

Title Postharvest water loss induces marked changes in transcript profiling in skins of wine grape berries

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Abstract

A large-scale transcriptome analysis was conducted using an oligo-based microarray (14,562 probes) on skins of wine grape (*Vitis vinifera* L.) berries dehydrated at different rates (slow, S and rapid, R) after harvest up to 10 and 30% of weight loss (WL). At 10% WL, a total of 84 and 68 probes were differentially expressed following S and R dehydration, respectively. At 30% WL, 309 and 262 differentially expressed probes were detected in S and R samples, respectively, indicating that grape berries are still reactive at advanced stages of postharvest dehydration. Bioinformatic analysis revealed that about 70% of the differentially expressed probes could be annotated and putative functions were assigned. Functional characterization highlighted that, independently of the rate and intensity of dehydration, differential expression occurred in particular for genes associated with general metabolism, regulatory processes, and responses to biotic and abiotic stimuli. A total of 16 (induced) and 10 (repressed) probes, common to all four dehydrated samples, were associated with hormone (ethylene) metabolism, transcription factors, carbohydrate and secondary (polyphenols) metabolism, transport and stress responses. Together with the total number of differentially expressed probes, enhancing the dehydration level from 10 to 30% WL also affected the distribution of genes within functional categories: this behaviour was observed in particular for R samples. A higher level of water stress in grapes appears to be associated with modification to the expression of genes mainly involved in hormone and sugar metabolism, and defence mechanisms. Besides the intensity of dehydration, a significant effect on gene expression was also associated with rate of water loss: an increase in the percentage incidence of differentially expressed probes was present for categories involved in defence and environmental stress when comparing R and S samples. The microarray data, validated by RT-PCR analyses, represent robust evidence for the marked effects of postharvest water loss on metabolic processes in fruit tissues.