Sequence analysis and gene expression of potential components of copper transport and homeostasis in *Thalassiosira pseudonana*

JIAN GUO[1], BEVERLEY R. GREEN[2] AND MARIA T. MALDONADO[3]

[1]Department of Earth, Ocean, and Atmospheric Sciences, University of British Columbia, Vancouver, BC, Canada (*correspondence: jguo@mbari.org)
[2]Department of Botany, University of British Columbia, Vancouver, BC, Canada (brgreen@mail.ubc.ca)
[3]Department of Earth, Ocean, and Atmospheric Sciences, University of British Columbia, Vancouver, BC, Canada (mmaldonado@eos.ubc.ca)

Copper (Cu) is an essential, redox-active metal for phytoplankton, playing key roles in, for example, respiration and photosynthesis. Furthermore, in some phytoplankton Fe limitation increases significantly the Cu demand. On the other hand, high Cu concentrations may cause oxidative damage. In the sea, Cu concentrations can range from low (0.5-6 nM) in open waters to high (2-150 nM) in coastal areas, suggesting that Cu can be either limiting or toxic. Despite the importance of Cu nutrition in marine phytoplankton, the specific genes and proteins involved in Cu transport and homeostasis are largely unknown. Using the diatom *T. pseudonana* as a model organism, we searched its genome for candidate genes involved in Cu assimilation and intracellular distribution. We then tested the transcriptional expression of these genes in cultures acclimated to various Cu and Fe levels. We identified genes encoding two putative homologs of high-affinity Cu transporters (CTR). These putative CTR-like Cu transporters have the conserved CTR Cu-binding motifs and transmembrane domains, and their gene expression was down-regulated by addition of Cu to low Cu acclimated cultures, which is typical of genes encoding CTRs. For intracellular Cu distribution, we identified genes encoding putative Cu transporting P_{1B}-type ATPases, and Cu chaperones delivering Cu to the trans-Golgi compartment, and to the mitochondria, respectively. The expression of these intracellular Cu transporters and chaperones genes was down-regulated by a Cu addition, indicating that they might be involved in Cu redistribution under low Cu. Furthermore, the vast majority of the genes identified were up-regulated by low Fe, suggesting a significant role for Fe in controlling the expression of Cu-related genes and a complex interaction between Cu and Fe cellular response networks.