

## CHARACTERIZATION OF GENETIC DIVERSITY FOR SALINITY TOLERANCE IN *SOLANUM LYCOPERSICUM*

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Salt stress is a major abiotic constraint limiting tomato (*Solanum lycopersicum*) productivity. It induces stomatal closure, reducing photosynthetic activity, and impairs nutrient uptake, leading to nutritional deficiencies, yield loss, and diminished fruit quality. The plant stress response triggers oxidative stress and reactive oxygen species (ROS) accumulation, which are regulated by redox homeostasis pathways. Among the key components of these pathways are glutathione S-transferases (GSTs), a multigene protein superfamily with diverse cellular functions. Previous studies indicate that GST genes modulate plant stress responses and tolerance.

Our research employs an integrative approach, combining targeted analysis of nucleotide diversity in GST genes, large-scale field phenotyping, and CRISPR/Cas9 functional validation, to identify stress-tolerant genotypes, key GST genes, and superior alleles. This strategy aims to develop knowledge-informed breeding programs for climate-resilient agroecosystems.

We first characterized GST allelic diversity in a reference core collection of *S. lycopersicum var. cerasiforme* accessions to identify structural variants associated with salt tolerance. Accession salinity tolerance was evaluated in a randomized block field trial with three replicates under

four treatments that is control (0.2 dS/m low-salinity water) and three saline irrigation regimes (SW1: 5 dS/m; SW2: 10 dS/m; SW3: 20 dS/m).

Environmental parameters (soil temperature, moisture, electrical conductivity) were monitored continuously using FDR sensors and weather stations. Physiological traits were assessed with a LI-600 porometer (LI-COR), SPAD meter (Minolta), and LP-80 AccuPAR ceptometer. UAV remote sensing (DJI Matrice 300 RTK with Sentera Double 4K NDVI/NDRE sensor) acquired multispectral vegetation indices. Yield, agronomic traits, and fruit quality were evaluated at harvest, identifying accessions with superior salinity tolerance-yield combinations.

Ongoing long-read sequencing of GST genomic regions will uncover allelic diversity underpinning salinity tolerance and enable molecular marker development. High-throughput phenotyping, comparative transcriptomics, and CRISPR/Cas9-generated GST mutants will characterize promising genotypes and elucidate regulatory mechanisms controlling salinity responses. These insights will accelerate the development of resilient tomato varieties for challenging environments under climate change.