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COMBINED TRANSCRIPTOMIC AND METABOLOMIC ANALYSIS OF AGLIANICO AND FALANGHINA FRUIT TISSUES DURING RIPENING

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Since the physiological and biochemical makeup of grape berries at harvest has a profound impact on the wine characteristics, there is great interest in understanding the molecular mechanisms triggered and regulated during berry maturation. Aglianico and Falanghina are grape varieties from Campania appreciated worldwide for the sensorial features of their wines, although the molecular mechanisms responsible of their distinctiveness remain largely unexplored. The aim of this work was to shed light on the transcriptional and metabolic regulations in Aglianico e Falanghina during berry formation and ripening. To this end, berries were collected during fruit-set, post-fruit set, véraison, ripening and technological ripening, dissected in skin and pulp and used for metabolome profiling through GC-MS and LC-HRMS and genome-wide expression analysis using mRNA-seq. As for metabolic profiling, Aglianico displayed a higher level of branched-chain amino acids (bcAA), phenylpropanoid and C5-lipid volatiles, whereas Falanghina exhibited increased levels of monoterpenoids, norisoprenoids and C6-lipid derived volatiles. Furthermore, we observed metabolites with cultivar- and tissue-specific accumulations. Regarding gene expression analysis, the overall trends were mainly related to temporal dynamics rather than tissue identity. Indeed, during different developmental stages, the magnitude of gene expression at véraison was the highest for most of the genes analysed both in skin and pulp. Genes involved in NADH-dependent cell respiration, electrons transport and catabolism of sucrose and starch, displayed a reduction of expression in all tissues and during all stages analysed. In contrast, the genes involved in the metabolism of glutathione and the anabolism of protoporphyrin and chlorophyll have showed a statistically significant expression increase from fruit-set on. Similar patterns have been observed for polyphenol biosynthesis genes. In conclusion, the data obtained provided a deeper knowledge on the correlation between genes and related metabolite in Aglianico e Falanghina useful to assist the development of wines of higher quality.