PETUNIA HYBRIDA AS A MODEL SYSTEM TO STUDY THE FUNCTION OF ANTHOCYANIN REGULATORS OF GRAPE

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Anthocyanins are accumulated during ripening of grape berries and represent the main source of pigment in wine. Besides the well characterized regulative role of the transcription factor VvMYBA1, the co-regulation of anthocyanin pathway by other members of the MYB family (VvMYB5a and VvMYB5b) has been proposed. The role of VvMYB5a and VvMYB5b has been mainly inferred by expression analyses and/or ectopic expression in heterologous systems.

We used functional complementation analyses of the well characterized Petunia anthocyanin regulatory mutants to gain information about the role of VvMYB5a, VvMYB5b and VvMYBA1 in the regulatory network in *Vitis vinifera*.

In petunia the mutation of orthologs of *VvMYB5a* / *VvMYB5b* (*PhPH4*) and of *VvMYBA1* (*PhAN2*) results in the increase of vacuolar pH and strong reduction of anthocyanin content of petals, respectively. The coding sequence of *VvMYB5a*, *VvMYB5b* and *VvMYBA1* was fused to the constitutive promoter 35S and transformed into *ph4* and *an2* petunia mutant lines. Analyses of transgenic plants revealed full complementation phenotypes. Deep analyses of pigment profile, vacuolar pH and expression of structural genes confirmed that restored phenotypes were attributable to an activation of target genes belonging to vacuolar acidification and anthocyanin pathways. Moreover, specific and/or partially overlapping effects could be observed, giving insights about their possible redundant roles of these MYB transcription factors in grape.