Summary, Conclusions

Summary

This thesis embodies the studies on genetic analysis of different qualitative and quantitative traits, combining ability, heritability and heterotic effects in G.hirsutum L. & G.barbadense L. The experiments were conducted at the Research Farm of Botany Department of Pune University (73°, 51'E longitude, 18°, 31' N latitude and altitude 559m). Nine cultivars of cotton (G. hirsutum L. & G. barbadense L.) viz; Delinter, Sindose-80, Barbadense, Bulgare-539, Termez-14, Red leaf, B-557, Brown fiber and Siokra of diverse genetic origin were crossed in a complete diallele fashion during 2005-2006. The parental lines along with F1 progenies were studied during 2006-2007.

Hayman's diallele analysis and further methods developed by Mather and Jinks were employed for genetic analysis like genetic components of variance D, H1,H2, Fh² and E, Wr/Vr graphs, Broad and narrow sense heritability to investigate the nature of gene action and their interactions for all the traits to identify promising hybrids for selection in the next generation. Griffing's approach considering Eisenharts Method I, Model Mixed-B was used for the study of general (GCA) and specific combining abilities (SCA). Heterosis and heterobeltiosis were studied in F1 generation.

The adequacy of additive – dominance model was tested through regression, ANOVA and correlation analysis. Analysis of variance for Simple Square Lattice Design (SSLD) showed more significant diversity (P< 0.01) among various parents and significant differences allowed genetic analysis by Hayman, Hayman-Jinks and Griffing's method. In F1 generation, it was apparent from the analysis of variance of arrays that significance of Wr/Vr for uniformity ratio, fiber bundle strength, seed index, seed cotton yield and boll weight indicated epistasis effects in them. Significance of Wr+Vr for all traits except boll weight indicating dominance effects in them and significance of b value for all traits except uniformity ratio indicated non-epistasis effects or confirmation of additive-dominance model for mentioned traits. Further it was observed that the assumptions of the Hayman-Jinks model are not fulfilled for some traits such as fiber bundle strength, seed index, seed cotton
yield and boll weight which makes the model partially adequate and non adequate for uniformity. There was existence of adequacy of additive-dominance model for remaining traits that there was no nonallelic interaction and independent gene action for random gene recombination. These results were confirmed with new scaling test of additive-dominance model by means of significant correlation between Wr and Vr.

Referring to genetic parameters in F1, the additive (D) and dominance (H1, H2) components were significant for all the traits, except fiber bundle strength and bolls/plant that for fiber bundle strength (H2) value was nonsignificant. Dominant component (H1) values in most of the traits were greater than additive component (D) indicating dominant effects of alleles in expression of related genes performance. The estimates of heritability, in broad, narrow sense and true sense for the traits were moderate to high indicating possibilities of improvement through selection. Also product of additive genes by dominance genes (F) effects was significant for all traits except for oil content and boll weight that showed frequencies of dominance and recessive genes related to negative and positive value of F for controlling of traits respectively. Average direction of dominance (h) was significant for all traits except staple length and uniformity ratio and proportion of dominant genes (Kd/Kd+Kr) was significant for all traits except bolls/plant this is also confirming dominant effects of genes for controlling these traits. These results are also confirmed by estimation of significant unequal and asymmetric distribution of positive and negative alleles (uv) for all traits except seed cotton yield and boll weight. Significant and more than 1 values of average direction of dominant components (VH/D) for all traits except nonsignificant and less than 1 value for bolls/plant and significant and less than 1 value for boll weight and bolls/plant also enunciate dominance of genes in controlling of these traits.

A contemplation of the Wr/Vr graph plotted for example for oil content and Fr values for F1 oil content, the regression line cuts Wr axis below the origin on negative side which suggests an over-dominance type of gene action. The distribution of array points along the regression line conceive that Barbadense(3) and Termez-14(5) having maximum and positive Fr values and being nearer to the origin, contain maximum dominant genes, while B-557(7) and Siokra (9) being farther and possessing minimum Fr values, had maximum recessive genes. This line intercepting Wr axis below the origin on negative side.
display over-dominance type of gene action for oil content, staple length, uniformity ratio, lint%, seed index, seed cotton yield and plant height and partial dominance type of gene action for rest with cutting of Wr axis above the origin on positive side.

<table>
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<tr>
<th>No</th>
<th>Pr</th>
<th>Wr</th>
<th>Vr</th>
<th>Fr</th>
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<tbody>
<tr>
<td>1</td>
<td>Delinter</td>
<td>2.184</td>
<td>2.498</td>
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<td>2</td>
<td>Sindore-80</td>
<td>1.736</td>
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<td>3</td>
<td>Barbadense</td>
<td>0.068</td>
<td>0.310</td>
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<tr>
<td>4</td>
<td>Bulgare-539</td>
<td>1.791</td>
<td>2.371</td>
<td>0.395</td>
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<tr>
<td>5</td>
<td>Termez-14</td>
<td>-0.592</td>
<td>0.519</td>
<td>0.997</td>
</tr>
<tr>
<td>6</td>
<td>Red leaf</td>
<td>2.291</td>
<td>2.025</td>
<td>0.374</td>
</tr>
<tr>
<td>7</td>
<td>B-557</td>
<td>2.607</td>
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<tr>
<td>8</td>
<td>Brown fiber</td>
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<td>1.972</td>
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<tr>
<td>9</td>
<td>Sokra</td>
<td>2.328</td>
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</table>

Scattering of Parents on Wr/Vr Regression Line and Limiting parabola for Oil Content and Their F₁ Fr Values (F₁ Generation).

Mean squares due to GCA and SCA were highly significant for all the traits in F₁ generation by Griffing method indicating importance of additive and nonadditive effects of genes for genetic controlling of traits. High estimations of MSGCA/MSSCA for all traits and also high narrow-sense heritability for all traits except uniformity ratio (non-adquate trait for additive-dominance model) and lint% by Griffing and Hayman method (differences of heritability between two method belong to interaction of environment and genetic parameters in Griffing method) display importance of additive effects of genes in genetic controlling of more traits. This is also confirming degree of dominance estimates near to 1 or less than 1 for some traits. Further for improvement and for breeding of these traits selection method will have more efficiency. Mean dominance deviation (b₁) was significant for all traits except uniformity ratio suggesting impotence of average heterosis. Dominance deviation of F₁ hybrids versus parents and dominance deviation of parents arrays (b₂) was significant for all traits except bolls/plant displaying impotence of some parent for having more dominance alleles and finally remaining discrepancy (b₃) in the reciprocal sum was significant for all traits except bolls/plant. Reciprocal effect was significant for all traits except earliness, bolls/plant and plant height enunciating significance of average maternal
effects of each parental line (c) or cytoplasmic effects and non-cytoplasmic effects (d) for mentioned traits.

Heterosis of varying magnitude was found in F1 generation. Plant height, seed cotton yield and earliness components showed maximum heterosis, while uniformity ratio and micronaire showed low heterosis and remaining traits showed moderate heterosis. This indicates the higher performance of F1 hybrids for related traits which is normal from physiological point of view.

It is concluded that the additive- dominance model was adequate for majority of the traits and partially adequate for some traits. Majority of the traits were influenced by additive genes in F1 generation. These results are encouraging for practical improvement through selection.

Significant variation for genotypic, general combining ability (GCA) effects, and specific combining ability (SCA) effects ($P < 0.05$) was identified for traits studied indicating potential for improvement through selection. In addition for other agronomic traits, it is suggested that improvements should be made utilizing a backcross approach. Also we can produce and use new hybrids that were the best crosses on the basis of our purpose and 12 studied traits commercially.

5.2 – Conclusions

The additive- dominance model was adequate for majority of the traits and partially adequate for some traits. These results are confirmed with new scaling test of additive-dominance model by means of significant and nonsignificant correlation between Wr and Vr. Majority of the traits were influenced by non-additive gene action in F1 generation. These results are encouraging for practical improvement through backcross method and for remaining which exhibited additive gene action through selection method. Significant variation for genotypic, general combining ability (GCA) effects, specific combining ability (SCA) effects and high narrow sense heritability ($P \leq 0.05$) was identified for traits studied.
indicating potential for improvement through selection on the other hand over-dominance
gene action, low and moderate rate of narrow sense heritability for some traits, suggest that
improvements should be made utilizing a backcross approach. Also we can produce and use
new hybrids that were the best crosses on the basis of our purpose and 12 studied traits
commercially. Plant breeders will be able to use data of mean performance, estimation of
heterosis, heterobeltiosis, combining ability (GCA and SCA) and interaction effects for all
traits while producing new cultivars depending on demand for fiber quality, oil content and
other characteristics in F1 generation annually. For example, traits including oil content,
staple length, uniformity ratio, micronaire, fiber bundle strength, earliness, Lint%, seed
index, seed cotton yield, boll weight, bolls/plant and plant height value of their top F1
hybrids have been increased by 25%, 7.22 mm, 3.4%, 1.08 µg/inch, 8.08 g/tex, -16.72 days,
11.69%, 5.62 g, 20.6 g, 1.96 g, 2.15 and 36.06 cm respectively in comparison with means of
their parents. In seed production programme we can use the best general combiner and the
best specific crosses in the view of their interaction effects.