

**IDENTIFICATION OF A MULTI-PARENT RMBUP POPULATION  
FOR SALT TOLERANCE IN COTTON**

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**Abstract**

Soil salinity is an accelerating threat to agriculture worldwide. Selection for improving crop salinity tolerance is a viable strategy for food security and sustainable agriculture worldwide. A multi-parent advanced generation inter-cross (MAGIC) population derived from a multi-parent random-mated RMBUP-C4 population of *Gossypium hirsutum* introgressed with *G. barbadense* alleles from 17 chromosome substitution lines (CSLs) was used to screen for salinity tolerance in a greenhouse water-culture system. A total of three screens are planned and two have been completed. A split plot design with three blocks was used with a starting population of 712 RILs and two treatments (control and 200 mM NaCl). Data collection included plant height, shoot and root fresh and dry weights, root to shoot dry weight ratio, and fresh to dry weight ratio. Significant genotypic differences were detected and the most tolerant genotypes (NMIL 265, 666, 063, 429, 150, 653, 668, 284, 383, and 711) show equal to or greater shoot and root dry weights than two parental standards, TM-1 and 3-79. Remaining work includes final screen and selection of most salt tolerant genotypes followed by RNA-seq from key tissues, genotyping of the RMBUP-based MAGIC population, and molecular analysis of genes for quantitative trait loci (QTL) contributing to salinity tolerance.