GENETIC ANALYSIS OF AFLP MARKERS ASSOCIATED WITH SEED QUALITY TRAITS IN UPLAND COTTON (*GOSSYPIUM HIRSUTUM*)

A. Badigannavar
G. Myers
LSU Agcenter
Baton Rouge, LA

Abstract

Cotton (*G. hirsutum*) is primarily grown for fiber production yet it is also the world's sixth largest source of vegetable oil and is an inexpensive source of seed oil and protein. Constituting nearly half of a seed’s weight, the cotton meal contains 23% of high biological-value protein. The present study explores the extent of genetic variability present in elite upland genotypes for several seed quality traits, so as to facilitate their selection in introgression breeding. A set of 75 upland cotton genotypes from different production regions were selected and analyzed for seed quality traits (seed oil, protein and fiber content). Based on the 234 polymorphic AFLP loci, the upland genotypes showed moderate genetic diversity. Population structure revealed that five subpopulations existed and was consistent with their geographical origin. There were a significant negative correlations between fiber content with oil and protein percentage and between protein and oil percentages. In order to reduce false positives that may arise in quantitative trait loci (QTL), identification, we utilized mixed model analysis incorporating both population structure and kinship estimates. The model identified 40 markers that were significantly associated with seed protein, oil and fiber content. In order to further validate markers selected from mixed models, multiple regression using 52 mixed-multiple regression models was performed. The mixed-multiple regression models confirmed the association of AFLP alleles E4M3_440, E4M3_200 and E5M7_195 markers with seed protein, oil, and fiber content, respectively. The mixed models enhanced the efficiency and robustness by reducing false positives and making the data more reliable.