

ABSTRACT

Gossypium hirsutum L. is main source of natural fiber in the world. High demand for textile products in the world resulted in high-speed spinning technologies; high production of upland cotton and demands high fiber quality. Narrow genetic base hinders improvement of cotton cultivars via conventional breeding. Therefore, it is necessary to assess genetic variation along with identification of strongly linked markers to quantitative trait loci (QTL) for to yield, yield related and quality traits to face high speed spinning technologies without breaking fiber. For this purpose, 100 cotton genotypes of *G. hirsutum* were studied to find out genetic diversity and relationship among the traits along with Genome wide association study. The dispersion of the genotypes on score plot indicated differences among genotypes. The 100 genotype of *G. hirsutum* were clustered into six groups. A strong positive relation was found among the yield, yield related traits and quality traits. All traits have inheritance value more than 80% except lint index. The "A" sub-genome carried 127 QTLs and "D" sub-genome 97 QTLs. Out of total, 72 QTLs were found for quality traits, 152 for yield and yield related traits. Maximum loci were located on the chromosome A08 (c08). Chromosome A07 (c07) and D01 (c15) carried QTL only for fineness of fiber and boll size respectively. SA02_9245903 exhibited highest value for R^2 while lowest R^2 value was recorded for SA07_35699558. It is concluded that cotton germplasm under study have considerable useful genetic variation. Identification of valuable genetic loci would help in marker-assisted breeding and transfer of genes in order to improve cotton genotypes in Pakistan.

Keywords: *Gossypium hirsutum* L., genetic diversity, association mapping, yield-related traits, fiber quality.