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A MOLECULAR LINKAGE MAP AND QUANTITATIVE TRAIT LOCUS ANALYSIS BASED ON A RECOMBINANT INBRED LINE POPULATION OF COTTON

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Abstract

A mapping population comprising of 98 recombinant inbred lines (RIL) was developed from a cross between TM-1, the genetic standard of upland cotton, and NM 24016, an Acala breeding line with substantial germplasm introgression from Pima cotton. The objectives of the study were to construct a molecular map using various DNA marker systems and to identify quantitative trait loci (QTL) of agronomic importance. The RIL lines, together with their parents were field tested in replicated trials in Las Cruces, NM and Maricopa, AZ in 2001 and 2002. Boll size, lint percentage, lint yield, and fiber quality traits were measured. A linkage map comprising of 23 linkage groups with 177 DNA markers was constructed. The majority of the markers were AFLP and SSR. Included were also other markers such as RFLP, RAPD, SRAP and STS. More than 60 QTL were identified for lint yield (16), boll size (5), plant height (3), fiber length (7), strength (13), elongation (9), and fineness (14) based on average data from the two locations in two years.