P72 – DAP-seq and GCN analyses to infer the role of the grapevine R_2R_3-MYB C2 repressors clade

Pirrello, Carlotta[1*]; Magon, Gabriele[1]; Magris, Gabriele[2]; Licursi, Valerio[3]; Matus, José Tomás[4]; Lucchin, Margherita[1]; Vannozzi, Alessandro[1]

[1]University of Padova, Department of Agronomy, Food, Natural Resources, Animals and Environment, Padova, Italy
[2]University of Udine, Udine, Italy
[3]University of Rome, Department of Biology and Biotechnologies "Charles Darwin"-"Sapienza", Rome, Italy
[4]Joint Centre Universitat de València-CSIC, I2SysBio, Institute for Integrative Systems Biology, Valencia, Spain

*carlotta.pirrello@unipd.it

Abstract

In grapevine, the involvement of the *VviMYB* family of Transcription Factors (TFs) in the key physiological processes that determine phenotypic variability is well known. Especially for members of the *R_2R_3-MYB* subfamily, which are mainly involved in fine-tuning the biosynthetic pathways of secondary metabolism. Transcription activation is orchestrated by the close interaction of several TFs such as basic Helix-Loop-Helix (bHLH) and WD40 with MYB proteins, which act by specifically targeting the promoter region. Among these MYB, a handful belonging to subgroup 4 are characterized by the presence of the C2 repressor motif, involved in the repression of transcription. The integration of data belonging to different *in silico* and wet-lab approaches is becoming increasingly important for the inspection and scouting of relevant genomic regions involved in the regulation of gene transcription. In this regard, DAP-seq (DNA Affinity Purification-sequencing) is a molecular technique capable of providing a collection of CREs (Cis-Regulatory Elements) on a whole genomic scale by combining the *in vitro* expression of TFs and NGS (Next Generation Sequencing) analysis. On the other hand, the information provided by transcriptomic data stored on public databases can be exploited using tools for GCN (Gene Co-expression Network) analysis. Taking advantage of the abovementioned approaches, the present study aims to characterize the role of *VviMYB4b, VviMYBC2-L1, VvMYBC2-L2* and *VviMYBC2-L3* genes belonging to C2 repressor motif clade, drawing up a list of candidate target genes, some of which are involved in biosynthetic pathways linked to secondary metabolism. The preliminary results shown here pave the way for the use of innovative investigation techniques which, once the target regulatory regions of TFs have been identified, allow the isolation of the protein complexes that regulate gene expression. This will entail an expansion of knowledge concerning the interaction TF-promoter region to serve as a basis for future genome editing experiments on CREs.

Keywords: *Vitis*, TFs, CREs, NGS, genome editing