ASSOCIATION OF SSR MARKERS WITH IMPORTANT FIBER TRAITS IN UPLAND COTTON

Sukumar Saha **USDA-ARS, Crop Science Research Laboratory** Mississippi State, MS Sharof S. Egamberdiev **Institute of Genetics and Plants Experimental Biology** Tashkent, Uzbekistan J. Wu South Dakota State University Brookings, SD Johnie N. Jenkins Jack C. McCarty **Dewayne Deng USDA-ARS, Crop Science Research Laboratory** Mississippi State, MS Ibrokhim Abdurakhmonov **Institute of Genetics and Plants Experimental Biology** Tashkent, Uzbekistan

<u>Abstract</u>

The objectives of this research are to: 1) report on the diversity in agronomic and fiber traits of the selected cotton germplasm, released by the public breeders and private industries, 2) detect the genetic diversity among these lines using SSR markers and 3) identify the SSR markers association with agronomic and fiber traits. The experiments were conducted with 43 improved Upland cotton lines including one Acala line for two years in two locations (four environments) at Mississippi State, MS. We detected genetic diversity following the standard PCR method using 182 SSR primer pairs in ABI3100 system. Both TM-1 (Gossypium hirsutum L.) and Pima 3-79 (G. barbadense) lines were used in the molecular analyses as the genetic standard lines. Seventy four percent of the selected primer pairs covering whole genome produced polymorphic amplicons. Mean values for agronomic and fiber traits over four environments were used to detect the coefficients of correlations between SSR markers and quantitative traits. SSR markers, significantly associated (α =0.05) with quantitative traits, were used in multiple linear regression analyses for all traits. Considering that some SSR markers may be correlated, the stepwise regression analyses and the cumulative coefficients of determination were used. Results revealed a wide range of phenotypic variation in fiber traits among these lines. The lint yield ranges from 183 to 999 kg/ha. The fiber strength and micronaire varies among these lines from 26 to 37g/tex and 3.8 mic to 5.0 mic respectively. Seventy four percent primer pairs were polymorphic and several markers were found to be strongly associated with some of the traits. The genetic diversity at the molecular level ranges from 0.07 to 0.23 among Gossypium hirsutum lines and 0.44 to 0.49 at the interspecific level. Multiple linear regression models with five markers for each trait explained 68% to 89% of the variability for individual trait. The Neighbor-Joining (NJ) analysis using SSR markers revealed the presence of six broad groups among these lines. Some of the markers was associated with more than one traits. For example, DPL0618 194 allele was associated with the highest and DPL0618 191 was associated with the lowest Upper Half Mean length and Uniformity index. The marker association analysis via stepwise regression analysis seems to be useful and concordant with the field data.