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

LETTERS

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To identify potential linkages between an initial response and eventual metabolic rearrangements under steady-state conditions, we identified groups of co-expressed genes based on a combined data set of 98 RNA sequencing and microarray data sets from a range of conditions, including our chemostat experiments. Of the 400 clusters of co-expressed genes, 160 exhibited significant correlation to CO2 partial pressure during transition or steady-state exposure. The clustering analysis yielded biologically meaningful insights, grouping together functionally related genes associated with energy metabolism including light harvesting, photosynthesis, and respiration. These energy metabolism gene clusters were differentially expressed only after acclimation to steady-state elevated CO2, along with other clusters containing genes implicated in cell signaling, suggesting a suite of gene clusters are probably involved in diatom metabolic rearrangement. High external CO2 is expected to reduce the need for the CCM as well as photorespiration, owing to the competitive inhibition of Rubisco’s oxygenase activity by CO2. Genes in the CCM/photorespiration cluster all share a short upstream sequence, TGACGT, recently identified as a *cis-*regulatory sequence that downregulates expression of the CO2 responsive β-CA in the distantly related diatom *Phaeodactylum tricornutum*. Furthermore, two transcription factors, one in each of 2 sub-clusters, exhibit close homology and are classified in the same phylogenetic groupas a cAMP-activated transcription factor in *P. tricornutum* shown to bind the *cis-*regulatory element and to contribute to downregulation of the β-CA gene in response to increased CO2. These lines of evidence suggest that the two transcription factors identified in the CCM/photorespiration cluster may function to downregulate transcription of their own cluster by binding to the common upstream *cis*-regulatory region. This further implies that these transcription factors repress their own transcription, creating a negative feedback on the repression of this cluster, a feature common in biological systems.

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

\_\_\_\_\_ downregulation \_\_\_\_\_chemostat \_\_\_\_\_ transcription factors

\_\_\_\_\_ metabolic/metabolism \_\_\_\_\_ photorespiration \_\_\_\_\_ microarray data

 \_\_\_\_\_ phylogenetic \_\_\_\_\_homology

 \_\_\_\_\_ steady-state \_\_\_\_\_ transition state \_\_\_\_\_ negative feedback

\_\_\_\_\_ competitive inhibition \_\_\_\_\_CCM \_\_\_\_\_upstream

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

downregulation-

chemostat-

transcription factors-

metabolic/metabolism-

photorespiration-

microarray data-

phylogenetic-

homology-

steady state-

transition state-

negative feedback-

competitive inhibition-

CCM-

upstream-

3. When the researchers looked at clusters (groups) of co-expressed genes, what did they find?

4. What does finding 2 similar transcription factors in a related diatom suggest?

5. The negative feedback resulting in repression of transcription factors is in response to what?

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

 levels of CO2 (climate change)?