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Salinity responsive genes profiling in tomato utilizing RNA sequencing and quantitative real time PCR

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Soil salinity and scarcity of fresh water resources are two of the most environmental constraints that negatively affect plant growth and productivity worldwide. Tomato (*Solanum lycopersicum* Mill.) has been classified as moderately sensitive to salinity at all plant developmental stages. Identification of salinity response genes that control tomato salt tolerance will provide important guide lines for breeding programs and genetic engineering in tomato. In this study, Illumina RNA-sequencing and qPCR were achieved in two improved tomato genotypes (L46 and L56) for salt tolerance evaluation, in order to differentially expressed genes estimation the two genotypes were affected by salinity treatment 0.5 d sm-1 as a control and 9.6 d sm-1 as a salt stress. cDNA libraries were constructed and sequenced. About 13.3 million short reads (92 bp) were generated from cDNA libraries originated from leaves of both genotypes. Genotype L56 showed over expression of major salinity- responsive genes that aid in the salinity tolerance mechanism. Genotype L46 showed different group salinity responsive genes. In conclusion, the salt tolerant breeding genotype L56 is genetically robust, as it shows enhanced expression of salt-responsive genes in response to saline conditions. By contrast, the salt susceptible genotype L46 showed some potential genetic background. These genotypes have great potential for future breeding programs.

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