Effects of stress memory on grapevine resilience in response to recurrent drought and recovery events

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Plants have evolved different strategies to cope with environmental stresses and, although still debated, it was observed that they can remember past stress occurrence.
Anatomical and physiological adjustments have been observed in different grapevine cultivars after repeated drought exposure, however epigenetic, transcriptional and biochemical changes associated with drought-primed ecological memory have been poorly studied.
This work was conceived to test whether exposure to recurring events of mild drought could prime vines to endure severe drought stress. Particularly, we investigated whether the expected improved stress tolerance of *Vitis vinifera* cv Nebbiolo plants subjected over years to moderate and long-lasting water stress events (WS-primed) depended on molecular memory phenomena or on resetting of stress-induced signals. To this aim, a combined multidisciplinary approach, involving eco-physiological, anatomical, biochemical and molecular analyses was adopted. First results revealed that WS-primed vines had reduced gas exchange in well-watered conditions, but at the end of WS imposition were able to maintain higher transpiration and assimilation rates with respect to unprimed plants. Moreover, WS-primed plants accumulated lower amounts of root abscisic acid and had higher content of resveratrol and viniferin, suggesting an increased antioxidant capacity that could help them in counteracting stress effects at the cellular level. WGBS analysis is ongoing to profile changes in DNA methylation landscapes in search of epigenetic signatures associated with specific transcriptome and physiological modifications.
In a future perspective, the gained information will deliver a predictive framework to estimate the impact of moderately dry periods on vine performance, considering memory-associated protective effects against drought.

Keywords: eco-physiology, recurring drought, priming, transcriptome reprogramming, epigenetic signature.