Title ACO gene expression in table grape berry development: Response to environmental factors and ethylene modulation

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Abstract

Veraison is an important stage during berry development since there are several physiological and compositional changes that determine quality in this stage. Among these, an increase in ethylene biosynthesis has been found in several varieties. However, due to the large number of grape varieties available and the presence of internal and external factors affecting berry development, it is a challenge to identify when this increase in ethylene biosynthesis occurs and how it is being modulated. The objective of this work was to study the expression of 1-aminocyclopropane-1-carboxylic acid oxidase (ACO) genes in different genotypes and how their expression is modulated under different conditions, such as ethylene inhibition/enhancement and growing regions. Experiments were performed using three varieties of table grapes grown in different areas that were sampled weekly from early stages of fruit development until maturity. In Thompson and Crimson Seedless, the *VvACO1* gene accumulated at higher levels in comparison to *VvAC02* and *VvAC03,* being this accumulation four to five-fold higher than at the harvest stage. The *VvACO1* transcript peak at veraison was concomitant with the characteristic changes observed at veraison, especially in terms of sugar accumulation rate. Red Globe showed a different pattern in *VvACOI* transcript levels, with a sharp increase at harvest time. There were not clear differences in *VvACO* expression levels among growing regions in all the varieties tested. In terms of ethylene modulation, the inhibition of ethylene action performed by 1-MCP application increased *VvACO1* expression levels but at lower levels than the ones observed by Ethephon application. Therefore, despite *VvACO1* expression seems to be a suitable measurement for identifying veraison in table grape, there are differences at the genotypic level that need to be investigated further. Ethylene effect on berry development is under research by NimbleGen cDNA array system (Funded by Fondecyt 1100273).