

## Mapping of QTL for Fiber Length Using Interspecific *Gossypium hirsutum* × *G. barbadense* F<sub>2</sub> Population

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Cotton occupies a pre-eminent place among cash crops as it guides the destiny of a large section of the farming community as well as that of a flourishing textile industry. As the yarn manufacturing industry has undergone a technological revolution, more emphasis is given to quality of the raw material in order to overcome high speed spinning. Though different yarn manufacturing technologies have various requirements in terms of basic fiber properties, fiber length has a premier role in deciding the spinning efficiency. So in the present study, we have focused on to identify the genomic regions associated with fiber length. An interspecific F<sub>2</sub> population generated by crossing two diverse parents KC2 (*Gossypium hirsutum* L.) possessing high drought enduring capacity and jassid resistance and Suvin (*G. barbadense* L.) noted for its exemplary fiber properties was utilized for mapping. Parents used in the present study revealed a polymorphism rate of 47.86 percent and 30.67 percent for SSR and SRAP markers respectively. Markers, which revealed difference between the parents, were used to establish the segregation pattern of F<sub>2</sub> individuals showing extremely high and low fiber length. Utilizing the data on fiber length segregation, a basic linkage map was constructed which included 173 marker loci distributed over 21 groups spanning 2264 cM of genome with an inter-marker distance of 15 cM. Based on the present map, nine QTL regions distributed over seven linkage groups were identified for fiber length. Among them two were found to be major QTLs and the association of some of the markers to fiber length shows colinearity with the earlier studies indicating the stable association of these markers to the trait the across populations.