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ADAPT: A MULTIDISCIPLINARY PROJECT TO DECODE THE INFLUENCE OF AGRO-CLIMATIC CONDITIONS ON THE GENE EXPRESSION AND MICROBIOME OF WINE GRAPES

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The grapevine has a remarkable ability to grow in different climatic environments. However, the genetic and molecular mechanisms underlying this extraordinary ability to adapt are poorly characterized. ADAPT is a PRIN project which aims to assess the impact of environmental conditions on grape and wine quality through the characterization of grapevine phenotypic plasticity. Two varieties were chosen for this purpose: Aglianico (AG) and Cabernet Sauvignon (CS). They were cultivated in three Italian sites: Molise, Campania, and Sicily. Here, we report the results of the 2020 vintage upon grapes harvested in the proximity of the ripe stage. The polyphenol fractions were quantified to understand the influence of agro-climatic conditions on grape metabolic profiles. A significant environmental effect was detected for skin compounds in both cultivars. Indeed, regardless of the cultivar, samples grown at higher latitudes displayed a greater content of all extractable phenolics. This behavior also interested the native anthocyanin acylations. The metabolomic data

were augmented with quantitative gene expression analyses to examine varietal differences and plasticity of genes involved in important oenological pathways. Among all genes analyzed, those related to the anthocyanin biosynthesis showed interesting patterns. In particular, the genes encoding flavonol 3’-hydroxylase (F3H) and dihydroflavonol 4-reductase (DFR) were found more active in CS than AG in all the sites. To deepen our knowledge of environmental influence on grape microbial populations, a culture-dependent approach was used, consisting in microbial culturing and DNA extraction, amplification, and sequencing. Results highlighted the presence of twelve different yeast species, with differences in their distribution and abundance linked to grape varieties and the grown environments. Only Hanseniasporaspp. was chosen in all grape samples under analysis, whereas Starmerella bacillariswas found only in AG from all sites. Finally, to correlate grape quality and water stress, we are monitoring the weather and soil conditions in each representative vineyard, collecting UAV multispectral images to support seasonal field plant monitoring, and taking satellite images for the vegetation indexes analysis. Taken together, our preliminary data suggest possible environment-dependent effects on metabolites, genes, and microbes. Further analyses in upcoming years will help us to understand whether 1) indigenous and international varieties exploit distinctive molecular mechanisms to cope with diverse climate regimes, 2) microbial communities present on the grape skin are affected by grapevine-specific plasticity and adaptation, 3) all previous factors impact musts and wines chemical compositions.