The role of UV-A light on flavonoid biosynthesis in *Vitis vinifera* L. cv. Cabernet Sauvignon callus cultures by targeted metabolomics and transcriptomics

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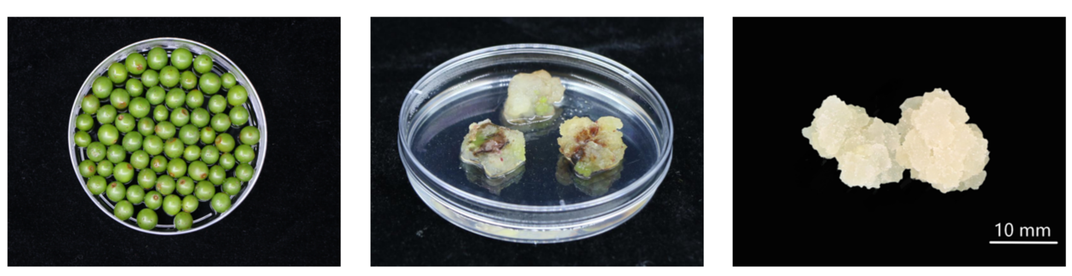
Introduction

Grapevine (*Vitis vinifera* L.) is one of the most widely cultivated horticultural plants worldwide with important economic values, producing a significant level of flavonoids (mainly including flavonol, flavan-3-ol, proanthocyanidins, anthocyanins, etc.) in berries, leaves, and flowers. The accumulation of flavonoids is not only affected by internal factors such as genotype, development period and tissues and organs, but also by external conditions such as climate conditions and cultivation measures. In order to explore the effects of climate factors on flavonoids metabolism, especially the effects of temperature, light and rainfall on flavonoids, we established a grape callus culture system in the laboratory. Here, we investigated the role of UV-A light on flavonoid biosynthesis in callus cultures of "Cabernet Sauvignon" (*Vitis vinifera* L.) . It was determined that UV-A light had remarkable promoting effects on the accumulation of flavonoids in the calli of Cabernet Sauvignon grape cultivar.

Materials

Callus was induced from the skin of grape berries at E-L 31 (pea-size) of "Cabernet Sauvignon" (*Vitis vinifera* L.) and then treated with three different intensities of UV-A light (low intensity UV-A treatment, high intensity UV-A treatment, and control).



Results

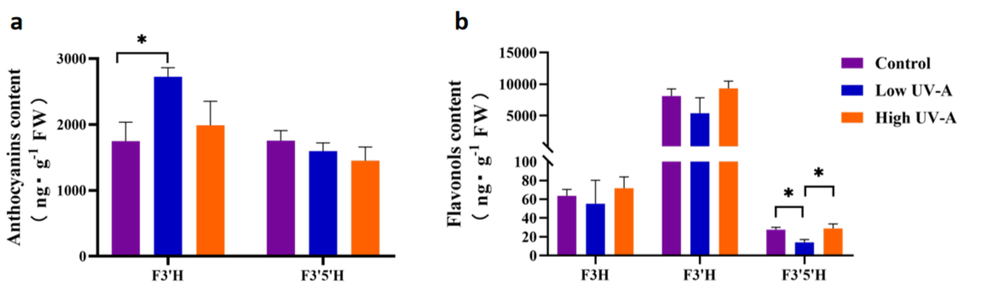


Figure 1. Anthocyanins (a) and flavonols (b) content in callus cultures of "Cabernet Sauvignon" (*Vitis vinifera* L.) treated with UV-A of different intensities. a. The low-intensity UV-A treatment significantly increased the anthocyanin content catalyzed by flavonoid 3' hydroxylase (F3'H) in callus, and there was no significant change in the high-intensity treatment group. **b.** The low-intensity UV-A treatment significantly reduced the flavonol content in calli by the catalysis catalyzed by the flavonoid 3'5' hydroxylase (F3'5'H), and the high-intensity UV-A treatment can recover this change.

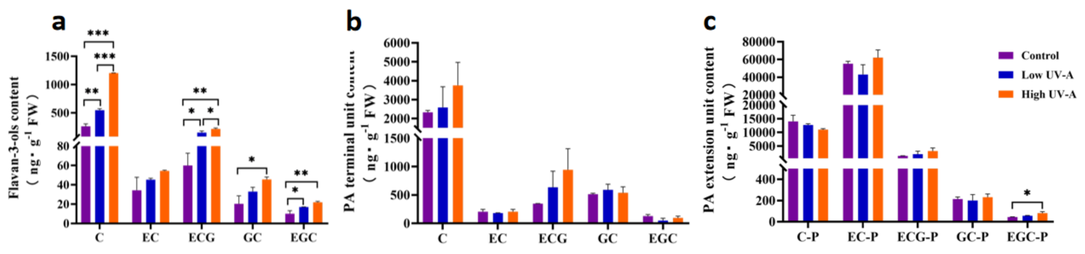


Figure 2. Flavan-3-ols (a), proanthocyanidins terminal unit (b) and proanthocyanidins extension unit (c) content in callus cultures of "Cabernet Sauvignon" (*Vitis vinifera* L.) treated with UV-A of different intensities. FW: fresh weight. Data are shown as the mean ± SD (for n = 3 biologically independent samples; **P* < 0.05, ***P* < 0.01, ****P* < 0.001, two-tailed unpaired Student's t tests).

Results

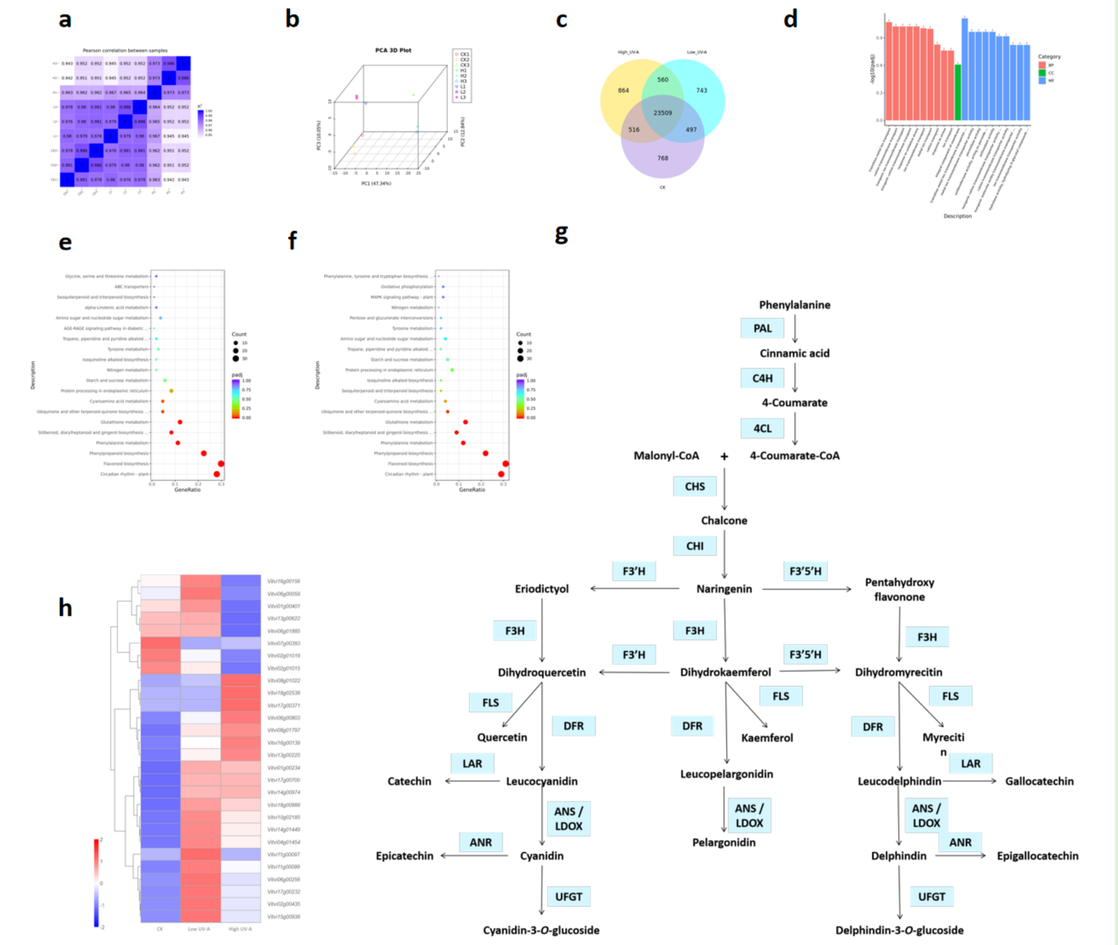


Figure 3. RNA-Seq expression profiling showed that callus cultures of "Cabernet Sauvignon" (*Vitis vinifera* L.) subjected to UV-A light processing of varying intensities involved in dynamic gene expression changes, including coordinated up- and down-regulation of metabolic pathway enzymes and transcriptional regulators. a. Pearson correlation between ssamples. **b.** The gene expression values (FPKM) of all samples were analyzed by PCA. In the PCA diagram, the samples between groups were scattered and the samples within groups were gathered together. **c.** Venn plot shows the number of genes co-expressed and specifically expressed between different UV-A treatment groups. **d.** The histogram shows the GO enrichment analysis of the differential genes between the low-intensity UV-A treatment and the control group. The results of KEGG enrichment analysis between high-intensity UV-A treatment and control group (**e**), as well as between high-intensity UV-A treatment and low-intensity UV-A treatment group (**f**), showed that DEGs were mainly enriched in the phenylpropanoid biosynthesis, phenylalanine metabolism and flavonoid biosynthesis pathway. **g.** Pathway of phenylpropane and flavonoid biosynthesis in grape. **h.** The gene expression clustering heat map shows up- and down-regulation of phenylpropane and flavonoid biosynthesis pathway enzymes and transcriptional regulators after UV-A light treatment.

Summary

In this study, we investigated the role of UV-A light on flavonoid biosynthesis in callus cultures of "Cabernet Sauvignon" (*Vitis vinifera* L.) by targeted metabolomics and transcriptomics, which may serve as a blueprint for the gene expression profile of grape berry response to the environment.