

EXPRESSION PROFILING OF RIPENING-ASSOCIATED MASTER REGULATORS IN GRAPEVINE BERRIES WITH ALTERED MATURATION TIME

BELLON O.*, FATTORINI C.*, FARALLI M.***, SHMULEVIZ R.*, TORNIELLI G. B.*, MOSER C.**, AMATO A.*, FASOLI M.*, ZENONI S.*

*) Department of Biotechnology, University of Verona, Strada Le Grazie 15, 37134 Verona, Italy

**) Research and Innovation Centre, Fondazione Edmund Mach, via Mach 1, San Michele all'Adige, TN 38098, Italy

***) Center Agriculture Food Environment (C3A), University of Trento, via Mach 1, San Michele all'Adige, TN 38098, Italy

grapevine, ripening, gene expression, transcription factors, hormones signalling

Vitis Vinifera, commonly known as grapevine, is an economically important fruit crop and grown worldwide for winemaking. The precise timing of grape ripening is crucial for producing high-quality wines well-balanced and with desirable flavors and aromas. However, in recent years, climate change led to fastened berry ripening dynamics and earlier harvest dates, posing challenges for harvesting logistics while negatively affecting grape and wine characteristics. These include high sugar concentration in the berries, decreased total acidity (TA) and primary aromas, and increased alcohol content in wines.

Unfortunately, the molecular mechanisms underlying berry ripening are still poorly understood and only a few genes have been identified as potential regulators of this processes so far. Recent functional studies performed for some of these candidates, such as the transcription factors (TFs) VviNAC60, VviNAC33, VviBHLH75, VviWRKY19 and VviERF45, strongly indicated their direct involvement in the control of the onset of berry ripening (veraison).

In order to better understand the role of these TFs, their expression was profiled in grapes with altered ripening kinetics due either to agronomic treatments or to somaclonal mutations.

A few management practices have been applied in a field trial located in San Michele all'Adige in cv Chardonnay with the primary aim of delaying harvest dates, i.e. reduction of leaf area by apical-to-bunch zone defoliation, application of a film-forming antitranspirant, and synthetic Auxin (1-Naphthaleneacetic acid, NAA) application.

These three approaches resulted in a significant delay of the onset of ripening in comparison to the control berries, with a major effect from NAA application. Control and treated Chardonnay berries were collected at regular intervals close to veraison and the expression profiles of VviNAC60, VviNAC33, VviBHLH75, VviWRKY19 and VviERF45 were analyzed by RT-qPCR.

In a similar experiment, NAA treatments were also applied onto clusters of the red-skinned cultivar Corvina, characterized by a later maturation date compared to Chardonnay. The same TFs are going to be analyzed also on the Corvina grapes to understand whether they act similarly to control berry ripening in both varieties.

These findings will be compared to a comprehensive transcriptomic analysis of berries collected from plants of a cross-breeding population segregating for slow/impaired ripening process in some individuals.

Altogether, the results obtained in this study will allow to better characterize the involvement and roles of these key transcription factors and define the molecular mechanisms at the basis of berry ripening onset. This fundamental knowledge represents a starting point for the development of potential strategies to counteract the negative effects of the climate change on wine quality.