

The role of NAC61 transcription factor in the regulation of berry ripening progression

Alessandra Amato^{1*}, Chiara Foresti¹, Luis Orduña², Oscar Bellon¹, Elodie Vandelle¹, José Tomás Matus², Giovanni Battista Tornielli¹, Sara Zenoni¹

¹ Department of Biotechnology, University of Verona, Verona, Italy

² Institute for Integrative Systems Biology, Universitat de València-CSIC, 46980 Paterna, Valencia, Spain

Corresponding author: alessandra.amato@univr.it

Abstract (250 words)

The undergoing global warming scenario is affecting grapevines phenology, including the timing of berry ripening and harvest date, negatively impacting production and quality. This work reports the crucial role of NAC61, a grapevine NAC transcription factor, in regulating metabolic processes occurring from the onset of ripening onwards. NAC61 high confidence targets mainly represent genes acting on stilbene biosynthesis and regulation, and in osmotic and oxidative/biotic stress-related responses. The direct regulation of the stilbene synthase regulator MYB14, the osmotic stress-related gene DHN1b, and the Botrytis cinerea susceptibility gene WRKY52, were all further validated. We demonstrate that NAC61 self-activates and is targeted by NAC60, another master regulator of grapevine organ maturation. Moreover, NAC61 physically interacts with NAC60 triggering the activation of common targets. In our studies, several NAC-NAC synergistic interactions were demonstrated, allowing us to suppose the existence of a NAC-dependent regulatory network orchestrating berry ripening and whose exploration is our current main purpose. As members of such regulatory network, we defined a core of 13 NACs highly correlated with NAC60, NAC61 and NAC33, the latter being a repressor of vegetative organ growth during the vegetative-to-mature phase transition. By using DAP-Seq combined with transcriptomic data and functional assays we reconstructed a hierarchical intra-family regulatory network. We confirmed NAC60 and NAC33 as high hierarchy activators and we traced the downstream network genes been active in fruit ripening. This work is of high interest as identifying key regulators governing berry ripening progression provides important biomarkers affecting quality of grapes and wine.

Keywords: Ripening, NAC transcription factors, Regulatory network, Functional analysis, DAP-Seq