

## IDENTIFICATION OF CIS-REGULATORY ELEMENTS ASSOCIATED WITH DIFFERENTIALLY EXPRESSED GENES UNDER DROUGHT STRESS IN GRAPEVINE

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*Vitis vinifera* L. is among the most important crops in the worldwide economy; however abiotic stresses, like drought, dramatically reduce its growth and grape production. Plant responses to these stresses include the reprogramming of transcription based on *cis*-regulatory elements (CREs) that both recruit trans-acting factors and chromatin complexes and interact with target genes by long-range DNA looping. Unfortunately, in contrast to protein-coding genes, little is known about the CRE-based regulatory response. Many CREs such as the abscisic acid (ABA)-, drought- and auxin-responsive, exhibit *bona fide* CRE properties such as strong position bias towards the transcription start site (TSS) and over-representation when compared with random promoters. Therefore, studying at molecular and sequence level CREs, specifically associated with differentially expressed genes under stress conditions, could provide insight into the mechanisms regulating their activity. In this work, we aimed at deepening the knowledge on the regulatory complexes of key genes involved in the response to drought in grapevine. By using *in silico* approaches, we were able to select 16 CREs associated with genes involved in drought responses in two different varieties (Italia and Autumn Royal). Notably among these, 7 CREs were never described before as involved in regulating water stress related genes. We studied the distribution and organization of the CREs in the promoters of genes differentially expressed (DE) under water stress

together with the CREs properties. Further insights into the biological role(s) of genes containing these CREs were achieved through a pathway enrichment analysis.