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DAP-SEQ ANALYSIS OF VVINAC03 TRANSCRIPTION FACTOR IN VITIS VINIFERA

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Vitis vinifera is both economically important and scientifically interesting. It is an economically since important crop that needs to comply with high quality standards for fruit, juice, and wine production. It is also scientifically intriguing because grapevine contains a complex genome of 487 Mb that exhibits extensive colonization by transposon elements, making it a useful model in which to study how gene expression is regulated. Understanding genetic variants in the non-coding portions of the genome is one of the current interests in molecular biology. This is not only for gaining more information on the complex relationship between molecular genotypes and phenotypes, but also for practical purposes to take part in a targeted manner on genes in order to modify their expression pattern. A large fraction of phenotypic variation appears to be determined by regulatory rather than coding variation. On this trend, the present project, aim to identified specific transcription factor (TF) binding site using the DNA affinity purification sequencing (DAP-seq). This technique combines next-generation sequencing with in vitro expression of affinity-purified TFs to generate cistrome and epicistrome maps. This study is contextualized in a broader project aimed to identify putative target genes of grapevine *MYB, WRKY* and *NAC* genes, that in several plant species are among the most important transcription factors, in terms of size and roles, involved in plant development and response to external stimuli. In particular, *NACs* are plant specific genes often involved in drought and salinity responses. Moreover, the *NAC* genes may represent important signalling components in the control of grapevine maturation processes such as late berry developmental and leaves senescence. Preliminary results here reported, focused on putative target genes of *VviNAC03* that is the closest homolog of *SlNOR* gene, the master regulator of fruit ripening in tomato.