

**IDENTIFICATION OF COTTON GERMPLASM AND MOLECULAR MARKERS
FOR SALT TOLERANCE****Rashmi Sharma Tiwari****Sanjay Bajaj****Jinfa Zhang****Department of Plant and Environmental Sciences, New Mexico State University****Las Cruces, NM****Michael D. Gill****New Mexico Department of Agriculture****Las Cruces, NM****James Mac Stewart****University of Arkansas****Fayetteville, AR****Sidney E. Hughs****USDA-ARS Southwestern Cotton Ginning Research Laboratory****Mesilla Park, NM****Don C. Jones****Cotton Incorporated****Cary, NC****Abstract**

Salinity imposes major abiotic stress on plants worldwide. About 20-40 % of world agriculture land and 50 % of irrigated land is affected by salt. Although cotton is classified as moderately tolerant to salt with a threshold of 7.7 dS m⁻¹, its growth is adversely affected by salinity at all stages of the plant's life cycle. Therefore, it is important to identify salt-tolerant genotypes in cotton germplasm for further improvement in cotton production under salinity conditions. The objectives of this study were to identify salt-tolerant genotypes from a backcross inbred line (BIL) population developed from Upland x Pima and to identify molecular markers associated with salt tolerance for marker-assisted selection. 146 BC2F4- derived BILs were developed using SG 747 (*Gossypium hirsutum*) as a recurrent parent and Pima S-6 (*G. barbadense*) as a donor parent. The 146 BILs were used for phenotypic screening at seed germination and seedling stage with 250 mM NaCl. Molecular markers were analyzed for linkage mapping and combined with phenotypic data to identify quantitative trait loci (QTL). *G. barbadense* (Pima S-6) was tolerant at seed germination with 87.75% of control germination with water, whereas *G. hirsutum* (SG 747) was sensitive with 38.52% of its control germination. Plant height, leaf number, shoot and root fresh and dry weight were significantly decreased by salinity. This phenotypic study allowed selecting BILs with significantly better salt tolerant. Three QTLs on one linkage group were identified for leaf number and plant height, and one QTL for plant height was identified on another linkage group. More DNA markers will be added to the linkage map for better genome coverage and identification of more QTLs for salt tolerance.