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GRAPE VOLATILE METABOLISM: A COMPARATIVE ANALYSIS OF TRANSCRIPTS AND METABOLITES' PROFILES IN AGLIANICO AND FALANGHINA RIPENING BERRIES

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The composition of grape berries at harvest determines the wine aroma. It is mainly defined by secondary metabolites such as terpenoids, methoxypyrazines, green leaf volatiles (GLVs), volatile thiols, carotenoids, phenylpropanoids and branched-chain aminoacids (BCAAs). Each includes hundreds of compounds whose amount and distribution in berries are finely regulated at the genetic level. In this study, we analyzed the aroma-related transcriptome and metabolome of ripe grape berries of two grapes, Aglianico Taburno (AT) and Falanghina del Beneventano (FB). Approximately 200 berries were harvested for each variety at the pre-veraison, veraison and ripening stages and separated into pulp and skin. As for transcriptome profiling, total RNA was sequenced using the Illumina HiSeq 2500 platform, providing 70M reads/samples. LC-MS and GC-MS were performed to detect and quantify volatiles and polar and non-polar precursors. In total, 441 and 442 aroma genes with about 250 and 221 differentially expressed genes (DEGs) have been found in AT and FB, respectively. One hundred thirteen metabolites were found in both varieties, 90 of which were differently accumulated metabolites (DAMs) in AT and 99 in FB. Among all, terpenes and

phenylpropanoids were highly accumulated in the berry skin of AT, while, in the same tissue, FB tends to gather primarily norisoprenoids. Lipids and BCAA showed opposite accumulation trends across samples, and their metabolic and expression profiles were variety-specific. We used a weighted gene co-expression network analysis (WGCNA) to identify co-expressed genes (“hub genes”) having regulatory functions and/or significant impacts on aroma bouquet determination. Overall, 22 and 16 DEGs were positively correlated with the secondary metabolites analyzed in AT and FB, respectively. This study provides new metabolomic and transcriptomic resources to understand the aroma genetic bases in grapevine further.