From Genes to Vineyards: System Biology and New Breeding Technologies for Water Stress Tolerance in Grapevines

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One of the major challenges for food security and sovereignty is to produce stress-tolerant plants without introducing foreign DNA, because the legislative process, that bans transgenics, challenges us to find new solutions for producing plants that can survive the drought. To achieve this goal, we need to identify genes that can be modified to improve stress tolerance in plants. In this work, we present an online tool for exploring the transcriptome of grapevines under water stress, which is one of the most important abiotic stresses affecting viticulture. The tool is based on a comprehensive collection of rna-seq data from 997 experiments, covering four different tissues (leaf, root, berry, and shoot), various levels of water stress, and diverse genetic backgrounds (cultivars and rootstocks) with different levels of tolerance to water stress. The tool will be integrated within VitViz and Grapedia, two web portals that provide access to genomic data of grapevine. The tool allows us to compare the expression of all grapevine genes, using the V3 genome of 'PN40024' as a reference. With this app, we discovered a couple of genes that could boost the drought tolerance of grapevines by cis/trans-genesis (such as the raffinose synthase and AQUILO) or by genome editing (GRETCHEN HAGEN gene). We applied these two methods to different rootstocks and cultivars of grapevines.

Keywords: Transcriptome, Abiotic stress, Drought, Rna-seq, Bioinformatics.