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INSIGHT ON THE VVIMYBC2-L4 TRANSCRIPTIONAL REGULATION ROLE IN VITIS VINIFERA THROUGH DAP-SEQ AND GCN ANALYSIS

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At present, transcription regulatory mechanisms are known to be the main determinants of phenotypic variability in plants. In grapevine, the VviMYB Transcription Factor (TF) family is involved in key physiological processes. In particular, the *R2R3-MYB* subfamily is involved in secondary metabolism regulation and its members belonging to the C2 repressor motif clade are known for their balancing activity on the transcriptional regulation acted by other TFs. The identification of candidate target genes for a given transcription factor can be achieved through both in silico and molecular approaches. In recent years, there has been an increasing use of gene co-expression network (GCN) analyses based on transcriptomic data stored on public databases to identify candidate targets. At the same time, molecular techniques have been developed capable of making the identification of TF binding sites (TFBS) and, consequently, target genes, fast and on a genome wide-scale. Amongst these is DAP-seq (DNA Affinity Purification-sequencing), an approach that combines NGS with TF in vitro expression providing screenshot of the whole cistrome for a given TF. In the present study, which enters a wider project aimed at investigating the genetic and epigenetic determinants of gene expression in grapevine, we tried to combine results obtained by DAP-seq with those retrieved by gene co-expression network (GCN) analysis, in order to investigate the putative role of *VviMYBC2-L4*. The combination of the evidences obtained on the basis of the correlation with those obtained on a molecular basis has made it possible to draw up a list of candidate target genes, some of which are involved in biosynthetic pathways linked to secondary metabolism. Although the results reported here are preliminary and partial, this study embodies a successful example of how the integration of data deriving from in silico and wet-lab approaches represents a valuable tool in the prediction of gene regulatory networks.