

## CHANGES IN GENOME METHYLATION AND TRANSCRIPTIONAL ACTIVATION OF STRESS RESPONSIVE GENES IN *POSIDONIA OCEANICA* PLANTS UNDER STRESS CONDITION

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DNA methylation is one of the most important epigenetic marks, which acts in the control of gene transcriptional activity in response to both endogenous factors and external stimuli (Dennis *et al.*, 1998; Finnegan *et al.*, 1993; Aina *et al.*, 2004; Boyko *et al.*, 2007). Despite the importance of DNA methylation, information on the classes of genes that are regulated in a coordinate manner by methylation in response to stress is still lacking. In our work, we have been studying whether changes in DNA methylation occur and face genes potentially involved in mediating plant tolerance /response in *Posidonia oceanica* (L.) Delile plants exposed to Cd-heavy metal (CdCl<sub>2</sub> 10 – 50µM for 6h, 2 or 4d). Noteworthy, this seagrasses which plays a relevant role in the Mediterranean coastal ecosystem as bioindicator, (Ott, 1980; Piazzini *et al.*, 1999), is able to absorb and accumulate metals from sediments (Pergent-Martini, 1998; Maserti *et al.*, 2005) thus influencing metal bioavailability.

Through Methylation-Sensitive Amplified Polymorphism (MSAP) analysis we were able to identify changes in genome methylation pattern involving both non-coding sequences and specific classes of genes in Cd-treated *vs* control plants. The expression level of three stress-responsive genes, directly or indirectly related to metal detoxification was also analyzed, via quantitative Real Time PCR (qRT-PCR): *PoHsp70* (*Posidonia oceanica* HEAT SHOCK PROTEINS70), *PoMIT* (*Posidonia oceanica* METAL ION TRANSPORT) and *PoCAT* (*Posidonia oceanica* CATALASE). We found that the transcription of these differentially methylated genes was up-regulated following Cd treatment, thus supporting a role for DNA methylation in modulating gene expression in response to stress.

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