

**COMPREHENSIVE META ANALYSIS OF QTLS AND DEVELOPMENT OF
A QTL DATABASE IN COTTON****J. Said****M. Song****J. Zhang****New Mexico State University****Las Cruces, NM****J. Knapka****University of Texas****El Paso, TX****H. Wang****Z. Lin****Xi. Zhang****Huazhong Agricultural University****Wuhan, Hubei, China****D. Fang****USDA-ARS Cotton Fiber Bioscience Research Unit****New Orleans, LA****Abstract**

Quantitative trait loci (QTL) studies in cotton, over the past 16 years have been done using a variety of mapping populations, markers, and trait types. Since QTL are a simple marker and trait association, false positive QTL exist. A QTL meta-analysis of previously identified QTL provides a means of reducing false positives and finding consensus regions of the genome including QTL clusters and hotspots. In this study, a QTL cluster is defined as a chromosomal region (usually 25 cM) where 4 or more QTL for different quantitative traits are located on the genome, while a QTL hotspot is a region with 4 or more QTL for the same trait. Previous meta-analysis done in cotton using fewer QTL quickly became obsolete as a number of succeeding QTL studies is published on a monthly basis. A comprehensive analysis of QTL cluster and hotspot regions over the genomes of both Upland and interspecific Upland x Pima was done using 2,134 QTL over 66 trait types. This meta-analysis provides the first meta-analysis comparison between Upland and interspecific Upland x Pima illustrating similarities and differences in QTL placement in both populations. In order to keep this study current and provide a tool for the cotton community, the CottonQTLdb database was developed as a QTL analysis, comparison, and visualization tool. QTL from the meta-analysis and succeeding QTL studies were added to the database for a current total of 2,274 QTLs. For each QTL, the database contains LOD scores, phenotypic variance explained, associated markers, chromosomal positions, and confidence intervals. QTL data selected by the user can be visualized on chromosomes and downloaded as publication ready images. QTL trait descriptions are provided to the user for each trait type as well as all data sources. The database will be updated by the curators and will also accept QTL submissions from the cotton community to remain current. The database is online and accessible through www.cottonqtladb.org.