

Identification of differentially methylated regions (DMRs) associated with leaf physiological acclimation to experimental long-term drought in holm oak (*Quercus ilex* L.)

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Abstract

Shifts in rainfall patterns and increasing temperatures associated with climate change are causing widespread forest decline, especially due to the increase and duration of droughts. Tree species may have to quickly adapt to these changing conditions, and epigenetic modifications are expected to play a key role in regulating rapid acclimation responses. In this study, we measured acclimation physiological responses and methylome responses in mature holm oak trees (*Quercus ilex* L.) subjected to 15 years of experimental accrued drought (-29% of rainfall) and their respective controls with ambient rainfall. We hypothesized that: i) oak trees exposed to long-term drought will exhibit different foliar traits due to adaptative phenotypic plasticity to drought, ii) methylation levels will differ between the drought and control trees allowing the identification of drought-induced differentially methylated regions (DMRs), and iii) these DMRs correlate with the differences in foliar traits. Our results confirmed all hypotheses. The methylome analysis revealed 84 drought-related DMRs among trees from different precipitation treatments, of which 17 DMRs were significantly associated with measured phenotypic responses. This study provides evidence of the role of epigenetic regulation for tree acclimation responses in natural populations of holm oak facing increased droughts and identified candidate genes potentially involved in drought adaptation.

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