6. SUMMARY AND CONCLUSIONS

1. Cotton fiber is the most important natural fiber. The textile industry is largely dependent on cotton not only in India but across the world. To make Indian textile industry globally competitive, improvement of cotton fiber quality (including both fiber length and strength) is essential. Fiber strength of most of the Indian varieties is only about 18-22 g/tex. This value is very low for the production of fine and superfine clothes by modern high speed rotor open end technology to ensure continuous spinning without breaks. Hence, there is a need to develop cotton varieties hybrids with improved fiber strength and change in the staple length so that the ratio of fiber length and strength is close to one. Therefore, there is an urgent need to develop improved cotton varieties hybrids having higher fiber strength, appropriate fiber length, finer fineness, higher yield and other agronomic traits.

Keeping the above in view, the present investigation on “Genetic analysis and molecular tagging of fiber strength and yield contributing traits in cotton (Gossypium hirsutum L.)” was undertaken with the following three objectives:

a. To study the genetics of seed cotton yield, yield components and fiber quality traits especially fiber strength.

b. To study the effect of yield contributing traits on lint yield.

c. To identify molecular markers linked to fiber strength and other economic traits.

2. A full 6 × 6 diallel cross involving six genotypes, P56-4, P56-6, P95-27-2P1, RS810, RS2013 and Bikaneri Narma (BN) was attempted to generate a set of 30 crosses for conducting genetic analyses of fiber and yield related traits. The data on parental genotypes and progenies were analyzed following method I model I of Griffing to study the combining ability of the parents and progenies.

3. In a separate experiment, the two genotypes, P56-4 and RS2013, identified as the most diverse parents based on Mahalanobis D² cluster analysis as well as molecular studies were used for conducting generation mean analysis to study the gene effects for various yield and fiber traits. The F₂ population and F₃
families of the cross P56-4 × RS2013 were also used to study the marker-trait associations.

4. Path coefficient analysis was carried out to study the direct and indirect effects of 13 different traits (plant height, number of monopodia per plant, number of sympodia per plant, lint index, ginning out turn, number of bolls per plant, boll weight, seed index, 2.5% span length, uniformity ratio, fiber strength, micronaire value and fiber elongation) on seed cotton yield. Separate direct and indirect contributions of the same on fiber strength were also worked out.

5. Forty seven (47) Indian genotypes of G. hirsutum, which including 14 released varieties, 14 germplasm lines and 19 advanced breeding lines were used to study the pattern of diversity among Indian cotton genotypes.

6. The analysis of variance for the 15 traits indicated significant differences among the six parental genotypes and 30 hybrids for all the traits under study except fiber maturity. The mean squares due to parent vs. hybrids and F₁ vs. reciprocals were also nonsignificant for fiber maturity. Thus fiber maturity was excluded from further analyses. The mean squares due to F₁s vs reciprocals were significant for six traits including seed cotton yield, lint index, boll weight, seed index and fiber strength suggesting presence of nuclear-cytoplasmic interactions.

7. The values of GCA and SCA variances and the GCA/SCA ratios suggested that both the additive and non-additive genetic components are important in controlling the different traits, although for most of the traits, the non-additive component is predominant. Results reaffirmed the relevance of heterosis breeding in cotton.

8. High broad sense heritability (>80%) was noted for sympodia per plant, seed index, uniformity ratio, fiber strength and fiber elongation. This indicated that these traits are less influenced by environment. Fiber strength, seed index and 2.5% span length showed high narrow sense heritability indicating predominance of additive gene effects, which are fixable and has more relevance in realizing gains during selection.

9. The parents with high general combining ability effects offer opportunities for the development of improved cotton genotypes. Considering the estimates of
GCA effects and the per se performance for different traits, it is suggested that P56-4, P56-6, P95-27-2P1, RS810, RS2013 and Bikaner Narma (BN) may be included in multiple crossing programme for obtaining high yielding good quality varieties of cotton.

10. The direct and reciprocal cross combinations with the highest mean performance differed for most of the traits (Table 5.1). Observations suggested significant nuclear-cytoplasm interactions in the expression of large number of yield and fiber quality related traits in cotton.

11. Dominance and epistatic interactions predominated for most of the traits. Six direct cross F1's and seven reciprocal cross F1's showed significant heterosis for seed cotton yield over the best parent. Out of these, two direct F1's (P56-4 x P56-6 and P95-27-2P1 x RS810) and two reciprocal F1's (RS2013 x RS810 and BN x RS2013) each showed highest heterosis for the seed cotton yield over the respective best parents. The F1's of the direct crosses P56-4 x P56-6 and P95-27-2P1 x RS810 also exhibited significant positive heterosis over the best parent for number of monopodia per plant, lint index, fiber strength and uniformity while the F1 of the reciprocal cross RS810 x RS2013 also showed significant and positive heterosis for sympodia per plant over the best parent. These four cross combinations are recommended for developing commercial hybrids for seed cotton yield and fiber quality traits in future.

12. Diversity analysis of the six parental genotypes used in diallel cross analysis following Mahalanobis D2 analysis based on four fiber traits (fiber strength, 2.5% span length, uniformity ratio and elongation) led to grouping of the six genotypes into three clusters. Three genotypes P95-27-2P1, P56-4 and P56-6 were placed in cluster I, two genotypes (RS2013 and RS810) were grouped in cluster II and the remaining sole genotype BN was grouped in cluster III. Based on this analysis, the P56-4 and RS2013 were identified as the two most diverse genotypes.

13. Six generations including two parental genotypes (P56-4 and RS2013), F1, F2, and the two backcrosses (BC1 and BC2) were used for generation mean analysis. Joint scaling test suggested higher order interactions for monopodia per plant, seed cotton yield, ginning percentage, number of bolls per plant and boll weight
For plant height, sympodia, ginning out turn, boll weight, seed index, 2.5% span length, uniformity ratio and fiber strength the additive effect was absent. These results indicated the preponderance of the dominance and epistatic components in controlling the genetic variation for almost all the traits in cotton.

14. Positive dominance (h) and negative dominance × dominance (l) interaction effects were noticed for plant height, lint index, seed index and 2.5% span length. Ginning percentage, boll weight, uniformity ratio and fiber strength showed negative dominance effects and positive dominance × dominance (l) interactions. This suggested the role of duplicate type of epistasis for these traits.

15. Path coefficient analysis showed a high direct and positive contribution of seed index, 2.5% span length, number of sympodial branches, ginning out of turn, uniformity ratio, fiber elongation, boll weight and boll number towards seed cotton yield. Fiber strength showed positive association with 2.5% span length, uniformity ratio and fiber elongation. The path coefficient analysis showed high direct contribution of 2.5% span length followed by uniformity ratio and fiber elongation towards fiber strength. Results suggested that both the seed cotton yield and fiber strength, the two most economically important traits, may be improved together through direct and indirect selection through component traits.

16. The genetic diversity in a collection of 47 accessions of *G. hirsutum* was studied using a set of 177 SSRs. Only 21.45% (38) of the 177 SSRs successfully detected polymorphism among the accessions. The number of alleles/SSR locus ranged from 2 to 4 with an average of 2.18 alleles/SSR locus. The polymorphism information content (PIC) ranged from 0.04-0.93 with an average of 0.32. Only seven (7) SSRs showed very high (>0.7) PIC values indicating their potential utility for detection of polymorphism among cotton genotypes.

17. The pair-wise genetic similarity values (Jaccard's similarity coefficient) ranged from 0.43 to 0.89 with an average of 0.67. Both dendrogram-based grouping and PCA approach grouped 47 cotton genotypes into three clusters. Cluster I was largest with 42 genotypes. UPGMA hierarchical clustering put two genotypes DHY286 and PKV081 in cluster II, while PCA placed two additional genotypes, namely AKH8828, LANKART57 in cluster II. SBYF428 was identified as an
out-group being represented in cluster III. The clustering pattern fitted poorly to
the similarity matrix with moderate co-phenetic correlation coefficient value
(r=0.73).

18. A minimal set of 10 SSRs could distinguish each of the 47 accessions. Fourteen
(14) markers detected heterozygosity in at least one accession. Of these, seven
markers detected heterozygosity in a majority of accessions. The fact that the
same loci were in heterozygous state across accessions suggested the possible
role of selection in retaining heterozygosity at these loci.

19. Out of 177 SSR primer pairs tested, only four (2.26%) SSRs, namely BNL3537,
BNL3463, BNL3502 and BNL840 detected polymorphism between the two
parents (P56-4 and RS2013), which were used to develop F2/F3 mapping
populations. Out of 50 AFLP primer combinations that were tested with the
above two parental genotypes, 32 (64%) primer combinations gave good
amplification and 28 primer combinations detected polymorphism with an
average of 12.3 polymorphic bands/primer combination. In all, 92 markers
showing polymorphism between the two parental genotypes of the mapping
population were identified.

20. Data of each of the 14 phenotypic traits were separately regressed on each of the
92 polymorphic markers to find out marker-trait associations through simple
regression analysis. A total of 23 markers showing association with eight traits
were identified. Of these, 15 markers were from the parent RS2013 and 8 were
from P56-4. Maximum number of markers (10) was associated with fiber
elongation followed by 2.5% span length (7 markers) and monopodial branches
per plant (4 markers). Only one marker each was associated with boll weight and
seed cotton yield.

21. Using the above 92 markers, step-wise backward multiple regression analyses
was also carried out and a total of 30 markers, 17 belonging to the parent
RS2013 and 13 belonging to P56-4 showed association with at least one of the
14 traits. A maximum of 14 markers were associated with 2.5% span length. The
markers could explain 3% to 41% variance for individual traits. Higher R² values
were obtained for traits like seed index, seed cotton yield, 2.5% span length and
uniformity ratio.
22. A maximum of seven common markers were associated with seed index in both F2 and F3. This is followed by uniformity ratio (6 markers), fiber strength (4 markers), 2.5% span length and micronaire (3 markers each). These markers accounting for a significant proportion of variance for the respective traits are of potential value for marker-assisted breeding. No marker was associated with number of bolls.

23. Majority of the markers involved in marker-trait associations showed association with more than one trait, particularly in multiple regression analyses. Such an association may arise due to pleiotropic effect of the linked QTL for different traits. In the present study, we found significant correlation between various agronomic and fiber quality traits; such associations were also evident in shared associated markers for these traits.

24. The marker-trait association analysis identified one highly reliable SSR marker BNL3502 linked with fiber strength, which can be used in breeding for high fiber strength. Other markers such as E3M7L71, E5M6L34, E5M6L72, E3M6L33, E4M7L82 and E5M6L42, which were consistent and showed associations with different fiber quality traits, may also be relevant for breeding quality cotton varieties. However, these AFLP markers need to be first converted to more readily usable PCR-based markers such as SCARs for use in routine MAS-based breeding programme.