

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

Salinity is a one of the major problems encountered for sustainable agriculture in arid and semi-arid areas including southwest of the United States. Although cotton is the second most salt tolerant herbaceous crop with 7.7 dS m^{-1} threshold, its growth is adversely affected by salinity at all stages of the plant's life cycle. Therefore, in order to increase crop yield in saline conditions, it is crucial to identify salt-tolerant genotypes for cotton breeding and production. The objectives of this study were to identify salt-tolerant genotypes from backcross inbred lines (BILs) developed from Upland x Pima and to identify molecular markers associated with salt tolerance for marker-assisted selection. A population of 146 BC₂F₄ BILs was developed using SG 747 (*Gossypium hirsutum*) as a recurrent parent and Pima S-7 (*G. barbadense*) as a donor parent. The 146 BILs were used for phenotypic screening at seed germination and seedling stage with 200 mM NaCl. Molecular markers were analyzed for linkage and combined with phenotypic data to identify quantitative trait loci (QTLs). The *G. barbadense* parent Pima S-7 was highly tolerant at seed germination with 87.75% of the control germination, where as the *G. hirsutum* parent SG 747 was sensitive with 38.52 % of the control germination. Plant height, leaf number, and shoot and root fresh and dry weight were significantly decreased with salinity, as compared with the seedlings under the control conditions without salt. This phenotypic study allowed to select significant salt-tolerant BILs. The correlation analysis between the traits showed that seedling growth, measured as plant height, leaf number, shoot and root fresh weight, and shoot dry weight, was negatively correlated with seed germination. This indicates that salt tolerances in seed germination and in seedling growth are under different genetic controls. Three QTLs on linkage group 12 were identified for leaf number and plant height and one QTL for plant height was identified on linkage group 16 that might be used for marker-assisted selection for salt tolerance.