Proceedings of the LXVI SIGA Annual Congress
Bari, 5/8 September, 2023
ISBN: **978-88-944843-4-2**

Poster Communication Abstract – 6.23

THE CISTROME OF THE WRKY TRANSCRIPTION FACTOR FAMILY IN GRAPEVINE (V. VINIFERA L.)

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DAPseq, CRE, TFBS

Transcription factors (TFs) are proteins that bind to DNA and control the expression of genes by recognizing specific short patterns located in the promoter region as well as other regions upstream and downstream of the transcriptional start site. In plants, approximately 10% of genes are responsible for encoding TFs, and many of these TFs are well-known for their involvement in various aspects of plant growth, development, and stress response. This particular study is part of a national research project (PRIN) involving the collaboration of three universities: Udine, Padua, and Rome. The research focuses on exploring the WRKY family of TFs in grapevines. The main objective of the study was to investigate the VvWRKY family using a technique called DNA affinity purification sequencing (DAP-Seq). DAP-Seq is a fast and cost-effective method for identifying TF binding sites. It involves cloning TF genes, expressing them in vitro, capturing target DNA sequences from a genomic DNA library, purifying the TF-DNA complexes, and analyzing the captured DNA using next-generation sequencing to create cistrome and epicistrome maps. We employed DAP-Seq to create cistrome maps for all 59 known VvWRKY proteins. We generated extensive DAP-Seq datasets by isolating DNA from young leaves of the Cabernet Franc grapevine cultivar and refined the data through statistical and bioinformatic analyses creating haplotype specific cistrome maps. Based on these findings and crossing data with gene centered co-expression networks based on a large transcriptomics dataset, we identified high

confidence target genes tracking regulatory modules and dependent biological mechanisms for this important plant gene family.