

## ***Cymodocea nodosa* response to simulated CO<sub>2</sub>-driven ocean acidification: a first insight from global transcriptome profiling**

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Global climate changes are imposing multiple pressures to marine organisms. The rising atmospheric CO<sub>2</sub> concentration is causing substantial changes in ocean physics, chemistry and biology. At least three synergic environmental stressors have been recognized as primary driven by CO<sub>2</sub> emissions: ocean warming, oxygen loss and ocean acidification. The effects of CO<sub>2</sub>-driven ocean acidification on seagrass metabolism remain largely understudied. A few studies have been conducted near submarine volcanic vents, which mimic the future ocean acidification scenarios, allowing researchers to investigate the performance of marine organisms under long-term exposure to high-CO<sub>2</sub> levels. Apart from these, some mesocosm-based experiments have investigated growth and physiological responses to high CO<sub>2</sub>.

For this work, we built an outdoor mesocosm facility at the Centre of Marine Sciences' field station in Algarve, Portugal, to experimentally manipulate CO<sub>2</sub> levels and investigate the effects of high-CO<sub>2</sub>/low pH on seagrass metabolism and underlying molecular mechanisms. *Cymodocea nodosa* plants were collected in Cadiz Bay at the end of January 2014 and transported to the mesocosm facility. After a one week acclimation period, *C. nodosa* were either kept under normal (400 ppm) or elevated (1200 ppm) CO<sub>2</sub> concentration for 12 days. Water physico-chemical parameters, irradiance, and chlorophyll-fluorescence-derived photosynthetic parameters were monitored on a daily basis. Here we present, for the first time in this species, results obtained using Illumina RNAseq technology and *de-novo* transcriptome assembly. Using *C. nodosa* RNAs extracted at the beginning and the end of the experiment, we assembled more than 70 thousands unique transcripts and were able to annotate more than 90% of them using the Annocript pipeline. Differential expression analysis revealed about 500 transcripts significantly differentially regulated between plants kept under control and high-CO<sub>2</sub> conditions. Pathways showing largest changes in gene expression included isoprenoid and amino-acid biosynthesis, porphyrin-containing compound metabolism, amine and polyamine biosynthesis, lipid and carbohydrate metabolism. Transcriptome sequencing also significantly increases the molecular resources available for *C. nodosa*, almost completely absent before this study.