# IDENTIFICATION OF DROUGHT TOLERANT GERMPLASM AND QTLS IN A BACKCROSS INBRED POPULATION OF COTTON

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## Abstract

With the advent of molecular markers, new methods for improving drought stress have been developed and it has been discovered that drought tolerance is a typically quantitative trait, controlled by multiple genetic loci, also known as quantitative trait loci (QTLs). The challenge now facing modern cotton breeders is to combine the most effective QTLs with elite cultivars, using effective selection methods to identify genotypes with the best performance in dry environments. Our project was initiated to use QTL analysis as a tool to identify genetic loci that confer drought resistance in cotton. A backcross inbred line (BIL) population was developed from a cross between Pima cotton as the non-recurrent parent and Upland cotton as the recurrent parent and followed by two generations of backcrossing and several generations of selfing. The BIL population of 146 lines together with their parents have been tested in two environments in 2008 and 2009 under normal and reduced irrigation conditions. Approximately 500 DNA markers have been developed for the population. Markers identified as drought responsive genes using microarray analysis are under development. This presentation will report the progress in identifying drought tolerant germplasm and drought responsive QTLs in the BIL population toward to the development of new drought resistant cultivars and a better understanding of mechanisms of drought tolerance in cotton.