34.21 *	42.86	-40.33**	-6.65	16.6
56	[ZCH 8 x (DB 533 x DB 534 F4 IPS 8)]	-8.75	6.78	-15.01	4.46	-20.29*	-4.97	-4.55	-3.29	110.00**	-43.04**	-16.23	4.63
57	[178-24 x (DB 533 x DB 534 F4 IPS 44)]	20.77	55.61**	23.85	26.45**	10.53	31.77**	-52.68**	-30.26*	51.43	-28.24**	8.19	35.14
58	[178-24 x (DB 533 x DB 534 F4 IPS 62)]	-34.16**	-14.80	-32.19*	18.96*	1.32	20.79*	-44.02**	-23.03	67.14*	-27.93**	11.98	39.86
59	[178-24 x (DB 533 x DB 534 F4 IPS 105)]	6.59	40.69*	11.97	-23.71**	-25.40**	-11.06	-61.6**	-36.84**	37.14	-59.08**	-33	-16.31
60	[178-24 x (DB 533 x DB 534 F4 IPS 26)]	-14.17	15.04	-8.44	-1.87	-18.38*	-2.69	-59.81**	-45.39**	18.57	-38.87**	-5.64	17.86
61	[178-24 x (DB 533 x DB 534 F4 IPS 71)]	1.18	21.09	-3.63	5.46	-9.38	8.03	-12.99	1.32	120.00**	-9.24	32.77	65.83**
62	[178-24 x (DB 533 x DB 534 F4 IPS 30)]	17.64	41.43*	12.56	-0.18	-16.45	-0.39	-26.54*	-21.71	70.00*	-49.96**	-24.5	-5.69

Contd...

Sl.No	Crosses	Lint index (g)			Photosynthetic rate (µmol $CO_2 m^{-2} s^{-1}$)			Stomatal conductance (µmol $m^{-2} s^{-1}$)			Transpiration rate (mmol $H_2O m^{-2} s^{-1}$)		
		H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2
		1	2	3	7	8	9	10	11	12	13	14	15
63	[178-24 x (DB 533 x DB 534 F4 IPS 25)]	-1.81	20.59	-4.02	-5.75	-9.22	8.22	-48.28**	-30.92*	50	-40.08**	-4.56	19.21
64	[178-24 x (DB 533 x DB 534 F4 IPS 49)]	-6.07	17.26	-6.67	18.83*	-2.92	15.74	17.87	23.68	168.57**	-11.42	32.77	65.83**
65	[178-24 x (DB 533 x DB 534 F4 IPS 23)]	-5.79	20.47	-4.12	-7.76	-23.92 **	-9.3	-59.88**	-55.92**	-4.29	-53.35**	-32.38	-15.54
66	[178-24 x (DB 533 x DB 534 F4 IPS 36)]	1.30	30.09	3.53	32.08**	5.99	26.36*	-13.82	-13.82	87.14**	-36.54**	-5.1	18.53
67	[178-24 x (DB 533 x DB 534 F4 IPS 15)]	-8.99	19.24	-5.10	-69.64**	-71.81**	-66.39**	**-90.67****	**-88.16****	**-74.29***	-64.08**	-43.28*	-29.15
68	[178-24 x (DB 533 x DB 534 F4 IPS 1)]	-18.81	8.01	-14.03	3.20	-19.25*	-3.73	-13.04	-14.47	85.71**	-19.04	20.25	50.19*
69	[178-24 x (DB 533 x DB 534 F4 IPS 33)]	-12.21	17.02	-6.87	-8.04	-21.63*	-6.56	-2.33	10.53	140.00**	-34.57**	-4.56	19.21
70	[178-24 x (DB 533 x DB 534 F4 IPS 24)]	-24.27*	1.36	-19.33	13.08	-6.15	11.89	-27.39*	-25	62.86*	-28.4**	7.73	34.56
71	[178-24 x (DB 533 x DB 534 F4 IPS 16)]	-34.3**	-10.36	-28.66	-68.52**	-69.90**	-64.11**	-89.9**	-86.84**	-71.43*	-67.5**	-48.38**	-35.52
72	[178-24 x (DB 533 x DB 534 F4 IPS 52)]	1.51	40.57*	11.87	8.28	-12.30	4.56	22.98	25	171.43**	-15.62	26.12	57.53*
73	[178-24 x (DB 533 x DB 534 F4 IPS 12)]	-4.91	12.33	-10.60	22.16*	-10.58	6.61	-47.68**	-48.03**	12.86	-45.02**	-23.49	-4.44
74	[178-24 x (DB 534 x DB 533 F4 IPS 22)]	1.82	20.84	-3.83	3.19	-26.77**	-12.69	29.41*	15.79	151.43**	-10.65	28.44	60.42**
75	[178-24 x (DB 533 x DB 534 F4 IPS 14)]	-8.90	10.48	-12.07	-38.38**	-48.50**	-38.60**	-34.46**	-23.68	65.71*	-23.19*	16.85	45.95*
76	[178-24 x (DB 533 x DB 534 F4 IPS 34)]	-38.6**	-24.29	-39.74**	26*	-13.10	3.6	19.85	5.26	128.57**	-20.84	12.98	41.12
77	[178-24 x (DB 533 x DB 534 F4 IPS 55)]	-25.89*	-5.92	-25.12	-15.54	-30.48**	-17.13	-54.57**	-52.63**	2.86	-39.92**	-15.61	5.41
78	[178-24 x (DB 533 x DB 534 F4 IPS 17)]	-9.57	15.29	-8.24	-1.15	-20.84 *	-5.63	-2.44	-7.89	100.00**	-19.23	17.16	46.33*
79	[178-24 x (DB 533 x DB 534 F4 IPS 32)]	-30.9*	-10.11	-28.46	-33.83**	-38.67 **	-26.88**	-75.07**	-69.74**	-34.29	**-79.1****	**-67.93****	**-59.94****
80	[178-24 x (DB 533 x DB 534 F4 IPS 38)]	-18.99	7.03	-14.82	8.01	-15.67	0.54	28.37*	19.08	158.57**	**-5.85**	35.63	69.40**
81	[178-24 x (DB 533 x DB 534 F4 IPS 48)]	0.15	21.21	-3.53	38.1**	-0.12	19.07	-45.35**	19.74	160.00**	-6.25	35.55	69.31**
82	[178-24 x (DB 533 x DB 534 F4 IPS 13)]	3.75	26.14	0.39	22.5*	-14.14	2.36	-51.57**	1.32	120.00**	-10.39	33.69	66.99**
83	[178-24 x (DB 533 x DB 534 F4 IPS 6)]	-8.74	13.32	-9.81	-6.14	-22.37**	-7.45	-56.55**	2.63	122.86**	-31.73**	7.57	34.36
84	[178-24 x (DB 533 x DB 534 F4 IPS 8)]	-17.83	3.70	-17.47	22.02*	-16.92*	-0.95	-53.09**	-2.63	111.43**	-14.99	25.97	57.34*
85	[DH 18-31 x (DB 533 x DB 534 F4 IPS 44)]	0.09	30.70	4.02	33.73**	0.50	19.82	-11.18	-11.18	92.86**	-30.79**	-2.4	21.91
86	[DH 18-31 x (DB 533 x DB 534 F4 IPS 62)]	23.46	61.90**	28.85	40.3**	2.31	21.97*	39.42**	25.66	172.86**	-28.84**	3.63	29.44
87	[DH 18-31 x (DB 533 x DB 534 F4 IPS 105)]	12.31	50.18**	19.53	22.77**	5.02	25.20*	-29.78**	-17.76	78.57**	-33.32**	2.7	28.28
88	[DH 18-31 x (DB 533 x DB 534 F4 IPS 26)]	12.26	52.40**	21.30	46.88**	4.17	24.19*	-4.83	-15.79	82.86**	-37.27**	-9.27	13.32
89	[DH 18-31 x (DB 533 x DB 534 F4 IPS 71)]	1.32	13.56	-9.62	24.02**	1.96	21.56*	-17.75	-8.55	98.57**	-34.44**	-0.39	24.42
90	[DH 18-31 x (DB 533 x DB 534 F4 IPS 30)]	9.69	23.55	-1.67	-15.67	-32.55**	-19.59	-31.17**	-30.26*	51.43	-55.32**	-30.06	-12.64
91	[DH 18-31 x (DB 533 x DB 534 F4 IPS 25)]	38.47**	59.56**	26.99	13.24	4.86	25.02*	-40**	-23.03	67.14*	-46.63**	-11.98	9.94
92	[DH 18-31 x (DB 533 x DB 534 F4 IPS 49)]	4.00	21.95	-2.94	33.2**	3.87	23.84*	-13.53	-13.82	87.14**	-37.79**	-3.25	20.85
93	[DH 18-31 x (DB 533 x DB 534 F4 IPS 23)]	12.63	42.42*	13.35	10.67	-3.54	14.99	24.04*	37.50**	198.57**	-23.17*	12.91	41.02
94	[DH 18-31 x (DB 533 x DB 534 F4 IPS 36)]	2.23	29.84	3.34	24.32**	5.58	25.86*	-21.82	-21.05	71.43*	-29.58**	6.72	33.3
95	[DH 18-31 x (DB 533 x DB 534 F4 IPS 15)]	-12.65	13.19	-9.91	-26.29**	-28.10**	-14.29	-32.13**	-13.16	88.57**	-53.37**	-25.43	-6.85

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Sl.No	Crosses	Lint index (g)			Photosynthetic rate (µmol $CO_2 m^{-2} s^{-1}$)			Stomatal conductance (µmol $m^{-2} s^{-1}$)			Transpiration rate (mmol $H_2O m^{-2} s^{-1}$)		
		H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2	H mp	H cc1	Hcc2
		1	2	3	7	8	9	10	11	12	13	14	15
96	[DH 18-31 x (DB 533 x DB 534 F4 IPS 1)]	-1.73	29.35	2.94	6.20	-11.93	4.99	-33.11**	-33.55*	44.29	-54.62**	-31.68	-14.67
97	[DH 18-31 x (DB 533 x DB 534 F4 IPS 33)]	-0.30	24.78	-0.69	7.05	-9.74	7.6	-10.84	-5.26	105.71**	-24.89*	15.69	44.5
98	[DH 18-31 x (DB 533 x DB 534 F4 IPS 24)]	-5.74	18.50	-5.69	21.6*	-0.19	18.99	-20.14	-23.03	67.14*	-36.08**	1.39	26.64
99	[DH 18-31 x (DB 533 x DB 534 F4 IPS 16)]	11.77	43.40*	14.13	-6.84	-11.78	5.18	-46.13**	-33.55 *	44.29	-44.52**	-7.34	15.73
100	[DH 18-31 x (DB 533 x DB 534 F4 IPS 52)]	15.61	50.68**	19.92	38.81**	11.17	32.53**	-4.86	-9.87	95.71**	-32.19**	6.88	33.49
101	[DH 18-31 x (DB 533 x DB 534 F4 IPS 12)]	-11.51	13.32	-9.81	12.30	-0.94	18.1	-34.36**	-15.79	82.86**	-40.34**	-6.49	16.8
102	[DH 18-31 x (DB 534 x DB 533 F4 IPS 22)]	-25.7*	-4.44	-23.95	15.82	-0.42	18.72	-30**	-17.11	80.00**	-33.37**	7.5	34.27
103	[DH 18-31 x (DB 533 x DB 534 F4 IPS 14)]	-14.10	12.70	-10.30	6.23	4.74	24.87*	-42.99**	-17.11	80.00**	-39.66**	2.4	27.9
104	[DH 18-31 x (DB 533 x DB 534 F4 IPS 34)]	-5.69	25.65	0.00	12.45	-5.56	12.59	-34.65**	-23.68	65.71*	-45.1**	-11.98	9.94
105	[DH 18-31 x (DB 533 x DB 534 F4 IPS 55)]	12.99	37.85*	9.72	39.82**	7.43	28.08**	-29.28**	-19.74	74.29*	-31.98**	2.09	27.51
106	[DH 18-31 x (DB 533 x DB 534 F4 IPS 17)]	-19.11	-0.86	-21.10	23.93*	-7.54	10.23	-14.29	-11.18	92.86**	-38.1**	-4.25	19.59
107	[DH 18-31 x (DB 533 x DB 534 F4 IPS 32)]	-16.16	4.93	-16.49	-1.84	-14.38	2.07	-37.53**	-18.42	77.14*	-40.47**	-2.94	21.24
108	[DH 18-31 x (DB 533 x DB 534 F4 IPS 38)]	-13.14	10.48	-12.07	33.18**	-3.30	15.28	-27.1*	-25.66	61.43*	-40.26**	-8.19	14.67
109	[DH 18-31 x (DB 533 x DB 534 F4 IPS 48)]	-14.80	8.63	-13.54	36.34**	-4.99	13.27	26.77*	35.53*	194.29**	-25.89*	10.74	38.32
110	[DH 18-31 x (DB 533 x DB 534 F4 IPS 13)]	5.92	35.64	7.95	57.92**	6.53	27.00**	-5.76	-8.55	98.57**	-38.99**	-6.03	17.37
111	[DH 18-31 x (DB 533 x DB 534 F4 IPS 6)]	-0.71	29.72	3.24	19.83*	-4.05	14.39	-30.5**	-13.82	87.14**	-40.28**	-3.01	21.14
112	[DH 18-31 x (DB 533 x DB 534 F4 IPS 8)]	-14.31	13.69	-9.52	40.83**	-7.82	9.9	26.9*	21.05	162.86**	-25.05*	14.68	43.24
95	**SEm+**	**0.65**	**0.75**		**2.11**	**2.44**		**0.09**	**0.10**		**1.01**	**1.17**	
	CD at 5%	**1.29**	**1.49**		**4.18**	**4.83**		**0.18**	**0.21**		**2.00**	**2.31**	
	CD at 1%	**1.71**	**1.97**		**5.53**	**6.39**		**0.24**	**0.27**		**2.65**	**3.06**	

* Significant at P = 0.05 ** Significant at P = 0.01

Appendix 8

Loading dye (6x)

0.25% Bromophenol blue

40% (w/v) sucrose in water

Stored at 4℃

DNA extraction buffer (Edwards *et al.*, 1991)

Tris HCl (pH 7.5) - 200 mM

NaCl - 250 mM

EDTA - 25 mM

SDS (w/v) - 0.5%

Sarcosine 5%

5 g of sarcosine in 100 ml of sterile distilled water

Lysis buffer

Components	MW	150ml	50ml
0.1 M Tri Hcl (PH 7.5)	157.60	2.36 g	0.79 g
20.0 mM EDTA	372.24	1.12 g	0.37 g
2.0 M Na Cl	58.44	17.53 g	5.84 g
55.0 mM CTAB	364.46	3.0 g	1.0 g

Appendix 9

Fix or Stop Solution

For 1 liter of solution we have to add 100ml of glacial acetic acid + 900 ml of distilled water

Staining Solution

2 gm of silver nitrate + 3 ml of formaldehyde + 2000 ml of distilled water

4% Acrylamide Solution

Dissolve 38 gm of acrylamide + 2 gm of bis- acrylamide (19:1) ratio in 50 ml (final volume 100 ml). Incubate at 65 ℃ for 10-15 minutes until it dissolves completetly.

100 ml 5X TBE + 250 ml of distilled water keep in oven for 2 minutes add 420 gm of urea, dissolve it completely (using stirrer). (Urea should be added with constant stirring)

Filter both of the above solutions separately and make up the final volume.

(Acrylamide and bis-acrylamide solution 100 ml

(Urea + TBE) solution to 900 ml.

3X STR Loading Solution : (for 10 ml)

0.02 ml (20 µl)- 5N NAOH

0.50 ml - Formaldehyde

5 mg BPB

5 mg Xylene cyanlo

Store at room temperature

5X TBE (For 1 Liter)

Add 54 gm of Tris base + 4.6 gm of EDTA + 27.6 gm of boric acid to 1000 ml of distilled water and dissolve completely.

Developing Solution

1500 ml of distilled water

45 gm of sodium carbonate anhydrous

3 ml of formaldehyde

300 µl of sodium thio – sulphate (10 mg/ml)

Solution A (For preparing bindiscilin and repulscilin) (for 10 ml)

500 µl of acetic acid + 9.5 ml of absolute alcohol.

10 % Ammonium persulphate (APS)

1 gm Ammonium persulphate in 10 ml of distilled water

1 gm 100 mg/ml (can be prepared in micro tubes)

Sodium thiosulphate

10 mg/ml

Appendix 10

YEMA medium (Yeast Extract Mannitol medium)

Mannitol - 10g

Yeast extract - 1g

K_2HPO_4 (2%) - 10 ml

$MgSO_4.7H_2O$ (1M) - 0.8 ml

$CaCl_2.2H_2O$ (1M) - 0.4 ml

Agar - 16 gm

Water - 1000 ml

Appendix 11

Plasmid extraction solutions

Sol I: Stocks 1. 1M glucose (stored at 4℃)

2. 0.5 M EDTA

3. 1M Tris-HCl (pH 8.0)

Working solutions: 5 ml of IM glucose + 2ml of 0.5M EDTA + 2.5 ml of IM Tris-HCl were combined and 5 mg/ml lysozyme was added to solution I before use.

Sol II: Stock solutions 1. 10 N NaOH

2. 10% SDS

Working solution: 0.8 ml 10 N NaOH + 4 ml 10% SDS + 35.2 ml of Sterile distilled water.

Sol III: Stock solution (stored at 4℃)

1.5 M Potassium acetate

Working solution: 60 ml of 5M potassium acetate was mixed with 28.5 ml of glacial aceticacid and 11.5 ml of sterile distilled water. pH of the final solution was adjusted to 4.8-5.3 using glacial acetic acid.

Sol IV: 3M sodium acetate

200 µl sodium acetate and 600 µl Isopropanol were added in sequence.

DEVELOPMENT AND EXPLOITATION OF HETEROTIC POOLS OF HIRSUTUM AND BARBADENSE FOR DEVELOPING POTENTIAL INTER SPECIFIC HYBRIDS, MOLECULAR MARKER AND GENETIC TRANSFORMATION STUDY IN COTTON

YANAL ALKUDDSI **2013** **Dr. S. S. PATIL**

Major Advisor

ABSTRACT

Reciprocal selection for improving combining ability was modified to suit cotton and tested. Based on earlier studies DB 533 and DB 534 the selected barbadense elite combiners were crossed and advanced to F_4 generation for creating recombinational variability for combining ability against the hirsutum testers (DH 98-27, ZCH 8, 178-24 and DH 18-31). In line x tester study, DB 533 and DB 534 were compared with barbadense lines in developing productive inter specific hybrids. Both of them recorded positive *gca* effects for seed cotton yield confirming potentiality to form heterotic groups of hirsutum *vs* barbadense cottons. Of the 23 hirsutum testers, four testers mentioned above exhibited positive *gca* values for yield. The potentiality of the heterotic box was also confirmed by comparing these eight bench mark crosses with 49 inter specific crosses and checks. Among the 53 F_5 barbadense lines, DB 533 x DB 534 F_5 IPS 18 showed exceptional superiority for productivity and fiber quality traits.

Among three methods of determining pooled score, weighted percent *gca* approach was efficient in identification of potential combiners. Based on mean and co-efficient of variability for productivity DH 98-27 was found to be efficient tester. Sub grouping the F_4 lines against pairs of hirsutum testers was done. Among the population used four F_4 lines revealed transgressive positive segregation for combining ability against all the four testers and the lines DB 533 x DB 534 F_4 IPS 49 and DB 534 x DB 533 F_4 IPS 22 were selected for developing sub populations against hirsutum testers. With the help of 40 SSR markers, molecular diversity was assessed and positive correlation was found between genetic distance (GD) and seed cotton yield of F_1 and heterosis over checks. In vivo transformation was attempted in hirsutum variety.