HIGH-DENSITY SNP-BASED MAPPING AND MULTI-TRAIT QTL ANALYSIS **OF ISOGENIC CHROMOSOME- SPECIFIC CS-B17 RILS** IN UPLAND COTTON (GOSSYPIUM HIRSUTUM L.) Yu-Ming Lin Luis M. De Santiago **Texas A&M University College Station**, TX Sukumar Saha **USDA-ARS** Mississippi State, MS **Robert Vaughn** Texas A&M AgriLife Research **College Station, TX** Johnie N. Jenkins Jack C. McCarty USDA-ARS Mississippi State, MS **Mauricio Ulloa USDA-ARS** Lubbock, TX **Russell Haves USDA-ARS** Mississippi State, MS B. Todd Campbell **USDA-ARS** Florence, SC David M. Stelly Texas A&M University

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<u>Abstract</u>

We have examined the feasibility of linkage mapping and agronomic/fiber trait quantitative locus detection and localization using a set of ~50 chromosome-specific CS-B17 RILs, each theoretically homozygous for a unique array of chromosome-17 segments from the two homozygous lines -- *G. hirsutum* line 'TM-1' and *G. barbadense* line '3– 79'. TM-1 was crossed with an isogenic BC5Sn inbred derivative CS-B17 that is homozygous for chromosome-17 Pima 3-79 in a TM-1-like genetic background. The F1 was iteratively selfed to create a population of 50 RILs. The RILs were phenotyped for 13 traits across two years; at four locations using RCBD. Initial efforts aimed at quantitative analysis with low numbers of markers proved difficult, so we ultimately resorted to using the CottonSNP63K Array. This yielded ~500 high quality SNP markers across chromosome 17 for the genotyping, linkage mapping and QTL analysis of the traits. Several programs were used for linkage mapping, JoinMap, and R – "OneMap" package. "qtl" package in R was mainly applied for QTL mapping analysis and QTL cartographer were also used for comparison. A condensed bin map from the 500 SNP markers was also tested with the phenotype datasets across four distinct locations. Zero to two QTLs were detected in chromosome-17 for various fiber quality traits. The results underscore the value of isogenic chromosome substitution lines and chromosome-specific RILs to interspecific cotton breeding, genetic diversification and genetic improvement of cotton.