



# Book of Abstracts

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## Direct impact of high temperature on Cabernet Sauvignon berries development and metabolism

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Among various environmental factors, temperature is a major regulator affecting plant growth, development and fruit composition. The molecular mechanisms involved in grapevine berries tolerance to high temperature, especially at the fruit level, are poorly understood. To better characterize the sensitivity of berries to the microenvironment, high temperature conditions (between 6°C and 9°C higher than the greenhouse ambient temperature) were locally applied to clusters from fruiting cuttings (*V. vinifera* cv Cabernet Sauvignon), at three phenological stages (middle-green, veraison and mid-maturation) and for 21 day periods. All the samples collected were subjected to transcriptomic (NimbleGen 12x135K array), proteomic (Label Free quantitative LC-MS/MS approach) and metabolic (primary and secondary metabolites) analyses. Results showed dramatic and specific physiological changes in developing grape berries exposed to heat stress. Two key players of the heat stress responses, namely *VvGOLS1* (galactinol synthase) and *VvHsfA2* (heat stress factor), were further characterized (Pillet *et al.*, 2012). The expression profile of *VvGOLS1* correlated positively with galactinol accumulation in heat stressed berries. Transient expression assays showed that *VvHsfA2* transactivates the promoter of *VvGOLS1* in a heat stress dependent manner. Taken together, our results highlight the intrinsic capacity of grape berries to perceive heat stress and to initiate adaptive responses suggesting that galactinol may play a signalling role in these responses Pillet *et al.* (2012). *VvGOLS1* and *VvHsfA2* are involved in the heat stress responses in grapevine berries. *Plant & Cell Physiology* 53:1776-92.

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## Identification of Metabolic Markers of Ripening Near Harvest in Pinot Noir

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Ripeness heterogeneity at maturity becomes a growing problem for the wine industry because it causes inferior crop quality and limits the identification of metabolic markers predicting maturity stage. Few



studies have attempted to assess the contribution of ripeness heterogeneity to the overall fruit composition at maturity. The greatest variability among berries is observed at the onset of ripening (véraison) wherein four developmentally different berry classes, representative of the ripening transition, coexist within the same cluster. When they reach harvest, these berry classes are assumed indistinguishable from one another but there is no scientific evidence to support this assumption. Therefore, the relevance of metabolic markers at maturity may rely not the physiological stage of a cluster near maturity but also the berry classes representative of a cluster. At OSU, we yield the first evidence of a reduction of the transcriptional variability among berry classes at harvest. As next step of a global approach, we developed an integrative analysis combining untargeted metabolomics using Liquid Chromatography Mass Tandem Spectrometry and multivariate technique (Bidirectional Orthogonal Projection to Latent Structures [O2PLS]) to determine putative metabolic markers between three maturity stages (Pre-Harvest, Harvest and Post-Harvest) among four predefined classes of berries. The rationale of the study is to determine the contribution of a berry class to the identification of metabolic markers specific to the maturity stages. Preliminary data suggest that the reduction of the overall metabolic variability among the four berry classes is observed at harvest stage but several metabolites were found to be specific to a given berry class at any of the three maturity stages studied. This suggests that these metabolic markers must reflect a minimal variability among berry classes in order to be considered putative metabolic markers of maturity stages.

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### Putative stage and tissue specific markers of the grape berry ripening transition

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Along with the emergence of high-throughput analysis method, our understanding of the grape berry ripening has been improved. “Omics” datasets have been generated to describe this biological process but no definitive mechanistic model was drawn to describe the ripening transition. One reason that explains such little advances in this area is the lack of strategies to limit biological variability in the sampling method and the low number of powerful analytical tools to integrate multiple datasets. In this context, there is a need to integrate rigorous sampling methodology and powerful multivariate analytical tools to be able to extract the most relevant information from a specific biological process like grape berry ripening. Using asynchronous cluster as fruit model, we developed a fine-tuned method, which focused on 1) the limitation biological variability among berry individuals by following linear stage-wise progression of individual berries (Green, Pink and Red) during the ripening transition; and 2) the use of Bidirectional Orthogonal Projections to Latent Structures (O2PLS) to identify, from transcriptomic datasets, tissue- and berry class-specific genetic markers of the ripening transition. Combining these two approaches, we have identified a series of genes that are stage- and tissue-specific of the ripening transition. A functional screening of some identified markers clearly identified genes relative to biological processes known to occur during the ripening transition, which confirms previous reports about the high relevance of O2PLS to identify putative ripening markers (Zamboni et al., 2010). The analysis also shed light on novel genes related to metabolic pathways that have never been suspected to play a physiological role during the ripening transition. Perspectives to use O2PLS to compare multiple datasets are discussed.

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