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The oversexpression of the grape *MYBPA1* gene triggers severe changes in the phenylpropanoid pathway in tobacco flowers

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Condensed tannins (CT) are minor compounds, originating from the flavonoid pathway, present in several plant species and tissues.

The interest in such compounds originates for their multiple utilisation, in industrial activity, but mainly for the beneficial effect of their presence in food and feed.

Since their share the biosynthetic pathway with anthocyanins it has been possible to identify and clone structural and regulatory genes in several species and describe the regulatory mechanism controlling their biosynthesis: three actors WD40-bHLH and MYB interact to activate/repress this route. Among this ternary complex, the MYB partner seems to be main player in specifying the competence of a given organ/tissue to accumulate CT. A large amount of MYB genes have been isolated from several species. They can exert both positive and negative action on the pathway.

In this work we tested the effects of the expression of *VvMYBPA1* in different tobacco tissues to test the possibility to use this gene as an activator of this route in different crop species.

In grape, *VvMYBPA1* is expressed in flowers and at the early stages of berry development, its expression correlates with CT accumulation and this gene complements *TT2* in *tt2* Arabidopsis mutants (Bogs et al, 2007).

Here we report on molecular and metabolic characterization of 3 T_2 progeny of tobacco plants transformed with *VvMYBPA1*. These plants have been selected for their different floral phenotypes: ranging from whitish to pale pink limbs, whereas the control plants show pink floral limb. Notably, the reduced accumulation of anthocyanins correlated inversely with the accumulation of CT and positively with the quantitative expression of the transgene. Among the genes tested CHS and ANR resulted the most positively affected by *VvMYBPA1.*

Metabolic analysis of flower tubes and limbs have shown that beside the anthocyanin derivatives, 41 additional phenolic compounds show different concentrations in the transgenics. Among those metabolites whose levels were markedly different between transgenic and control lines are the flavan-3-ols, catechin and epicatechin, the building blocks of CT, and their dimers and polymers. Notably, the concentration of epicatechin, that is about an order of magnitude higher than catechin in any genotype investigated, increased almost linearly with the decrease of the anthocyanin content. Interestingly, none of these compounds have been detected in wild type tubes. Other compounds such as chlorogenic, cryptogenic and neochlorogenic acid followed the same rule as the flavan-3-ols. In particular, chlorogenic and neochlorogenic acids displayed an increment in their accumulation both in limbs and tubes of the transgenic lines; interestingly, this increment mirrors the steady state levels of the transgene to suggest a specific action of the exogenous transcription factor on this branch of the phenylpropanoid pathway.