

IS A MEMBER OF UDP- GLYCOSYLTRANSFERASE REGULATING ELLAGITANNINS METABOLISM IN STRAWBERRY?

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Fresh strawberries are a popular and important component of the human diet. The demand for high-quality fruits is increasing globally, challenging breeders to develop modern strawberry cultivars that fulfill all desired characteristics. Fruit flavor and nutritional characteristics are key quality traits and ones of the main factors influencing consumer preference. Shikimate and phenylpropanoid pathways produce many chemical compounds, like phenolic compounds, polyphenols and tannins, that are highly valuable in human nutrition offering antioxidant protection and contribute to the prevention of some diseases. Among them, the hydrolysable tannins, like ellagitanins and ellagic acid, have an effect on health in some human diseases such as breast and prostate cancers or neurodegenerative diseases (Basu *et al.*, 2014). In a previous study, Pott *et al.*, (2020) found 110 stable QTL for secondary metabolism by studying the F1 population derived from the crossing of '232' and '1392' (Zorrilla-Fontanesi *et al.*, 2011). Among these QTLs, we highlighted one that was responsible for 50-70% of the variation of ellagic acid hexose. A RNAseq with contrasting lines in ellagic acid hexose content was performed to reveal 11 differentially expressed genes (DEGs) with a false discovery ratio under 0.05. Candidate genes were functionally annotated using MapMan software. One gene raised as a candidate gene, annotated as UDP-glycosyltransferase suggesting to participate in the glycosylation of ellagic acid. In addition, we found that the gene expression of this candidate was negatively correlated with proanthocyanidin and flavan-3-ols content, providing an evidence of possible metabolic flux redirection through the synthesis of ellagitannins. However, further experiments are needed to confirm the role of this gene in the synthesis of ellagitannins.

References:

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