

A molecular phenology scale of grape berry development

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Fruit growth and development consist of a continuous succession of physical, biochemical, and physiological changes driven by a genetic program that dynamically responds to environmental cues. Establishing recognizable stages over the whole fruit lifetime represents a fundamental requirement for research and fruit crop cultivation. This is especially relevant in perennial crops like grapevine (*Vitis vinifera* L.) to scale the development of its fruit across genotypes and growing conditions.

In this work, molecular-based information from several grape berries transcriptomic datasets was exploited to build a molecular phenology scale (MPhS) and to map the ontogenic development of the fruit. The MPhS allowed the alignment of time-series fruit samples proving to be a complementary method for mapping the progression of grape berry development with higher detail compared to classic time- or phenotype-based approaches. We demonstrated that the MPhS application allows defining the shifts of fruit development driven by various agronomic and environmental factors such as cluster thinning, defoliation, water limitation, and varying temperature regimes. Our efforts are to make the R-based MPhS scripts fully available to all users for their research purposes and applications.

Given the global importance of grapevine and the strict relationship between grape quality and the environment, the precise definition of fruit growth stages is of crucial interest to develop and apply mitigation strategies. This is especially important in the context of climate change, which is anticipating the onset of ripening with a negative impact on the overall sustainability of the wine-growing sector.