

Title Phenol compound metabolism and gene expression in the skin of wine grape (*Vitis vinifera* L.) berries subjected to partial postharvest dehydration

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Abstract

Specific polyphenol compound concentrations and gene expression patterns were determined by both microarray and qRT-PCR analyses in the epicarp of red-skinned grape berries (*Vitis vinifera* L. cv ‘Raboso Piave’) dehydrated, after harvest, at slow (S) and rapid (R) rates of up to 10 and 30% weight loss (WL). Increases in flavonols (quercetin) and *trans*-resveratrol concentrations were observed in the skins of all dehydrated samples, whereas flavan-3-ols concentrations showed a decreasing trend, which was more pronounced in S samples. The decrease in flavan-3-ol concentrations was paralleled by a reduction in procyanidin B1 and, particularly B2. Computational analysis of microarray data revealed that several key genes of the flavonoid pathways were unaffected or down-regulated during berry dehydration, with the exception of flavonol synthase, which was induced as well as one *MybB* transcription factor. Chalcone synthase (*CHS*), flavanone 3-hydroxylase (*F3H*), leucoanthocyanidin dioxygenase (*LDOX*) and *MybA* were markedly down-regulated, particularly in relation to 30% WL, whereas UDP-glucose:flavonoid 3-O-glucosyltransferase (*UFGT*) was unaffected in all the samples considered. Specific genes involved in the lignin biosynthetic pathway, including laccase, were induced in the most dehydrated samples. Considering the accumulation pattern and gene expression profiles, stilbenes and flavonols may represent useful biomarkers to monitor postharvest dehydration.