



## Response of key stress-related genes of the seagrass *Posidonia oceanica* in the vicinity of submarine volcanic vents

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**Abstract.** Submarine volcanic vents are being used as natural laboratories to assess the effects of increased ocean acidity and carbon dioxide (CO<sub>2</sub>) concentration on marine organisms and communities. However, in the vicinity of volcanic vents other factors in addition to CO<sub>2</sub>, which is the main gaseous component of the emissions, may directly or indirectly confound the biota responses to high CO<sub>2</sub>. Here we used for the first time the expression of antioxidant and stress-related genes of the seagrass *Posidonia oceanica* to assess the stress levels of the species. Our hypothesis is that unknown factors are causing metabolic stress that may confound the putative effects attributed to CO<sub>2</sub> enrichment only. We analyzed the expression of 35 antioxidant and stress-related genes of *P. oceanica* in the vicinity of submerged volcanic vents located in the islands of Ischia and Panarea, Italy, and compared them with those from control sites away from the influence of vents. Reverse-transcription quantitative polymerase chain reaction (RT-qPCR) was used to characterize gene expression patterns.

Fifty-one percent of genes analyzed showed significant expression changes. Metal detoxification genes were mostly down-regulated in relation to controls at both Ischia and Panarea, indicating that *P. oceanica* does not increase the synthesis of heavy metal detoxification proteins in response to the environmental conditions present at the two vents. The up-regulation of genes involved in the free radical detoxification response (e.g., CAPX, SODCP and GR) indicates that, in contrast with Ischia, *P. oceanica* at the Panarea site faces stressors that result in the production of reactive oxygen species, triggering antioxidant responses. In addition, heat shock proteins were also activated at Panarea and

not at Ischia. These proteins are activated to adjust stress-accumulated misfolded proteins and prevent their aggregation as a response to some stressors, not necessarily high temperature.

This is the first study analyzing the expression of target genes in marine plants living near natural CO<sub>2</sub> vents. Our results call for contention to the general claim of seagrasses as “winners” in a high-CO<sub>2</sub> world, based on observations near volcanic vents. Careful consideration of factors that are at play in natural vents sites other than CO<sub>2</sub> and acidification is required. This study also constitutes a first step for using stress-related genes as indicators of environmental pressures in a changing ocean.

### 1 Introduction

Seagrass meadows rank amongst the most valuable ecosystems to society in terms of the flow of services and values they support (Costanza et al., 1997; Seitz et al., 2014). They form multidimensional habitats for organisms directly participating in the trophic dynamics (Mazzella et al., 1992) and are a primary food source for herbivores on coral reefs, lagoons, and other shallow habitats (Orth et al., 2006). Seagrasses reduce sediment resuspension and their roots enhance sediment accretion, thus maintaining high water quality. Seagrass ecosystems also represent key sites for carbon storage in the biosphere and are important as CO<sub>2</sub> sinks (McLeod et al., 2011; Fourqurean et al., 2012; Pendleton et al., 2012; Pergent et al., 2012).