

Heat-stress responses regulated via a MYB24-MYC2 complex

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Throughout the growing season, grapevine frequently encounters environmental challenges associated with heat and light radiation stress, especially during the ripening stage, thereby constraining the yield and quality of berries. MYB24 has been previously proposed to control light responses during late fruit ripening stages, and it has been found to require the co-factor MYC2. We have generated transcriptomic data from grapevine leaves transiently co-transformed with MYB24 and MYC2. Differential expression analysis revealed 179 up-regulated genes (URGs). Considering tissue specificity, where MYB24 is specifically and highly expressed in flowers and late-ripening berries, the expression of these URGs was explored using a previously published Berry Development Atlas gathering berry development data of cv. 'Pinot Noir' and 'Cabernet Sauvignon' in different vintages. Half of URGs highly co-express with MYB24, and MapMan analysis discloses many significantly enriched heat-related terms. Specifically, 18 co-expressed URGs were reported as heat-induced genes. Due to the DNA-binding capacity of MYB24 and MYC2, we investigated their regulatory potential by taking advantage of DAP-seq data. More than 40 of these co-expressed URGs, named as MYB24/MYC2 high confidence targets (HCTs), are bound by both TFs or one of them in their 5kb upstream region. In particular, some HCTs have been previously and functionally validated as heat regulators or heat-induced genes. Furthermore, MYB24, MYC2, and a high proportion of their HCTs were significantly induced in reanalyzed heat-treatment transcriptomic studies. To sum up, our data suggests that the MYB24-MYC2 complex plays a key role in the hierarchical regulation of heat responses.

Keywords: MYB24, MYC2, heat stress, transcriptomics, transcriptional regulation.