Proceedings of the 56th Italian Society of Agricultural Genetics Annual Congress
Perugia, Italy – 17/20 September, 2012
ISBN **978-88-904570-1-2**

Poster Communication Abstract – 7.27

THE STILBENE SYNTHASE AND CHALCONE SYNTHASE COMPEETING PATHWAYS IN GRAPEVINE: FROM GENOMIC ORGANIZATION TO TRANSCRIPTOME DINAMICS

VANNOZZI A.*, DRY B.I.**, FASOLI M.***, ZENONI S.***, LUCCHIN M.*

*) Department of Agronomy, Food, Natural resources, Animals and Environment, University of Padova, Agripolis, Viale dell'Università 16, 35020 Legnaro (Italy)
**) CSIRO Plant Industry, PO Box 350, Glen Osmond, SA 5064 (Australia)
***) Dipartimento di Biotecnologie, Università degli Studi di Verona, Strada Le Grazie 15, 37134 Verona (Italy)

stilbene synthase, chalcone synthase, downy mildew, abiotic stress, Vitis vinifera

Plant stilbenes are a small group of phenylpropanoids, which have been detected in at least 72 unrelated plant species and accumulate in response to biotic and abiotic stresses such as infection, wounding, UV-C exposure and treatment with chemicals. Stilbenes are formed via the phenylalanine/polymalonate-route, the last step of which is catalysed by the enzyme stilbene synthase (STS), a type III polyketide synthase (PKS). STSs are closely related to chalcone synthases (CHS), the key enzymes of the flavonoid pathway, as illustrated by the fact that both types of enzymes share a high amminoacidic omology, the same crystallographic structure and even the same substrates. *STS* genes appear to exist as a family of closely related genes in the majority of stilbene producing plant species. Also *CHS* genes are organized in a small family in grapevine, comprising three members (*CHS1*, *CHS2* and *CHS3*). In this study a complete characterization of the grapevine *STS* multigenic family has been performed, in order to shade light on its controversial size based on predictions obtained from the two sequenced genomes now available. The analysis has been coupled with a comprehensive set of gene expression analyses on both the PKS families (*CHS* and *STS*) including healthy tissues at differential developmental stages and leaves exposed to both biotic (downy mildew infection) and abiotic (wounding and UV-C exposure) stresses. At least thirty-three full length sequences encoding *VvSTS* genes were identified, which, based on predicted amino acid sequences, cluster in 3 principal groups designated A, B and C. The majority of *VvSTS* genes cluster in groups B and C and are located on chr16 whereas the few gene family members in group A, which are also the closest to the CHS scaffold, are found on chr10. Microarray and mRNA-seq expression analyses revealed different patterns of transcript accumulation between the different groups of *VvSTS* family members and between *VvSTSs* and *VvCHSs*. Indeed, under certain conditions the transcriptional response of *VvSTS* and *VvCHS* genes appears to be diametrically opposed suggesting that flow of carbon between these two competing metabolic pathways is tightly regulated at the transcriptional level. This study represents an overview of the expression pattern of each member of the *STS* and CHS gene families in grapevine under both constitutive and stress-induced conditions. The results strongly indicate the existence of a transcriptional sub-functionalization amongst *VvSTSs* and provide the foundation for further functional investigations about the role and evolution of this large gene family. Moreover, it represents the first study to clearly show the differential regulation of *VvCHS* and *VvSTS* genes, suggesting the involvement of transcription factors (TFs) in both the activation and repression of these genes.