

THE ROLE OF SMALL NON-CODING RNAS (SMALL NCRNAS) IN PHENOTYPIC PLASTICITY OF GRAPEVINE

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The cultivated grapevine (*Vitis vinifera*) has a remarkable phenotypic plasticity, namely the ability of a genotype to produce different phenotypes in response to environmental cues. However, the molecular mechanisms underlying this extraordinary ability to adapt are poorly characterized due to their complex nature. Here, we aimed to assess the role of small non-coding RNAs (small ncRNAs) in regulating plasticity-related traits in ripened grapevine berries using high throughput technologies.

The material consists of three biological replicates of two varieties (Aglianico and Cabernet Sauvignon) cultivated in three sites characterized by different latitudes and located in Molise, Campania, and Sicily regions. A total of 604 miRNAs and 181 phasiRNAs were predicted. Among them, small RNAs with low expression levels (lower than one count per million [cpm]) were filtered out. Hence, the final dataset resulted in 302 miRNAs (94 known miRNAs and 208 novel miRNAs) and 181 phasiRNAs. The results revealed that Cabernet Sauvignon showed a similar response to the environment between the three sites. On the contrary, Aglianico was characterized by greater variability, which, interestingly, reflects the geographic distance between the three growing environments. In particular, out of 483 small RNAs employed in the analysis, 135 and 131 were differentially expressed between Molise – Sicily and Campania – Sicily vineyards, respectively, whereas only 15 were differentially expressed between Molise – Campania

vineyards. Moreover, the southernmost vineyard (Catania) maximized the differences between the two cultivars, promoting the differential expression of 158 small RNAs between Aglianico and Cabernet Sauvignon. The in-silico prediction of small RNA targets suggested their involvement in response to biotic/abiotic stresses, berries development, and secondary metabolite accumulation, such as polyphenols and genes involved in the biosynthesis of final aroma components of the wine (e.g., thiols, branched amino-acids, terpenes, norisoprenoids). Therefore, the small-RNA profiling was augmented with transcript (RNA-seq) and metabolites (HPLC) analyses. DEGs showing an inverse relationship with DESs were used to construct a smallRNA – mRNA interaction network. We are currently performing a weighted gene co-expression network analysis (WGCNA) to cluster small RNA into groups (modules) and identify significant statistical associations between modules and phenotypic traits, such as polyphenol content in berries and pedo-climatic data. This study paves the way for a deeper understanding of the involvement of small RNAs in genotype x environment interaction in grapevine