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TRANSCRIPTOME AND METHYLOME DYNAMICS DURING BUD DORMANCY AND DEACCLIMATION IN GRAPEVINE

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Temperature represents the main parameter controlling grapevine's phenological development, placing its global increase among the top factors affecting viticulture. Higher temperatures lead to early bud deacclimation and dormancy release, which in turn translate into the anticipation of budbreak together with subsequent developmental stages, including ripening and harvest. These conditions may result in a substantial increase of spring frost damage risk in several areas of the world, as well as challenge traditional wine production. For these reasons, understanding the molecular regulation of dormancy release in buds is essential to direct breeding efforts towards the production of climate-smart late-budbreak varieties, better suited to the new climatic scenario.

In order to investigate the molecular changes associated with the release from dormancy, we implemented an experimental system to monitor potted plants of Cabernet Sauvignon, assessing bud cold hardiness by Differential Thermal Analysis (DTA), during the transition from cold acclimation to deacclimation. Then, we carried out transcriptome and DNA methylome analyses from buds collected in the three critical stages. The developmental reactivation expected during deacclimation is supported by the overexpression of several genes related to cell cycle and DNA replication, as well as various components of major epigenetic regulatory pathways, such as *de novo* DNA methylation. However, significant and more directional changes in DNA methylation appeared to have already occurred through the dormancy stage prior to deacclimation, especially in genes. The function of such epigenetic variation remains elusive as demethylation events outnumber hypermethylation events, but the latter are greater in

magnitude. The fact that hypermethylation, albeit more infrequent at the genomic level, is often greater in genes containing transposons in their introns than in their transposon-free counterparts suggests a reinforcement of the silencing of repetitive sequences in bud meristems. Nevertheless, the overall dynamics of such silencing appear very different from and more subtle than the scenario previously observed in embryonic tissues. The biological implication of expression and DNA methylation modulations over different genomic features during bud dormancy and deacclimation will be discussed.