

IMPROVING GRAPEVINE WATER STRESS RESILIENCE BY A SPRAY INDUCED GENE SILENCING (SIGS) APPROACH ON TWO GLUTATHIONE TRANSFERASE GENES

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Water is one of the major factors limiting the productivity of agricultural ecosystems worldwide. Since the last century, the average temperatures have increased dramatically, leading to extreme weather conditions that inevitably made crucial the role of water management practices in the control of plant growth and yields. Due to ongoing climate change, drought events are and will become more frequent and severe, hardly limiting the availability of freshwater resources with water demand exceeding the supply capacity of the natural ecosystems. In this context, the emerging SIGS technique could represent a useful strategy to improve crop adaptability and fitness by elucidating mechanisms involved in stress resilience responses. SIGS is based on the high-pressure application of double stranded RNAs (dsRNAs) directly on the leaf surface. In this study, we in vitro produced dsRNAs targeting specific grapevine endogenous gene sequences, putatively involved in drought stress tolerance responses. Previous studies demonstrated that the downregulation of a glutathione S-transferase (GST) gene in Arabidopsis mutants increases endogenous abscisic acid (ABA) levels and triggers the plant anti-oxidant system, in turn improving drought resilience of the primed plants. We thus focused our survey on two putative VvGST genes are inhibited by drought stress in different species, including grapevine, and we evaluated the plant ecophysiological and molecular behaviour of potted vines of 'Chardonnay' after high pressure spraying the leaves (dsGST). Leaf gas exchange, leaf water potential (ψ_{Leaf}), and expression of stress-related and silencing machinery-associated genes were monitored in dsGST and dsGFP (the latter used as negative control of the technique) plants either submitted or not to water deprivation. Interestingly, the dsGST-treated plants revealed increased resilience to severe water deficit condition, as attested by the ecophysiological measurements. To deepen these responses further, molecular (transcript analysis of stress- and ABA-related genes) and biochemical (ABA quantification in leaves) analyses are ongoing.