

***IN SILICO* CHARACTERIZATION OF GRAPEVINE STILBENE SYNTHASE MULTIGENIC FAMILY**

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Grapevine represents one of the major agronomically interesting species on a world scale. The always growing economic relevance of this species and the challenge to reach higher and higher excellence levels regarding productivity and quality has led to an intensification in physiology and genetic studies in the last decades. On August 26th 2007 a great step forward in biology field and grapevine research was done: the first detailed grape genome draft was published on “Nature” journal and a few months later a second draft of a heterozygous grapevine variety was presented on “Plus One” journal.

The Grape-genome public issuing represents a fundamental goal *per se*, but, at the same time it is a formidable starting point for several studies aimed at understanding the gene function and variation in this species. The present work rises from this awareness, and deals with the bioinformatic characterization of the stilbene synthase (STS), an important grapevine multigenic family. Stilbene synthase enzymes catalyze the last metabolic step in the biosynthesis of simple stilbenes (cis- and trans-resveratrol). Resveratrol belongs to the phytoalexins family, showing its role in plant resistance response to biotic and abiotic stresses. Resveratrol is also present in wines and beneficial effects on human health have been consistently reported. Based on interpretation supplied with grapevine genome, the stilbene synthase family includes as many as 43 members. All representative hits that in the grape genome matched with sequences belonging to this family were analyzed. The existence of an organization in smaller sub-families potentially linked to differential responses to various elicitations or to specificity in tissue localization were investigated. Multiple alignments of all these sequences and selection of all those showing a functional catalytic site have let us to design several member-specific primers to amplify 23 different STS members and to study their expression pattern in different organs and tissues and under different elicitations, such as downy mildew infection and UV exposure.