NACs intra-family hierarchical transcriptional regulatory network orchestrating grape berry ripening

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Abstract

Considering that global warming is changing berry ripening timing and progression, uncovering the molecular mechanisms and identifying key regulators governing berry ripening could provide important tools in maintaining high quality grapes and wine. NAC (NAM/ATAF/CUC) transcription factors represent an interesting family due to their key role in the developmental processes control, such as fruit-ripening-associated genes expression, and in the regulation of multiple stress responses. Between the 74 *NAC* family members, we selected 12 of them as putative regulators of berry ripening: *NAC01*, *NAC03*, *NAC05*, *NAC11*, *NAC13*, *NAC17*, *NAC18*, *NAC26*, *NAC33*, *NAC37*, *NAC60* and *NAC61*. Genome wide analyses and functional assays permitted to reconstruct a hierarchical intra-family regulatory network in which most of the selected NACs resulted as transcriptional activators of other *NACs*. Moreover, to investigate the common regulative role of the selected NACs on the grapevine transcriptome, all the annotated *V. vinifera* genes were listed and the most represented genes between all the DAP-seq results were identified. Interestingly, at the top of the ranking we found many genes related to maturation and senescence such as an *indole-3-acetic acid-amido synthetase*, which could be involved in the establishment and maintenance of low IAA concentrations in ripening berries, a *laccase*, encoding for a phenylpropanoid pathway-related enzyme, the *senescence-inducible chloroplast stay-green protein 1*, triggering Chl degradation, and the *UTP-glucose-1-phosphate uridylyltransferase*, encoding for a carbohydrate-metabolism-related enzyme which is highly expressed in berries at veraison. All these results lay a foundation stone in understanding the genetic regulation of such a complex process as fruit ripening.

Keywords: Berry ripening, cistrome, NAC, hierarchical intra-family network.