

TRANSCRIPTOME ANALYSIS REVEALS PLASTICITY OF GENE EXPRESSION IN WINE GRAPE CULTIVARS GROWN AT DIFFERENT LATITUDES IN SOUTHERN ITALY

SICILIA A.*, VILLANO C.**, DI SERIO E.**, AVERSANO R.**, FERLITO F.***, NICOLOSI E.*, LO PIERO A. R.*

*) Department of Agriculture, Food and Environment, University of Catania, Via Santa Sofia 100, 95123 Catania, Italy

**) Department of Agricultural Sciences, University of Naples Federico II, Via Università 100, Naples 80055, Italy

***) Council for Agricultural Research and Economics, Research Centre for Olive, Fruit and Citrus Crops, Corso Savoia 190, 95024 Acireale, Italy

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The ability of a genotype to produce different phenotypes according to its surrounding environment is known as phenotypic plasticity. The resulting variegated responses are then caused by gene-by-environment interactions (GxE) whose understanding is particularly important since selected varieties might have divergent phenotypes according to their growing environment. Moreover, studying plasticity in gene expression in natural systems is crucial for predicting and managing the effects of climate change on plant species. Grapevine (*Vitis vinifera* L.) is one of the most economically important plants in modern agriculture and post-genomic era studies can provide a wide and unbiased view of its physiology in different environmental conditions. Transcriptomics represents a powerful approach to quantify changing expression levels in distinct and varied conditions. The aim of our work was to investigate the GxE interactions of two red grape varieties, the international Cabernet Sauvignon (C) and the indigenous Aglianico (A), at berry commercial maturity. Using a *de novo* RNA-seq approach, their transcriptomes has been analyses in three regions of southern Italy characterized by different latitudes, such as Sicilia (SIC), Molise (MOL) and Campania (CAM). Firstly, PCA analysis indicated that both genotypes in Campania and Molise sites behaved similarly in terms of qualitative traits and transcriptomic response compared with the Sicilian

site. Congruently, the highest number of differential expressed genes (DEGs) resulted in the comparisons involving the Sicilian site, such as A_SIC vs A_CAM (4711), A_SIC vs A_MOL (3397), C_SIC vs C_CAM (2504) and C_SIC vs C_MOL (2328), compared to the C_CAM vs C_MOL (1914) and A_CAM vs A_MOL (1937) comparisons. The main enriched pathways found de-regulated in all the comparisons are “Biosynthesis of secondary metabolites” and “Phenylpropanoid biosynthesis”. “Fatty acid biosynthesis” pathway is de-regulated only in comparisons involving Aglianico genotype, whereas “Photosynthesis” and “Carbon fixation in photosynthetic organism” categories are de-regulated only in the Cabernet sauvignon comparisons. A weighted gene co-expression network analysis (WCGNA) was applied to correlate DEGs with either climatic data (air temperature, relative humidity, dew point, total precipitation, evapotranspiration and solar radiation) or qualitative parameters (°Brix, pH, titratable acidity, polyphenols, anthocyanins and maturity index) revealing highly co-expressed clusters of genes (modules). Furthermore, the role of small non-coding RNAs (small ncRNAs) in regulating plasticity-related traits was deepened using high throughput technologies. These results, within the PRIN2017 “ADAPT” project, can contribute to an advanced understanding on the relationship between genotype and environmental variables in wine grape also leading to the identification of the best performing genotype for each latitude.