TISSUE SPECIFIC TRANSCRIPTOME CHANGES DURING WATER DEFICIT STRESS IN TETRAPLOID COTTON

Megan Bowman
USDA-ARS
Florence, SC
Wonkeun Park
Clemson University
Florence, SC
Philip J. Bauer
USDA-ARS
Florence, SC
Joshua A. Udall
Justin T. Page
Joshua Raney
Brigham Young University
Provo, UT
Brian Scheffler
USDA-ARS
Stoneville, MS
B. Todd Campbell
USDA-ARS
Florence, SC

Abstract

As decreasing water resources continue to be a concern for cotton production, it is essential to develop new molecular tools in an effort to understand the regulation of water deficit stress, and subsequently apply these tools towards the improvement of available cotton germplasm resources. Towards that end, we have used RNA-seq analysis to identify global transcriptome changes occurring in either the root or leaf tissue of field grown upland cotton (*Gossypium hirsutum*). The identification of tissue specific transcripts regulated under drought stress is a major step towards candidate gene evaluation and the development of molecular tools in cotton breeding for drought tolerance.