

**MAPPING OF COTTON FIBER LENGTH AND STRENGTH
QUANTITATIVE TRAIT LOCI USING MICRO SATELLITES**

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Abstract

An abundance of new sources of microsatellites identified within the cotton genome are making possible the construction of a linkage map containing a significant proportion of these convenient markers. An F₂ population consisting of 98 plants derived from the cross of *Gossypium hirsutum* cv Tamcot SP37 by *G. barbadense* cv Pima S-7 were phenotyped for fiber length and strength. The F₂ distribution of both traits indicated polygenic inheritance. A simple method of genotyping using a subset of the population has been adapted for identification of markers. This population subset contained plants selected from the extremes for both fiber length and strength characteristics. Two electrophoresis systems, high resolution agarose and acrylamide gel, were modified to facilitate visualization of markers in an inexpensive, rapid, and less laborious fashion. Seventy-five microsatellite loci were assayed over the population subset. Based on the single-point analysis, microsatellite loci JESPR-U21, JESPR-U92, CM13, CM30, and CM68B are contributing 11.7%, 11.7%, 14.3%, 16%, and 12.5% to fiber length, respectively. Similarly, for fiber strength, markers BNL3279, CM30, CM140, JESPR-D14, JESPR-G6, JESPR-G31, and JESPR-U30 explained 20.3%, 16%, 20.6%, 8%, 12.5%, 11.7%, and 17.7% of total variation, respectively. Some of the identified markers have been located on chromosomes 3, 7, 20, and 25 using aneuploid stocks. Presently, validation of these markers over the entire population and incorporation of additional microsatellites is being pursued for identification of major QTLs using interval mapping.