

META-ANALYSIS OF TOMATO RNA-SEQ DATA REVEALS IMPORTANT MULTIPLE-STRESS RESPONSIVE GENES

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Tomato (*Solanum lycopersicum*) is an extensively cultivated food crop which yield can be affected by several losses due to the combination of biotic and abiotic stresses. Our purpose was to perform a tomato meta-analysis between biotic and abiotic stress RNA-sequencing experiments, to find out genes involved in multiple stress responses. In particular, for biotic stress we analyzed RNA-seq data of tomato interaction with eight pathogens: *Cladosporium fulvum*, *Phytophthora infestans*, *Pseudomonas syringae* pv *syringae*, *Ralstonia solanacearum*, *Sclerotinia sclerotium*, *Southern tomato virus* (STV), *Tomato spotted wilt virus* (TSWV), and *Tuta absoluta*. As for abiotic stress, RNA-seq experiments analyzed data includes tomato plants challenged with drought, salt, cold and oxidative stress. In our study, we first identified three main groups of common-response genes in fungi, bacteria, and abiotic stress datasets: 268 and 545 genes resulted up and down-regulated among fungi, 277 up and 233 down-regulated genes among bacteria, and 71 up and 99 common down-regulated genes among all the abiotic stresses. Then, to identify genes involved in both abiotic and biotic stress response, we compared fungi, bacteria, viruses, and pests against two groups of abiotic stresses: drought and salt stress and low temperature and oxidative stress. From all the comparisons made, we identified 223 genes that resulted differentially expressed in at least 3 of these groups of stresses. Among these we identified new genes that could be important for multiple stress resistance as transcription factors; aquaporins, PR-genes (Pathogen-Related genes) differentially regulated during both abiotic and biotic stress. By contrast, in our DEGs lists, several genes have been previously reported in other studies. We are aimed to provide a list of tomato target genes that can be used in tomato genetic engineering programs. To test the robustness of our dataset we chose to knock out two genes: Solyc12g009650 (HyPRPI) and Solyc04g080940 (WATI) which resulted down-regulated during abiotic stress and during fungi infections (HyPRPI) and down-regulated during Bacterial infections (WATI) respectively. We designed two gRNAs for each gene, edited plants showed both monoallelic and biallelic mutation (with deletions of the entire fragments between the gRNAs). Further studies to assess the resistance of these plants against both biotic and abiotic stresses are in progress.