

DEFINITION OF THE VVIWRKY3 TRANSCRIPTIONAL ORCHESTRATION IN GRAPEVINE INTEGRATING GENE CO-EXPRESSION NETWORK (GCN) AND DNA-AFFINITY PURIFICATION SEQUENCING (DAP-SEQ) APPROACHES

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In grapevine, the increasing accumulation of transcriptomic data from many different experimental conditions made the use of gene co-expression networks (GCN) as a noteworthy tool to predict gene function. In fact, the application of network-based methods in multi-omics data analysis is providing additional resources to address important questions related to grapevine fruit quality and composition. Since most of the phenotypic variability of an organism seems to be due more to regulatory rather than coding variations, the full comprehension of those processes controlling gene expression passes through the analysis of the transcription factors (TFs) and the localization of their binding motifs, in this way revealing the relative putative target genes. In this regard, in the last years was developed the DAP-Seq, a novel high-throughput assay which combines *in vitro* expression of TFs with NGS-technologies. This study, which is part of a more comprehensive and articulated project aimed at deciphering the genetic

and epigenetic determinants of gene expression in grapevine, focuses on the transcriptional orchestration of VviWRKY3, a TF putatively involved in stilbenes synthase (STS) pathway regulation. Here we present results obtained integrating data deriving from our DAP-Seq analysis performed on young leaf of Cabernet Franc, with those obtained by GCN analysis performed on transcriptional data collected from public repositories and corresponding to 670 runs deriving from 42 SRA experiment. Preliminary results showed an overlap between the target genes of both analyses, making the description of VviWRKY3 network more reliable and stronger. Among VviWRKY3 target genes, some had been previously identified and characterized as phenylpropanoids biosynthetic process regulators, e.g. VviMYB14 and VviMYB15, some others were novel targets never functionally characterized. As matter of fact, we identified VviMYB108A that in *Arabidopsis thaliana* seems to be involved in anther development and pollen fertility. More detailed studies are yet on going to give the functional characterization in grapevine.