

CONTENTS

	Page no.
1. INTRODUCTION	1
2. REVIEW OF LITERATURE	6
2.1 Biometrical tools in cotton improvement	7
2.1.1 <i>Diallel analysis in cotton</i>	7
2.2 Generation mean analysis	13
2.3 Heterosis and inbreeding depression	15
2.4 Path analysis	17
2.5 Molecular studies	19
2.5.1 <i>DNA markers in fingerprinting and diversity studies in cotton</i>	21
2.5.2 <i>Molecular markers in linkage studies in cotton</i>	25
2.5.3 <i>Methods of QTL analysis</i>	27
2.5.4 <i>QTL analysis in cotton</i>	29
3. MATERIALS AND METHODS	34
3.1 Biometrical studies on cotton yield and fiber quality traits	34
3.1.1 <i>Plant material</i>	34
3.1.2 <i>Experimental design and layout</i>	35
3.1.3 <i>Recording of data</i>	36
3.1.4 <i>Statistical analysis</i>	37
3.1.4.1. Combining ability analysis	37
3.1.4.2. Estimation of heterosis in experimental crosses	40
3.1.4.3. Estimation of gene effects through generation mean analysis	41
(a) Calculation of generation means and variances	41
(b) Scaling tests	42
(c) Estimation of gene effects and interactions	42
(i) Estimation of gene effects and interactions according to six parameter model	42
(ii) Joint scaling test	43
3.1.5. <i>Path coefficient analysis</i>	44
3.2. Application of molecular markers for genetic diversity analysis and identification of markers linked to fiber strength and other economic traits	45
3.2.1 <i>Diversity studies using SSR markers</i>	45
3.2.1.1. Genetic materials	45
3.2.1.2. DNA extraction, purification and quantification	45
3.2.1.3. DNA amplification and SSR analysis	47
3.2.1.4. Diversity studies using SSR markers	48
3.2.2 <i>Marker-trait association using AFLP and SSR markers</i>	48
3.2.2.1. Plant Material	48
3.2.2.2 Phenotyping of F ₂ population	49
3.2.2.3 Genotyping of F ₂ population	49
(a) AFLP analysis	49
(b) SSR analysis	53
3.2.2.4 Marker association with quantitative traits	53

CONTENTS

	Page no.
1. INTRODUCTION	1
2. REVIEW OF LITERATURE	6
2.1 Biometrical tools in cotton improvement	7
2.1.1 <i>Diallel analysis in cotton</i>	7
2.2 Generation mean analysis	13
2.3 Heterosis and inbreeding depression	15
2.4 Path analysis	17
2.5 Molecular studies	19
2.5.1 <i>DNA markers in fingerprinting and diversity studies in cotton</i>	21
2.5.2 <i>Molecular markers in linkage studies in cotton</i>	25
2.5.3 <i>Methods of QTL analysis</i>	27
2.5.4 <i>QTL analysis in cotton</i>	29
3. MATERIALS AND METHODS	34
3.1 Biometrical studies on cotton yield and fiber quality traits	34
3.1.1 <i>Plant material</i>	34
3.1.2 <i>Experimental design and layout</i>	35
3.1.3 <i>Recording of data</i>	36
3.1.4 <i>Statistical analysis</i>	37
3.1.4.1. Combining ability analysis	37
3.1.4.2. Estimation of heterosis in experimental crosses	40
3.1.4.3. Estimation of gene effects through generation mean analysis	41
(a) Calculation of generation means and variances	41
(b) Scaling tests	42
(c) Estimation of gene effects and interactions	42
(i) Estimation of gene effects and interactions according to six parameter model	42
(ii) Joint scaling test	43
3.1.5. <i>Path coefficient analysis</i>	44
3.2. Application of molecular markers for genetic diversity analysis and identification of markers linked to fiber strength and other economic traits	45
3.2.1 <i>Diversity studies using SSR markers</i>	45
3.2.1.1. Genetic materials	45
3.2.1.2. DNA extraction, purification and quantification	45
3.2.1.3. DNA amplification and SSR analysis	47
3.2.1.4. Diversity studies using SSR markers	48
3.2.2 <i>Marker-trait association using AFLP and SSR markers</i>	48
3.2.2.1. Plant Material	48
3.2.2.2 Phenotyping of F ₂ population	49
3.2.2.3 Genotyping of F ₂ population	49
(a) AFLP analysis	49
(b) SSR analysis	53
3.2.2.4 Marker association with quantitative traits	53

	Page no.
4. RESULTS	55
4.1. Biometrical studies involving seed cotton yield and fiber quality traits	55
4.1.1. <i>Diallel analysis</i>	55
4.1.1.1. Analysis of variance	55
4.1.1.2. Genetic components of variance	57
4.1.1.3. GCA and SCA effects	59
4.1.1.4. Heterosis	67
4.1.2. <i>Generation mean analysis</i>	78
4.1.2.1. Analysis of generation means	80
4.1.2.2. Scaling tests and estimates of gene effects and interactions	82
4.1.2.3. Joint scaling tests and estimates of gene effects and interactions	82
4.1.3. <i>Path coefficient analysis</i>	86
4.1.3.1. Phenotypic correlation coefficient analyses involving seed cotton yield and fiber quality contributing traits	86
4.1.3.2. Phenotypic path coefficient analysis	86
4.2. Molecular marker studies	90
4.2.1. <i>Diversity studies using SSRs and fiber quality traits</i>	90
4.2.1.1. Diversity studies using SSRs	90
4.2.1.2. Diversity analysis using fiber quality traits	93
4.2.2. <i>Identification of QTL using AFLP and SSR markers</i>	94
4.2.2.1. AFLP and SSR analysis	94
4.2.2.2. Marker-trait Associations	96
4.2.2.3. Single marker regression analysis	96
4.2.2.4. Multiple Regression analysis	98
5. DISCUSSION	100
5.1 Variability, nature and magnitude of gene effects in cotton	101
5.2 Combining ability analyses and choice of parents	104
5.3 Heterosis and its utilization in cotton	107
5.4 Character association analysis	107
5.5 Diversity analysis using SSR markers in cotton	109
5.6 Marker-trait association analysis	112
6. SUMMARY AND CONCLUSIONS	119
7. REFERENCES	125
ANNEXURE A: Details of SSR primers used for diversity analysis with sequences, size and repeat motif	i
ANNEXURE B: Per cent total SS explained by various sources in ANOVA for cotton	vii
ANNEXURE C: Fitting of three parameter model by joint scaling test for cotton yield and quality contributing traits	viii
ANNEXURE D: Jacard's similarity coefficients among the 47 cotton genotypes	ix
ANNEXURE E: List of publications	xii