Antioxidant and stress-related genes in the seagrass *Posidonia oceanica* in the vicinity of natural CO₂ vents at different nutrient conditions

Lauritano Chiara[1], Bulleri Fabio[2], Ravaglioli Chiara[2], Tamburello Laura[2], Buia M. Cristina[1], Procaccini Gabriele[1]*

[1] Stazione Zoologica Anton Dohrn, Napoli, Italy

[2] Dipartimento di Biologia, Università di Pisa, CoNISMa, Italy

* gpro@szn.it

Studies on stress genes are fundamental to understand how marine organisms maintain or re-estabilish a normal metabolism in face of physical or chemical disturbances. Aquatic organisms are in fact constantly exposed to environmental stimuli and natural and/or dissolved anthropogenic variables/compounds, including both physical (e.g. cold, heat, salinity and pH) and chemical (e.g. heavy metals, hydrocarbons and other pollutants) stressors. Human activities have intensified in coastal area, increasing the number of stressors that act simultaneously over natural systems (e.g. ocean acidification and eutrophication).

In this study, Reverse Transcription-Quantitative Polymerase Chain Reaction (RT-qPCR) was used to characterize metabolic processes at the cellular level in response to natural CO₂-enrichment and artificial nutrient-enrichment in proximity of a volcanic vent located in the Ischia island (Gulf of Naples, Tyrrhenian Sea). We evaluated the differential expression of selected stress genes in the seagrass Posidonia oceanica collected in a control site and in the vicinity of the CO₂ vents. In each location, plants experienced three different nutrient concentrations: natural (without adding any nutrient), low- and high- enrichments.

Results show that nutrient addition mainly induced an over-expression of genes codifying for antioxidant proteins, in sites not influenced by CO₂-enrichment. In particular, we observed an increase in the activity of glutathione synthase, responsible of the synthesis of the antioxidant protein glutathione. In addition, we also observed the up-regulation of glutathione peroxidase, catalase, ascorbate reductase and cythocrome P450. When analysing the effects of nutrients in the acidified site, trends in expression changes were similar, but expression levels were notably lower. Interestingly, the over-expression of the above mentioned genes was always higher at low nutrient exposure, while other antioxidant enzymes (i.e. glutathione S-transferase and glutathione reductase) were more activated in high nutrient conditions. The difference in response between acidified and control site and in different nutrient conditions seems to derive from the combined affect of multiple stressors, in a way that still remains obscure. Effects of different stressors should be disentangled in order to identify stress-specific genes as early indicators of stressful conditions at sea and during laboratory experiments.