

Vineyard environments influence Malbec grapevine phenotypic traits and DNA methylation patterns in a clone-dependent way

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Abstract

Clonal selection and vegetative propagation determine low genetic variability in grapevine cultivars, although it is common to observe diverse phenotypes. Environmental signals may induce epigenetic changes altering gene expression and phenotype. The range of phenotypes that a genotype expresses in different environments is known as phenotypic plasticity. DNA methylation is the most studied epigenetic mechanism, but only few works evaluated this novel source of variability in grapevines. In the present study, we analyzed the effects on phenotypic traits and epigenome of three *Vitis vinifera* cv. Malbec clones cultivated in two contrasting vineyards of Mendoza, Argentina. Anonymous genome regions were analyzed using Methylation-Sensitive Amplified Polymorphism (MSAP) markers. Clone-dependent phenotypic and epigenetic variability between vineyards were found. The clone that presented the clearer MSAP differentiation between vineyards was selected and analyzed through Reduced Representation Bisulfite Sequencing. Twenty-nine differentially methylated regions (DMRs) between vineyards were identified and associated to genes and/or promoters. We discuss about a group of genes related to hormones homeostasis and sensing that could provide a hint of the epigenetic role in the determination of the different phenotypes observed between vineyards and conclude that DNA methylation has an important role in the phenotypic plasticity and that epigenetic modulation is clone-dependent.

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