Merging two genomes: a holistic approach to disentangle rootstock-mediated drought and recovery responses

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Abstract (250 words)

Viticulture is facing many challenges due to climate change effects with increasingly attention to save resources, such as water, considering that drought events have been predicted to dramatically increase over the next future. Thanks to the -omics techniques, research pushed forward knowledge to deepen facets of drought response in diverse grapevine-rootstock combinations. However, the regulatory mechanisms orchestrating adaptation strategies during drought and recovery in grafted grapevines need further exploration. Herein, we combined ecophysiological, biochemical and molecular approaches to unravel drought and recovery-induced changes in potted Nebbiolo (NE) plants grafted onto three different rootstocks (3309, Kober5BB, Gravesac), by analysing root and leaf tissues. Rhizosphere bacterial dynamics and arbuscular mycorrhizal fungi (AMF) colonization have also been investigated during drought and recovery phases. Leaf ecophysiology and water relations were monitored over time, revealing diverse behaviours at severe stress (SS) and recovery (REC) conditions. Overall, combining anatomical, biochemical and gene expression data of stress-associated markers involved in ABA metabolism, osmolytes, antioxidant pathways and xylem features from both bionts, different ABA- or osmotic-dependent responses were observed at SS and REC for NE/3009 and NE/Gravesac combinations. Conversely, the NE/Kober5BB combination appeared to be in a *priming* state, displaying higher root ABA content and AM colonization prior to stress imposition, along with a lower scion xylem area. These findings underscore the varied strategies employed by different grafted combinations in drought recovery, considering grapevines not as standalone entities, but rather as holobionts (with their inhabiting microbes) interacting collectively with the surrounding environment.

Keywords: Rootstock, metabarcoding, gas exchange, AMF, Multi-omics.