2006 Beltwide Cotton Conferences, San Antonio, Texas - January 3 - 6, 2006

ASSOCIATION ANALYSIS OF MORPHOLOGICAL CHARACTERS WITH MOLECULAR MARKERS IN A TM-1 X 3-79 RI POPULATION GROWN IN THREE DIVERSE ENVIRONMENTS

Roy Cantrell
Cotton Incorporated
Cary, NC
Steven Hoffman, Russell Kohel, Jaemin Cho and Zhanyou Xu
USDA-ARS
College Station, TX
C. Wayne Smith and Alan Pepper
Texas A&M University
College Station, TX
John Z. Yu
USDA-ARS
College Station, TX
Mauricio Ulloa
USDA-ARS, WICS Res. Unit, Cotton Enhancement Program
Shafter, CA

Abstract

An element lacking in *Gossypium* is the availability of large RIL populations that can be shared among the cotton research community. For integrated mapping of the cotton genome, we developed and used such a permanent population of 191 RILs derived by single seed decent from the cross TM-1 x 3-79, the genetic standards for *G. hirsutum* and *G. barbadense*, respectively. The TM-1 x 3-79 RIL population exhibited a great range of the variability seen throughout the *Gossypium* genus offering an opportunity to locate or map important morphological traits and fiber properties. Plant height, total node count, canopy density and number of vegetative branches were analyzed with SAS 8.0 Proc Mixed (The SAS Institute, Cary NC) over all three locations, allowing us to estimate the covariance associated with the RILs, the Environment x RIL interaction and the Environmental effect on each of the morphological traits. Plant height, number of vegetative branches, seed cotton yield, and number of bolls all exhibited the heritability that imply their usefulness for QTL mapping studies in this population. Stem diameters and the number of vegetative branches were significantly higher in the Burleson County than the Brazos county location indicating much greater allocation of biomass to vegetative growth as seen in the reduced lint yield at the Burleson county location. There were a wide variety of leaf shapes and morphologies. Flower morphology was completely consistent over all three locations with results were consistent with those seen in the past with this RIL population. We are now associating these morphological characters with SSR molecular markers that have been mapped on this TM-1 x 3-79 RIL population. Cluster analysis with both newly developed SSRs and those publicly available markers was conducted on Nei's genetic distance two main sub clusters do not have any apparent relation to simple % contribution from each parent.