

Title: Dynamics of DNA methylation in *Posidonia oceanica* (L.) Delile from different environments

Abstract

The dynamics of DNA methylation play important roles in the regulation of gene expression and genome stability. These epigenetic modifications are regulated by environmental factors through the activation of different writers/erasers that can be at the basis of the appearance of different phenotypic responses to environmental stresses. In the context of climate change, understanding the impact of ocean warming in combination with local pressures is fundamental for exploring resilience capacity of marine organisms. Seagrasses, which are marine angiosperms particularly vulnerable to environmental changes, display high degree of phenotypic plasticity colonizing heterogeneous environments. Here we explore, for the first time, the dynamics of DNA-methylation in *Posidonia oceanica* shoots from meadows experiencing different nutrient conditions (oligotrophic, Ol; eutrophic, Eu). The expression of key genes involved in the *de novo* DNA methylation, maintenance, demethylation and histone modifications were selected and analysed after one, two and five weeks of exposure to single (temperature and nutrients) and combined stressors (nutrients + temperature). Global DNA methylation levels were also measured in both Ol and Eu plants at the same time points. Our results revealed that the global DNA methylation and the expression dynamics of selected genes were influenced by both plants origin and the duration of the imposed stresses. Temperature was the main driver modulating gene expression during the experiment. These findings suggest that DNA methylation in marine plants is a dynamic process that could potentially regulate phenotypic responses to environmental changes.

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