

## GENOMIC CHARACTERIZATION AND EXPRESSION ANALYSIS OF GENES BELONGING TO A FAMILY OF ABC TRANSPORTERS INVOLVED IN RESPONSE TO STRESS IN *VITIS VINIFERA* L.

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This project arose from the analysis of data obtained from a whole transcriptome sequencing approach, aimed at investigating the response of grapevine (*Vitis vinifera* L.) stilbene synthase (*STS*) genes to biotic (*Plasmopara viticola* infection) and abiotic stress (wounding and UV-C exposure). By means of Next Generation Sequencing (NGS) technology (mRNA-seq, Illumina), the pattern of expression of each member belonging to this large multigenic family was analyzed. At the same time, in an attempt to identify other class of genes potentially related to the *VvSTS* expression and activity, mRNA-seq data sets were also searched for genes displaying specific expression pattern matching that observed for the majority of *STS* genes, using Pavlidis Template Matching (PTM) analysis, a statistic tool of the Multi Experiment Viewer (MeV) software package. Expression patterns of approximately 33000 predictions, based on the 12X V1 coverage assembly of the PN40024 grapevine genotype, were screened in the analysis, leading to the identification of a vast range of genes co-expressed with *VvSTS*. Amongst them we identified genes involved in defense, secondary metabolism (general phenylpropanoid pathway), regulation (TFs), signaling and transport. In particular, the PTM analysis revealed a significant co-expression between *VvSTS* and several members of the pleiotropic drug resistance (PDR) sub-family of ABC transporters which are an important class of membrane-bound proteins with an ATP-binding cassette thought to be involved in the transport of secondary metabolites. Analysis of the 12X V1 grapevine genome sequence indicates the presence of at least 33 *PDR* genes in grapevine. Neighbor-joining analysis of the deduced protein sequences of these 33 *VvPDR* genes together with the already annotated *Arabidopsis PDR* genes led to the identification of seven major clusters. A number of *VvPDR* genes which show similar expression patterns to *VvSTS* genes, in response to stress treatments, were found to cluster with AtPDR12 and NpPDR1, an *AtPDR12*-like gene isolated in *Nicotiana plumbaginifolia*. Previous studies have demonstrated that NpPDR1 confers resistance against *Botrytis cinerea* infection. Furthermore, the *AtPDR12*-like ABC transporter-encoding gene *BcatrB* from *B. cinerea*, appears to be up-regulated by treatment with resveratrol and confers resistance of this pathogen against this phytoalexin, suggesting it may be acting as a resveratrol transporter. We are currently validating the expression patterns of individual *VvSTS* and *VvPDR* genes by qPCR in leaf discs following wounding, UV-treatment and downy mildew infection and studying protein localization using GFP fusion constructs in order to determine whether any of these *VvPDR* candidates might be involved in the resveratrol transport. A resveratrol transporter on the plasma membrane of grape cells would be crucial to avoid the accumulation of this compound to toxic

concentrations within the cell while ensuring it is delivered to the extracellular space to act as a deterrent to fungal attack.