

The grapevine single-berry clock, practical tools and outcomes

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Abstract (250 words)

The dynamic sequence of physiological events along the three-months of berry development from anthesis to ripe stage has been thoroughly investigated. Most studies were performed on average samples, taking care to crush enough fruits to fairly represent the overall trend of the future harvest. However, phenological stages like 30% caps off (EL25) highlights the asynchronous nature of this population. Consequently, softening, onset of sugar accumulation and coloration were melted by asynchrony in a developmental mumbo jumbo, until their respective timing could be clarified by single berries approaches. To alleviate any statistical bias from pooling unsynchronized fruits, we have gathered a set of approaches on single berries, including non-destructive analysis of time-lapse images, Near InfraRed Spectrometry, basic phenotyping, transcriptomics and metabolomics. In this pertinent reference system, the sugar and acid pathways noticeably accelerated and metabolic transitions were sharpened. Transcripts encoding membrane transporters abruptly switched on during either growth phases were identified, enlightening the special design and bioenergetics of the phloem unloading and vacuolar accumulation pathways, in full quantitative agreement with our new appraisal of the sugar/acidity ratio. Single berries did not depart from strict developmental paths on PCAs from transcriptomic or metabolomic data. It led to the identification of a very small set of genes differentially expressed between clones, without interfering with developmentally regulated ones. This study shows that single berry omics alleviates random noise and temporal ambiguities inherent to mixed fruits, thereby improving the accuracy of the molecular clocks to just a few days.

Keywords: *Vitis vinifera* L., untargeted metabolites, single berry, phenology