

LEGENDS OF FIGURES

		After page no.
Fig. 1	Phenotypes of the plants of parental lines used in 6 × 6 diallel analysis	35
Fig. 2	Phenotypes of the plants of the parental lines P56-4 and RS2013 and the derived F ₁ used for developing mapping population	35
Fig. 3	Gel picture showing restriction endonuclease digested DNA of the parental genotypes of the cross P56-4 × RS2013	49
Fig. 4	Phenotypic path analysis of seed cotton yield and its contributing traits in cotton (<i>Gossypium hirsutum</i> L.)	86
Fig. 5	Phenotypic path analysis of fiber strength and its contributing traits in cotton (<i>Gossypium hirsutum</i> L.)	90
Fig. 6	DNA amplification profile of SSR BNL3650 in 48 cotton genotypes	90
Fig. 7	Diagrammatic presentation of DNA fingerprints using 10 most informative SSR markers	92
Fig. 8	Dendrogram of cotton (<i>G. hirsutum</i> L.) accessions derived using UPGMA cluster analysis	92
Fig. 9	Two dimensional (a) and 3 dimensional (b) projections of principal components of the cotton (<i>G. hirsutum</i> L.) genotypes using SSR data	92
Fig. 10	D ² cluster analysis based on fiber quality traits of six parental genotypes used in diallel analysis in cotton	93
Fig. 11	AFLP Polymorphism between P56-4 and RS2013 using MCTG+EACA primer combination	94
Fig. 12	Detection of AFLP polymorphism between P56-4 (odd number lane) and RS2013 (even number lane) with 15 primer combinations using ABI377	94
Fig. 13	AFLP genotyping of P56-4 (lane 1) and RS2013 (lane 2) and 30 F ₂ individuals (lanes 3-32) with multiplexing primers [MCAC+(EACC+EACT+EAGG)] using ABI377	94
Fig. 14	DNA amplification profile in cotton genotypes P56-4 (odd number lane) and RS2013 (even number lane) using 12 SSRs	94
Fig. 15	A representative segregation pattern of SSR BNL3563 in 48 individuals of the F ₂ population derived from the cross P56-4 × RS2013	94