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IDENTIFICATION OF GENES RESPONSIVE TO MULTIPLE-STRESS BY COMPARATIVE TOMATO TRANSCRIPTOMIC ANALYSIS

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Identification of genes responsive to multiple-stress by comparative tomato transcriptomic analysis

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Tomato (Solanum lycopersicum) is susceptible to various biotic and abiotic stress, which can occur separately or in combination, leading to significant decreases in yield. In this study, the transcriptomic response of resistant and susceptible tomato plants exposed to biotic factors such as fungi, bacteria, virus and insects and abiotic factors such as drought, salinity, low temperatures and oxidative stress was compared. This approach, allowed the identification of 1474 DEGs common between biotic and abiotic stress. In particular, RLKs, MAPKs, FLAs, glycosyltransferases, phytohormones and transcription factor genes were found. Genes involved in cellulose deposition, were mainly activated by resistant plants to TSWV and during oxidative stress. By contrast, UGEs participating in pectin metabolism were induced in resistant genotypes to fungi and during low temperatures conditions. A list of signaling-responsive genes to both biotic and abiotic stress was obtained. Among these, four RLKs exhibited divergent regulation during exposure to fungi, bacteria, T. absoluta, and TSWV and 4 were in common in all genotypes susceptible to abiotic stress. Thirteen genes encoding for phytohormones responsive to both biotic and abiotic stress were pointed out. Auxin-related genes were activated during abiotic stress and by resistant genotypes to fungi, and four of them were repressed by the resistant genotype to TSWV. Two ethylene relate genes were activated in abiotic stress and in fungi resistant plants and repressed in

TSWV resistant genotype. By contrast two genes involved in JA signaling that were downregulated during salinity and low temperature and induced by the R genotypes to TSWV and fungi. Two candidate genes (SlHyPRPI and SlWATI),involved in multiple-stress response, were selected for CRISPR/Cas9 validation. Currently, the T3 generation plants are under analysis. Our approach is aimed to demonstrate that the exploration of multiple transcriptomic datasets may help the identification of target genes for plant breeding programs.