Proceedings of the LXV SIGA Annual Congress Piacenza, 6/9 September, 2022 ISBN: **978-88-944843-3-5** 

Poster Communication Abstract - 5.38

## ANALYSIS OF SALINITY TOLERANCE IN TOMATO INTROGRESSION LINES (ILS) BASED ON MORPHO-BIOMETRIC PARAMETERS AND DIFFERENTIAL GENE EXPRESSION

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abiotic stress, stress tolerance, tomato, morpho-biometric parameters, Introgression Lines

Global warming is one of the most dangerous artificial phenomena that has ever affected planet Earth, then farming and cultivation. Among its several side issues, exponentially rising temperatures are causing the reduction of available freshwater, leading to a frequent use of saline water for agricultural purposes. This practice global warming is leading to a sharp increase in soil salinity which in turn, exposes crops to salt stress and secondary osmotic stresses. The presence of high salt concentrations in the soil close to the root system severely impedes the normal development of the plant, resulting in a reduced growth of shoots and roots, so as a loss of yield and eventual plant death. Nowadays, agriculture requires new tolerant varieties, with high resilience to salt stress and fine agronomic commercial quality. Cultivated plants are related to manv wild and relatives capable of growing in sub-optimal conditions, such as in the presence of abiotic and biotic stresses. These wild species own genetic variants needed to face today's climate challenges. Solanum pennellii is a wild non-commercial species of tomato, endemic to the Andean region, where arid and saline habitats are widely spread. The extreme tolerance to saline stress makes *S. pennellii* a perfect candidate for commercial tomato ( Solanum lycopersicum) genetic improvement. For this purpose, a collection

of *S. pennellii* (LA0716) x *S. lycopersicum* (UC82) Introgression Lines (ILs) was analyzed in salt stress and control condition to monitor the effect of the single introgressed chromosomic regions on the IL phenotype. Several studies identified chromosome 7 of *S. pennellii* as a potential source of salt tolerance candidate genes (Frary et al., 2010; Bolger et al., 2014).

This study aims to analyse morpho-biometric parameters of several *S. lycopersicum* subjected to salt stress. To reach this aim, IL 7-4-1 (LA4068), IL 7-5-5 (LA4070) and the parental UC82 were grown in vitro, using both MS medium added with 40mM NaCl and MS medium not including salt, as control. After one month of growth, root fresh weight (FW) and root dry weight (DW) data were collected. LA4068 (IL 7-4-1) and LA4070 (IL 7-5-5) resulted to be the most tolerant accessions (Ferrari et al., 2022; Submitted).

Afterwards, RNA was extracted from the roots using the Direct-zol<sup>™</sup> kit by Zymo-Research. Three biological replicates were taken for each sample, for a total of 18 samples. In the perspective of carrying out a RNAseq experiment and in order to combine the morpho-biometric parameters with analysis of gene expression, sequencing is in progress.