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The regulation of ABA-induced anthocyanin accumulation in grape berry

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Abstract

Color is a key quality trait for grape berry and the producing wines. Berry color of red genotypes is mainly determined by the quantity and composition of anthocyanins accumulated in the skin and/or pulp. Both genetic and environmental factors could influence the quantity and composition of anthocyanins, while the underlying mechanisms are not fully clear. To explore the mechanisms underlying the diversity of anthocyanin accumulation in grape berry, we compared two grapevine genotypes showing distinct sensitivities to ABA-induced anthocyanin biosynthesis, where one genotype showed minor responses to exogenous ABA application while the other showed significant increase in anthocyanins after exogenous ABA application. Transcriptome and metabolome were conducted and their analysis pointed out that the cis-element of *MYBA1* might be responsible for the observed phenotypes. The promoters of *MYBA1* were then cloned from both genotypes and several differences in their sequences were observed, but without any mutations in the ABRE elements. Dual-luciferase assay was applied to test the promoter activity and their responses to ABA, with a series of fragmented promoters of *MYBA1* from both genotypes. The mutations in a portion of promoter not containing any ABREs were identified as the core for determining the sensitivity of ABA-induced anthocyanin accumulation. These results show the importance of sequence context on the function of cis-element and provide novel insights into the understanding of the mechanisms underlying the diversity of anthocyanin accumulation in grape berry.

Keywords: color, cis-regulation, sequence context, anthocyanin diversity, metabolism.