2024 open GPB
Open Conference on Grapevine Physiology and Biotechnology
LOGROÑO - LA RIOJA
7-11 July 2024

Exploring the gene regulatory networks of WRKY family in grapevine (*Vitis vinifera* L.) using DAP-Seq

Gabriele Magon[1*], Giovanni Gabelli[1], Carlotta Pirrello[2], Sara Zenoni[3], Valerio Licursi[4], Luis Orduña Rubio[5], Gabriele Magris[6], Margherita Lucchin[1], Josè Tomàs Matus[5], Mario Pezzotti[3], Michele Morgante[6] and Alessandro Vannozzi[1]

[1] *Department of Agronomy, Food, Natural resources, Animals and Environment (DAFNAE), Università degli Studi di Padova, Viale dell'Università 16 - 35020 Legnaro (PD), Italy*
[2] *Research and Innovation Center, Fondazione Edmund Mach, Via Edmund Mach 1 - 38098 San Michele all'Adige (TN), Italy*
[3] *Department of Biotechnology, Cà Vignal 1 – Università degli Studi di Verona, Strada Le Grazie 15 - 37134 Verona (VR), Italy*
[4] *Department of Biology and Biotechnology "Charles Darwin" – Università "La Sapienza" di Roma, Piazzale Aldo Moro 5 - 00185 Roma (RM), Italy*
[5] *Institute for Integrative Systems Biology (I2SysBio), Universitat de València-CSIC, Carrer del Catedràtic Agustín Escardino Benlloch – 46980 Paterna, Valencia, Spain*
[6] *Department of Agricultural, Food, Environmental and Animal Sciences (D4A) – Università degli Studi di Udine, Via delle Scienze 206 – 33100 Udine (UD), Italy*

[*] *Corresponding author: gabriele.magon@unipd.it*

Abstract

The recent development of regulatory genomics has raised increasing interest in plant research since transcriptional regulation of genes plays a pivotal role in many biological processes. By shedding light on the target genes of the various transcription factors (TFs), it is therefore possible to infer the influence they exert on the different molecular mechanisms. In this regard, the attention was focused on WRKYs, a family of TFs almost exclusively found in plant species. In grapevine, WRKYs are involved in several biological processes, playing a key role in berry development, hormonal balance and signalling, biotic and abiotic stresses responses, and secondary metabolites biosynthesis. In this study, DAP-Seq was used to investigate the regulatory activity of the whole WRKY family in gDNA from young leaves of Cabernet Franc. This approach allowed the definition of the WRKYs cistrome (*i.e.*, the set of bound genes). 46 out of 59 WRKYs gave results, outlining a total number of 674,407 binding events along whole grapevine genome, of which 459,791 (68%) are localized in the perigenic region, according to its intense regulatory activity. Cistrome maps were integrated with gene centred co-expression networks based on a large transcriptomics dataset, and with the results of an ATAC-Seq. This allowed to isolate some High Confidence Targets, characterized by high degree of co-expression with the related TF and laying down in genomic regions of open chromatin. The networks generated can be used to provide a complete regulatory map of WRKY family, shedding light on its biological role in grapevine.

Keywords: DAP-Seq, WRKY, transcription factors, gene regulation, regulatory network