

IDENTIFICATION CANDIDATE SSR, SNPS AND GENES ASSOCIATED SALT TOLERANCE IN ASIATIC COTTON (*GOSSYPIUM ARBOREUM*)

Tussipkan Dilnur, Shuga Manabayeva*

National Center for Biotechnology, 13/5, Qorghalzhyn Hwy., Astana, 010000, Kazakhstan

*Correspondence: Shuga A. Manabayeva manabayeva@biocenter.kz

Soil is a vital resource for feeding the growing global population. Increased salt tolerance of perennial species used for fodder or fuel production is an important and natural method for controlling the spread of secondary salinity. This study was carried out to identify marker-trait association analysis using 7 traits and one comprehensive index of salt tolerance (CIST) and SSR and SNP markers for 215 accessions of Asiatic cotton (*G. arboreum*). The traits related to salt tolerance like germination rate (GR), fresh weight (FW), stem length (SL), water content (WC), chlorophyll content (ChlC), electric conduct (EC) and methylene dioxyamphetamine (MDA), of 215 cotton accessions were screened out using 150mM NaCl concentration after 7 days of seed growth. According to a comprehensive index of salt tolerance (CIST), 215 accessions were mainly categorized into four groups, and 11 accessions (top 5%) with high salinity tolerance were selected for breeding. Group 1 contained 12 accessions that were sensitive to high salt treatment (<0.6), group 2 contained 26 accessions that were moderate tolerant to salt treatment (0.6~1.5), group 3 includes 153 accession that were tolerant (1.5~2.5), and group 4 had 24 accessions that were highly tolerant to salt treatment (>2.5).

The natural population of 215 accessions of *G. arboreum* was first classified into 3 main groups by phylogenetic analysis, in which Group 2 (G2) and Group 3 (G3) represented the Yellow River and Yangtze River accessions respectively, while Group 1 (G1) contained mixed cotton accessions which belongs to different cotton growing areas in China. The grouped accessions results were largely congruent with the breeding history and ecological region, which indicates the extensive genetic diversity of *G. arboreum* accessions both in phenotype and genotype.

The relative value (R) of the traits was used for marker-trait association analysis. Twenty-two strong SSR marker-trait associations were ob-

tained with strict significant P value i.e. $P < 0.01$ and four makers including NAU1023, NAU1099, JESPR222, and NAU2783 were significantly related to salt tolerance. The marker NAU2783 was highest associated ($P = 1.98E-12$) with REC, and with the highest phenotype variation of 20.87%. Some markers are significantly associated with more than two traits. MUSS020 was significantly ($P < 0.01$) related with RFW, and RMDA, NAU1375 was associated with RFW and RSL, while NAU3468 was significantly associated with RFW, RGR, and RWC.

By applying the threshold of $-\log_{10} P \geq 4.0$, the 2062 SNP markers covered all 13 chromosomes and 100 SNP markers locations that were unknown. Among these 2062 marker-trait associations, 61 markers were associated with RGR, 187 markers were associated with RFW, 255 markers were associated with RSL, 370 markers were associated with RWC, 190 markers were associated with RChlC, 583 markers were associated with REC, 335 markers were associated with RMDA and 81 markers were associated with CIST. The nine SNP rich regions analysis revealed 143 polymorphisms that distributed 40 candidate genes and significantly associated with salt tolerance. Notably, two SNP rich regions on chromosome 7 were found to be significantly associated with two salinity related traits, RFW and RSL, by the threshold of $-\log_{10} P \geq 6.0$, and two candidate genes (Cotton_A_37775 and Cotton_A_35901) related to two key SNPs (Ca7_33607751 and Ca7_77004962) were possibly associated with salt tolerance in *G. arboreum*. The classification information derived from these studies may be used to facilitate the development of salt tolerant cotton accessions that could give economic yield in salinity prone areas. The strong marker-trait association results might provide insights for marker-assistant selecting salt-tolerant varieties and will be useful for future cotton breeding programs.