

TRANSCRIPTOMIC ANALYSIS OF STEVIA REBAUDIANA (BERTONI) PROVIDES NOVEL INSIGHTS INTO STEVIOL GLYCOSIDES AND PHENOLIC COMPOUNDS BIOSYNTHESIS AND ACCUMULATION

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Stevia rebaudiana (Bertoni) is a perennial shrub of the Asteraceae family spread across Asia, Europe, and North America. It is a valuable crop, particularly for the significant amount of steviol glycosides (SGs) and phenolic compounds (PCs) in its leaves. SGs are natural no-calorie sweeteners that are a hundred times more potent than sucrose, exhibiting antibacterial, antioxidant, antidiabetic, and renal protective effects. On the other hand, PCs have drawn significant attention due to their beneficial health-related effects and multiple biological activities. The global market for *S. rebaudiana* was estimated at \$447M in 2016, and by 2023, it is expected to reach \$1045M. Although the crucial role of several genes involved in the SGs and PCs biosynthesis has been investigated, the contribution of many genes and transcription factors in the biosynthesis of specific SGs and PCs in stevia has not been fully elucidated. With the aim of investigating putative genes and transcription factors (TFs) involved in the biosynthesis of specific SGs and PCs, three genotypes with high and three genotypes with low content of these compounds were selected for RNA-seq analysis. In total, 2997 differentially expressed genes (DEGs) were generated. Among the DEGs, various genes involved in the biosynthesis of SGs already known in the literature, like MCT, KS, UGT85C2 and UGT91D2, were found. Furthermore, a variety of genes implicated in the monolignol biosynthesis were retrieved as over-expressed in the genotypes with high content of PCs. In addition, co-expression analysis (WGCNA) showed genes that positively correlate with several biochemical traits of the six

genotypes of stevia. In particular, UGT85A8 and UGT76H1 turned out to be putative candidates for producing specific SGs, like rebaudioside E. Finally, several TFs, which resulted specifically regulated, such as WRKY65 and MYB12, could putatively be involved in regulating the biosynthesis of specific SGs and PCs, respectively. In conclusion, this work provided various putative candidate genes and TFs involved in the biosynthesis of specific SGs and PCs that could be useful for future *S. rebaudiana* breeding programs. Further studies are being carried on in order to fully define the function of such candidate genes.