

A recombinant inbred population of cotton for QTL and DNA marker association

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ABSTRACT

We grew 192 recombinant inbred (RI) lines of cotton, *Gossypium hirsutum* L., developed from a cross of HS26 x MARCABUCA8US-1-88 and measured yield traits and fiber properties in multiple environments. We also analyzed the lines using Amplified Fragment Length Polymorphisms (AFLP) markers. This paper describes variation for yield and fiber traits and associations of specific traits with AFLP markers. RI lines were grown in replicated plots for two years in Mississippi. Sufficient variation was measured for each trait to indicate that these RI lines represented a good data set. Minimum and maximum values for each trait were as follows: Seed cotton yield, 1128 and 6002 kg per ha; lint yield, 386 and 2119 kg per ha; lint percentage, 31.72 and 41.37; boll weight, 3.97 and 6.67 g; micronaire, 3.45 and 5.10; fiber elongation, 4.75 and 9.75 percent; fiber T_1 strength on stelometer, 162 and 263 kNm per Kg; 50% span length, 12.7 and 15.5 mm; 2.5% span length, 26.41 and 31.24 mm. Additional measurements were made using an arealometer instrument that measures the resistance to air flow of a plug of cotton fibers at two air pressures, A (low) and AH (high). Minimum and maximum arealometer fiber measurements were as follows: A, 378 and 549; AH, 396 and 595 square mm air flow per cubic

mm of fiber. From these two arealometer measurements several parameters are calculated. Minimum and maximum calculated values were: D (difference between A and AH and relates to fiber shape and fineness with higher D values being more ribbon like and more immature), 3 and 46; I (immaturity ratio), 1.10 and 2.06; maturity, 71.50 and 108.00%; P (perimeter), 32.50 and 58.26 microns; WF (weight fineness is mass per unit of length), 2.62 and 5.34 micrograms per 25.4 mm of fiber length; and WT (wall thickness), 2.13 and 3.68 microns. All traits segregated normally based upon skewness and kurtosis statistics. From measurements comparing the mean of all RI lines with mid-parent values significant negative additive x additive epistasis was indicated for seed and lint cotton yield, lint percentage, micronaire, T_1 strength, weight fineness, and wall thickness. Significant positive additive x additive epistasis was indicated for boll size and arealometer measurements AH and A. Significant genotype by environment interaction was detected for all agronomic and fiber traits. The classical statistical analyses suggested that the use of epistasis and G x E genetic models and corresponding methods should be appropriate to detect associations between AFLP markers and Quantitative Trait Loci (QTL). These results should be of value for marker-assisted selection.