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# SHAPING THE ROLE OF VITIS R2R3-MYB C2 REPRESSORS IN TRANSCRIPTIONAL REGULATION BY INTEGRATING DAP-SEQ AND GCN DATA

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The *VviMYB* family of Transcription Factors (TFs) is well-known, in grapevine, for its role in key physiological processes that determine phenotypic variability. Members of the $R_2R_3$-MYB subfamily, in particular, are involved in fine-tuning secondary metabolism biosynthetic pathways. The close interaction of several TFs such as basic Helix-Loop-Helix (bHLH) and WD40 with MYB proteins, which act by specifically targeting the gene promoter region, orchestrates transcription activation. A handful of MYB belonging to subgroup 4 are distinguished by the presence of the C2 repressor motif, which is involved in transcription repression. For the inspection and scouting of relevant genomic regions involved in gene transcription regulation, the integration of data from various *in silico* and wet-lab approaches is becoming increasingly important. DAP-seq (DNA Affinity Purification-sequencing) is a molecular technique that combines *in vitro* TF expression with NGS (Next Generation Sequencing) analysis to provide a collection of CREs (Cis-Regulatory Elements) on a whole genomic scale. On the other hand, GCN (Gene Co-expression Network) analysis tools can be used to exploit the information provided by transcriptomic data stored in public databases. Using the methods described above, the current study aims to characterize the role of C2 repressor motif genes *VviMYB4b, VviMYBC2-L1, VvMYBC2-L2,* and *VviMYBC2-L3*, as well as a list of candidate

target genes, some of which are involved in biosynthetic pathways linked to secondary metabolism. The preliminary findings presented here pave the way for the application of novel investigation techniques that will allow the isolation of protein complexes that regulate gene expression once the target regulatory regions of TFs have been identified. This will entail a greater understanding of the TF-promoter interaction, which will serve as the foundation for future genome editing experiments on CREs.