P41 – DAP-Seq analysis on MYB108A/B transcription factors identified candidate target genes involved in anther development and biotic stress response in grapevine

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Abstract

Since the usability of a crop pass throught the full comprehension of the genetic mechanisms at the base of flower and fruit tissues development, which in grapevine represent the economically important part, we think it is pivotal make clear the molecular occurrence defining gene expression. For this purpose, we produced a floral expression atlas using an RNA-Seq approach isolating the absolutely and highly specific genes for each tissue using a τ and WGCN analysis. Amongst all the results, we focused attention on those transcription factors specifically expressed in each floral whorl. Of particular interest was *VvMYB108A,* a gene expressed exclusively in anther tissues before anthesis. This gene, which is paralogous of *VvMYB108B* and orthologous of the *Arabisopsis* gene *MYB108*, seems to be involved in male fertility and stamens development by controlling pollen viability, filament elongation and anther dehiscence. Moreover, *MYB108* was shown to be involved in plant-pathogen relationship during *Botrytis cinerea* infection. In order to identify the gene targets of *VvMYB108A/B,* we took advantage of a novel NGS tecnique, namely DAP-Seq (DNA-Affinity Purifcation Sequencing), able to identify all the genomic regions bound by a given transcription factor. Results were crossed with gene coexpression networks already available on public repositories. *MYB108A* and *MYB108B* overexpression in tomato and *Arabidopsis* plants together with dual reporter luciferase assays are now in progress aiming to functionally characterize these genes and to validate results obtain by DAP-Seq.

Keywords: grapevine, NGS, flower, *Botrytis cinerea*, MYB