Spatial Variability of Grape Berry Maturation Program at the Molecular level

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The application of sensors in viticulture is a fast and efficient method to monitor grapevine vegetative, yield and quality parameters and determine their spatial intra-vineyard variability. Molecular analysis at the gene expression level can further contribute to the understanding of the observed variability by elucidating how pathways responsible for different grape quality traits behave in zones diverging for one or the other parameter. The intra-vineyard variability of a Cabernet Sauvignon vineyard was evaluated by a standard Normalized Difference Vegetation Index (NDVI) mapping approach, employing UAV platform, accompanied by detailed ground-truthing (e.g. vegetative, yield, and berry ripening compositional parameters) that was applied in 14 spots in the vineyard. Berries from different spots were additionally investigated by microarray gene expression analysis, performed at five time points from fruit set to full ripening. The relationships between NDVI and ground measurements were explored by correlation analysis and revealed high variability in the vineyard. Comparison between the transcriptome data of spots with the highest and lowest NDVI values unraveled 968 differentially expressed genes. Among them, were ripening-related genes, found to feature the low vigor spots, and genes involved in photosynthesis mechanisms that were prevalent in the high vigor spots. Spatial variability maps of the expression level of key berry ripening genes showed consistent patterns, aligned with the vineyard vigor map and with spatial maps generated for several vine and berry parameters. These insights suggest that berries from different vigor zones present distinct molecular maturation programs, hence, showing potential in predicting spatial variability in fruit quality.

Keywords: berry ripening, vegetation indices, gene expression analysis, sensors, precision viticulture