**Diatom acclimation to elevated CO2 via cAMP signalling and coordinated gene expression**

LETTERS

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Metabolic and regulatory genes were differentially impacted by changes in CO2. The initial response to an abrupt increase in CO2 included upregulation of genes required for transcriptional regulation and kinase activity, potentially reflecting CO2 specific signaling mechanisms. Once steady-state conditions with elevated CO2 were attained, genes required for energy-producing metabolic pathways, including oxidative phosphorylation, TCA cycle and photosynthesis, were preferentially downregulated, as were genes involved in transcriptional regulation, ion transport, kinase activity and protein degradation, suggesting a general reduction in metabolism under high CO2. This corroborates our previous physiological measurements of decreased respiration and photosynthetic oxygen production under elevated CO2 and nitrate limitation. A significant upregulation of components of the ribosome under steady-state high CO2 may reflect either an increased capacity for protein synthesis or a high turnover of ribosomal proteins, whereas the downregulation of the same gene category in transition suggests disparate modes of regulation between transition and steady-state exposure to elevated CO2.

The metabolic rearrangement we observed under steady-state elevated CO2 and nitrate limitation resulted from downregulation of the energy-consuming processes of CCM and photorespiration because cells were unable to increase growth rate owing to nitrate limitation, a common limiting factor in the oceans. Diatoms are also limited by other factors, such as iron or light, in vast regions of the ocean, and may exhibit different metabolic rearrangements or growth rate enhancement in response to elevated CO2 under these other conditions. Our analysis discovered genes that exhibit CO2 responses regardless of nitrogen status, and provide insights into the mechanisms of CO2 sensing, signaling and metabolic rearrangement necessary to predict how diatoms will acclimate in future oceans.

**1. Highlight in the text and then check off the terms that you find in this section:**

\_\_\_\_\_ upregulation \_\_\_\_\_ active site \_\_\_\_\_ downregulation

\_\_\_\_\_ metabolic/metabolism \_\_\_\_\_ oxidative phosphorylation

\_\_\_\_\_ steady-state \_\_\_\_\_CCM \_\_\_\_\_ corroborates \_\_\_\_\_ synthesis

\_\_\_\_\_ disparate modes \_\_\_\_\_signaling \_\_\_\_\_acclimate

**2. Use a science dictionary (text or online) for help in defining the following terms.**  Be prepared to help your group make meaning of these terms by taking notes for each word.

upregulation-

active site-

downregulation-

metabolic/metabolism-

oxidative phosphorylation-

steady state-

CCM-

corroborates-

synthesis-

disparate modes-

signaling-

acclimate-

3. Which genes were downregulated in a steady-state, elevated CO2 environment?

4. How is this different than what happened in a transition state (abrupt increase in CO2)?

5. Why did the researchers examine gene expression in low nitrogen conditions?

6. Make a prediction: how will diatoms such as *Thalassiosira pseudonana* respond to high

levels of CO2 (climate change)?