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ORIGINAL ARTICLE

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Genomewide transcriptional reprogramming in the seagrass *Cymodocea nodosa* under experimental ocean acidification

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Abstract

Here, we report the first use of massive-scale RNA-sequencing to explore seagrass response to CO_2-driven ocean acidification (OA). Large-scale gene expression changes in the seagrass *Cymodocea nodosa* occurred at CO_2 levels projected by the end of the century. *C. nodosa* transcriptome was obtained using Illumina RNA-Seq technology and *de novo* assembly, and differential gene expression was explored in plants exposed to short-term high CO_2/low pH conditions. At high pCO_2, there was a significant increased expression of transcripts associated with photosynthesis, including light reaction functions and CO_2 fixation, and also to respiratory pathways, specifically for enzymes involved in glycolysis, in the tricarboxylic acid cycle and in the energy metabolism of the mitochondrial electron transport. The upregulation of respiratory metabolism is probably supported by the increased availability of photosynthates and increased energy demand for biosynthesis and stress-related processes under elevated CO_2 and low pH. The upregulation of several chaperones resembling heat stress-induced changes in gene expression highlighted the positive role these proteins play in tolerance to intracellular acid stress in seagrasses. OA further modifies *C. nodosa* secondary metabolism inducing the transcription of enzymes related to biosynthesis of carbon-based secondary compounds, in particular the synthesis of polyphenols and isoprenoid compounds that have a variety of biological functions including plant defence. By demonstrating which physiological processes are most sensitive to OA, this research provides a major advance in the understanding of seagrass metabolism in the context of altered seawater chemistry from global climate change.

KEYWORDS

carbohydrate metabolism, *Cymodocea nodosa*, ocean acidification, protein folding, seagrasses, transcriptome

1 | INTRODUCTION

Ocean acidification (OA) is a direct consequence of the oceanic uptake of atmospheric CO_2 (Caldeira & Wickett, 2003) that is causing fundamental ecological transformations as a result of changes in physical, chemical and biological environments (Gruber, 2011; Hoegh-Guldberg & Bruno, 2010). A drop of ocean pH of about 0.1 pH units from ≈ 8.21 to 8.10 has already been recorded (Royal Society 2005), and a further reduction of 0.3–0.5 units is predictable by the end of the century (Caldeira & Wickett, 2005; Feely, Doney, & Cooley, 2009). In this process, the relative proportion of the

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