

**UNVEILING THE POSITION AND EFFECTS ON SALT STRESS RESILIENCE OF WILD *S. PENNELLII* GENOME IN *S. PENNELLII* X *S. LYCOPERSICUM* INTROGRESSION LINES THROUGH INTEGRATED DNA AND RNA SEQUENCING APPROACH**

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Salinity stress disrupts plant metabolisms, affecting crop yield and restricting the utilization of agricultural land. The high concentration of salt in the root zone severely hinders the normal growth of plants, leading to stunted development, reduced yield and eventual death. Crops have close association with numerous wild relatives capable of growing even under suboptimal conditions. *Solanum pennellii* is a non-commercial wild tomato species endemic to the Andean region, characterized by arid and saline habitats, making it an ideal donor of resilience traits for commercial tomato (*Solanum lycopersicum*). A collection of *S. pennellii* (LA1706) x *S. lycopersicum* (UC82) introgression lines (IL) was realized in the laboratory of Professor Dani Zamir (Hebrew University of Jerusalem) to assess the effect of the single genomic regions on plant's phenotype and several studies identified chromosome 7 of *S. pennellii* as a potential source of salt tolerance. Previous experiments selected IL 7-4-1 as the genotype with the highest performance in root development under salt stress conditions.

This work has been designed to identify candidate genes, derived from *S. pennellii* and introgressed in the *S. lycopersicum* genome, associated with improved root growth under salt stress conditions. Seeds of the two promising ILs (IL 7-4-1, IL 7-5-5), and UC82 were cultivated in vitro for

one month under two salt concentrations (0mM and 40mM) and subjected to RNAseq analysis. Differentially Expressed Genes (DEGs) through nine comparisons, including both intra- and inter- genotype analyses, were identified. The genome of ILs was sequenced (Illumina technology) and VCF (Variant Call Format) files were generated using the M82 genome as a reference. The developed genomic tool allowed the analysis of SNP (Single Nucleotide Polymorphism) density, to determine physically the introgressed regions and to generate a preliminary physical map of ILs' chromosome 7.

By integrating the data from RNA and DNA sequencing, a list of DEGs located within the introgressed regions was generated. Further analysis revealed that several of them are associated with hormonal pathways, specifically the auxin, cytokinin, and ethylene pathways. The identification of these DEGs suggests their potential involvement in the response to salt stress and highlights the significance of hormonal regulation in the genetic improvement of *S. lycopersicum*.