World Academy of Science, Engineering and Technology
International Journal of Biotechnology and Bioengineering
Vol:17, No:01, 2023

Transcriptome and Metabolome Analysis of a Tomato Solanum Lycopersicum STAYGREEN1 Null Line Generated Using Clustered Regularly Interspaced Short Palindromic Repeats/Cas9 Technology

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Abstract : The SGR1 (STAYGREEN1) protein is a critical regulator of plant leaves in chlorophyll degradation and senescence. The functions and mechanisms of tomato SGR1 action are poorly understood and worthy of further investigation. To investigate the function of the SGR1 gene, we generated a SGR1-knockout (KO) null line via clustered regularly interspaced short palindromic repeats (CRISPR)/Cas9-mediated gene editing and conducted RNA sequencing and gas chromatography tandem mass spectrometry (GC-MS/MS) analysis to identify the differentially expressed genes. The SlSGR1 (Solanum lycopersicum SGR1) knockout null line clearly showed a turbid brown color with significantly higher chlorophyll and carotenoid content compared to wild-type (WT) fruit. Differential gene expression analysis revealed 728 differentially expressed genes (DEGs) between WT and sgr1 #1-6 line, including 263 and 465 downregulated and upregulated genes, respectively, for which fold change was >2, and the adjusted p-value was <0.05. Most of the DEGs were related to photosynthesis and chloroplast function. In addition, the pigment, carotenoid changes in sgr1 #1-6 line was accumulated of key primary metabolites such as sucrose and its derivatives (fructose, galactinol, raffinose), glycolytic intermediates (glucose, G6P, Fru6P) and tricarboxylic acid cycle (TCA) intermediates (malate and fumarate). Taken together, the transcriptome and metabolite profiles of SGR1-KO lines presented here provide evidence for the mechanisms underlying the effects of SGR1 and molecular pathways involved in chlorophyll degradation and carotenoid biosynthesis.

Keywords : tomato, CRISPR/Cas9, null line, RNA-sequencing, metabolite profiling
Conference Title : ICGEPB 2023 : International Conference on Genetic Engineering and Plant Biology
Conference Location : Tokyo, Japan
Conference Dates : January 09-10, 2023