



## Vineyard microclimate alterations induced by black mulch through transcriptome reshaped the flavoromics of Cabernet Sauvignon

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### Abstract

To alter the vineyard microclimate and produce quality wine under a semi-arid climate, black geotextile inter-row mulch (M) was applied for two vintages (2016-2017). The grapes were sampled at three growing stages to conduct the untargeted metabolome and transcriptome analysis. The upregulated genes related to photosynthesis and heat shock proteins confirmed that M weakened the total light exposure and grapes suffered severe heat stress, resulting in lower sugar and higher acids at harvest. The integration of metabolome and transcriptome analysis identified the key genes responsible for the enhancements in phenylalanine, glutamine, ornithine, arginine, and C6 alcohol concentrations, and the downward trend in  $\epsilon$ -viniferin, anthocyanins, flavonols, terpenes and norisoprenoids concentrations in M grapes. The effects of metabolites and transcriptome were more evident in vintage with weaker light indicating the key regulator of light exposure under semi-arid regions. In addition, the potential key transcription factors regulating the biosynthesis of the above metabolites including *VviGATA11*, *VviHSFA6B*, and *VviWRKY03* were identified through weighted correlation network analysis. Taken together, this study provides a valuable overview of metabolic and transcriptomic responses of grapes exposed to inter-row mulch treatment in semi-arid climates, which could facilitate understanding the complex regulatory network of metabolites in response to microclimate changes.

**Keywords:** grape, floor management, microclimate, phenolic compounds, volatile compounds.