

1891 Comparative Analysis of Gene Expression in Developing Fibers between Upland and Sea Island Cottons

Mr. Mark Goebel , Texas A&M University, College Station, TX
Dr. Magdy S. Alabady , Texas Tech University, Lubbock, TX
Dr. C. Wayne Smith , Texas A&M University, College Station, TX
Dr. Thea Wilkins , Texas Tech University, Lubbock, TX
Dr. Hong-Bin Zhang , Texas A&M University, College Station, TX

Upland and Sea Island cottons represent two major cultivated cotton species that significantly differ in fiber yield and quality. It has long been a major goal of cotton breeding to combine the desirable fiber traits from the two species into cultivars. The goals of this project are to advance the molecular knowledge of cotton fiber development and develop a genomics-assisted system to help effectively manipulate the genes involved in fiber development for cotton breeding. As the initial step of this effort, we are analyzing the expression of genes in the 10-dpa fibers collected from four cultivars of the species, the parents of three RIL populations for fiber QTL mapping, cloning and characterization, using the cotton fiber gene-specific long oligo arrays newly developed by the Wilkins Laboratory at Texas Tech University. The results will provide the molecular basis and tools to decipher the molecular mechanism of fiber development and to design the genomics-assisted system to effectively manipulate desirable fiber genes from both Upland and Sea Island cottons for high fiber yield and quality cultivar breeding.