

## **SHORT-TERM TRANSCRIPTOME RESPONSE TO LOW NITRATE REVEALED N-RELATED DIFFERENTIALLY EXPRESSED GENES IN TWO NUE-CONTRASTING TOMATO GENOTYPES**

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Improving the nitrogen use efficiency (NUE) and understanding the mechanisms underlying the nitrogen (N) stress response in crops are crucial for a sustainable agriculture. As the main N source for plants, nitrate ( $\text{NO}_3^-$ ) acts as essential nutrient and signal molecule regulating the expression of many genes inducing genotype and tissue-dependent responses. In the present study, a RNA-seq approach was performed to compare the spatio-temporal transcriptome patterns in response to low  $\text{NO}_3^-$  in two NUE-contrasting tomato genotypes, Regina Ostuni (R0, high-NUE) and UC82 (low-NUE). A time-course analysis (0, 8 and 24h) was performed to highlight the differential expression patterns of all genes (DEGs) identified by an ANOVA modeling analysis taking into account all factors and their interactions (G; GxN; GxT; GxNxT). Three hundred ninety-five (395) and 482 N-responsive DEGs between genotypes (R0vsUC82) were identified in shoot and root, respectively. Among the low N-responsive genes, many were involved in protein kinase signaling pathways and plant hormone signal transduction, and interestingly almost induced in R0 compared to UC82. Low and high affinity nitrate transporters as well as many genes involved in proteolysis processes, like E3 ubiquitin ligases, were specifically induced in response to low N in R0 shoot compared to UC82, while many proteinase/protease inhibitors appeared significantly down-regulated. In addition, genes involved in phenylpropanoid and flavonoid biosynthesis resulted more expressed in R0 root compared to UC82. Furthermore, several transcription factors (TFs) specifically induced in response to low N in both R0 tissues were identified. More interestingly, nine (9) and 5 hubs genes were identified throughout a co-expression network analyses in shoot and root,

respectively. Among the shoot hubs, we found a stress-activated protein kinase (SAPK2) and a CBL-interacting protein kinase (CIPK) involved in response to abiotic stresses and Ca<sup>2+</sup> signaling cascade in response to N-stress and ABA signaling pathways. In addition, a CONSTANS-LIKE 9 TF, implicated in circadian rhythm and the negative regulation of long-day photoperiodism, and a Golden2-like protein 2 (GLK2), regulating chloroplast development by the activation of nuclear photosynthetic genes involved in chlorophyll biosynthesis, light harvesting and electron transport, were identified. In root, an IAA-amido synthetase GH3.6 involved in endogenous auxin homeostasis critical for plant stress adaptation and a Lateral Organ boundaries TF (LOB37) involved in nitrogen metabolism appeared among the most connected genes. Our results revealed potential key genes that may independently and/or concurrently regulate low N short-term response in the high-NUE genotype R0, useful for NUE improvement in tomato.