Nucleotide sequence and phylogeny of a plastocyanin gene in the marine diatom, *Thalassiosira oceanica*.

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Preface

All experiments and analyses were designed and carried out by the author. Holly Nikiforuk performed a large portion of the work associated with culturing of the specimen used in the experiments. Sarah-Ann Quesnel translated the English abstract into French. All ideas, experiments and written communication were completed in collaboration with the author's supervisor, Dr. Neil Price.

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Chapter 1. Background

Introduction

The world's oceans are a major sink for carbon dioxide and are increasingly important to offset rising atmospheric CO_2 levels as terrestrial sinks become limited (Hurtt *et al.*, 2002, Canadell *et al.*, 2007). Phytoplankton, which contribute to the oceanic uptake, represent only 1-2% of global carbon but account for roughly 40% of total global carbon (C) fixation (Falkowski *et al.*, 2000). Their photosynthetic production drives the biological pump that delivers carbon to the deep ocean through deposition of particulate organic matter (Raven & Falkowski, 2002). A variety of chemical and environmental factors such as nutrient resources limit the rate of oceanic photosynthetic C fixation. Trace metal nutrients are especially important because they are present at exceedingly low concentrations in surface water and are essential co-factors for phytoplankton growth. Current estimates are that iron, for example, limits phytoplankton growth in ~30% of the world's oceans (Morel *et al.*, 1991, Tsunda et al., 2003). To better understand the constraints on oceanic C production we need to know how trace metals affect phytoplankton growth and specifically how phytoplankton have adapted to lower trace metal concentrations.

Trace Metal Requirements

Trace metals are important constituents of enzymes and proteins (Da Silva & Williams, 1991) and in some secreted proteins such as ferretin (Castruita *et al.*, 2006). In

virtually all organisms, they function in such enzymes as Cu, Fe, Zn or Ni superoxide dismutases, Fe-S proteins and cytochromes. In oxygenic photosynthetic organisms, trace metals are largely involved in the photosynthetic machinery (Raven *et al.*, 1999). Iron, for example, is required for core photosynthetic proteins in photosynthetic center (PS) I and II and in the electron transport carriers ferrodoxin and cytochrome b_6f (Raven et al., 1999). Other trace metals such as Cu are required for such proteins as plastocyanin (Sigfridsson, 1998), a congeneric protein to Fe-containing cytochrome c_6 (Kerfeld & Krogmann, 1998). The amounts and types of trace metals required by photoautotrophs may be largely determined by the presence and use of specific photosynthetic proteins. For example, most of the Cu requirement in some green algae and diatoms can be attributed to the use of plastocyanin (Li *et al.*, 1996, Peers & Price, 2006).

Differences exist in the trace metal requirements of the two evolutionary distinct lineages of photosynthetic organisms; the red and green supergroups. These two supergroups of phytoplankton diverged early in the evolution of eukaryotic phytoplankton and gave rise to 2 plastid lineages (Falkowski *et al.*, 2004). The green group, which utilizes chlorophyll b, has increased requirements for Cu, Zn and Fe while the red group, which utilizes chlorophyll c, has increased requirements for Cd, Co and Mn (Quigg *et al.*, 2003). Variations in trace metal availability are thus predicted to affect the relative abundance of the red and green phytoplankton by affecting differentially their photosynthetic ability and viability.

Trace metal concentrations, in the ocean, varies in time and space and thus may affect phytoplankton ecology and evolution. In both the proterozoic and archean oceans, Fe was much more bioavailable than present day. An abundance of Fe is thought to have

contributed to the early ecological dominance of the green algae and their relatives (Falkowski *et al.*, 2004); groups of organisms unified by a common plastid origin. Oxygenation of the environment led to Fe precipitation and decreased availability and eventual succession by members of the red plastid line (Falkowski et al., 2004). Other trace metals, such as Cu, increased as Fe decreased. The low Fe and Mn requirements and high Cd, Co and Mo requirements of the red supergroup are thought to be an adaptation to changes in availability of trace metals that allowed for its ecological success (Quigg *et al.*, 2003). The disparity in metal concentrations between the paleo and modern day oceans also exists today between the near shore and offshore waters. Coastal waters contain far more nutrients, including trace metals, than oceanic waters because they receive inputs from terrestrial sources. Although the red supergroup has come to dominate modern oceans, certain members have a greater ability and propensity to proliferate in low nutrient waters than their counterparts found under high nutrient conditions (Ryther & Kramer, 1961, Sunda & Huntsman, 1995, Peers *et al.*, 2005, Price, 2005).

Regardless of evolutionary heritage, trace metal requirements for growth of phytoplankton exceeds availability in the ocean (Boyd *et al.*, 2000, Coale *et al.*, 1996, Morel et al., 1991). This imbalance is a common theme in biology and is found in many systems. In the human body, for example, Fe is sequestered to limit bacterial growth (Moeck & Coulton, 1998) and provides a barrier to potential pathogens. Likewise, some regions of the oceans contain such low concentrations of some metals that primary production and hence photosynthesis is inhibited (Boyd et al., 2000, Coale et al., 1996, Morel et al., 1991, Marchetti *et al.*, 2006). For organisms in the oceanic environment, the

imbalance is exacerbated by complex chemical reactions that affect the speciation of the metals and greatly reduce their bioavailability (Hudson, 2005).

Responses to Trace Metal Limitations

Reconciling the imbalance between the concentrations of metal required for growth and the concentrations present in the environment is a significant obstacle for photosynthetic organisms to overcome. Some species of phytoplankton have adapted and developed specific mechanisms to respond to trace nutrient limitation. Under Fe limiting conditions, for example, phytoplankton from Fe-limited environments increase Fe transport capacity (Maldonado & Price, 1999), produce siderophores (Trick *et al.*, 1983), reduce Fe (III) chelates (Maldonado & Price, 2001) and ingest insoluble particulate Fe (Nodwell & Price, 2001). Other physiological and biochemical responses act to decrease the cellular requirements for metals.

One such adaptation involves changes in the stoichometry of components of the light reaction of photosynthesis to decrease the amount of Fe needed. Comparison of *Thalassiosira oceanica* and *Thalassiosira weissflogii* reveals that the former species has reduced the amount of photosystem I (PSI) and cytochrome b_6f, which are disproportionately iron rich (Strzepek & Harrison, 2004). Other adaptations in other species include the biochemical pathways that completely replace metal demanding biochemical pathways (Posey & Gherardini, 2000) or the replacement of metal-containing enzymes with non-metal containing enzymes. Indeed, the replacement of the Fe-based photosynthetic electron carrier, ferrodoxin, with a functionally equivalent flavin-based flavodoxin under Fe-limiting conditions has been observed in the laboratory

and in the field (LaRoche *et al.*, 1996). This adaptive response appears to be common to many species of plankton with the exception of some species isolated from Fe-rich environments (Erdner *et al.*, 1999). The expression and presence of flavodoxin follows a habitat-dependent pattern that corresponds to the availability of iron in the environment, occurring in habitats where trace-nutrients are limiting (Erdner & Anderson, 1999, Erdner *et al.*, 1999). Adaptations such as these have helped oceanic phytoplankton survive in metal poor regions of the sea. What other adaptations do oceanic phytoplankton posses?

Horizontal and Vertical Gene Transfers

The adaptations described above depend on the genetic make up of the organism in question. After all, the sum of the genetic composition of an organism is the product of its historical or recent adaptations. The genetic composition of an organism is determined by the inheritance of genes. These genes may be inherited vertically from progenitors or, less frequently, horizontally from exogenous sources. In bacteria, horizontal transfer of genes from exogenous sources may be a significant mechanism of gene acquisition and play a role in survival. Indeed, it is been proposed that the majority of operational genes are continuously exchanged among some species (Jain *et al.*, 1999). The observation is not restricted to terrestrial bacterial communities. Within the marine environment, multiple species of the cyanobacteria, *Prochlorococcus* and *Synechococcus*, have acquired the eukaryotic Calvin cycle genes and fructose bisphosphate aldolase, resulting in partial or complete replacement of the endogenous homologues (Rogers *et al.*, 2007). Other cases of transfer between domains have been reported, for example, asmuch as

24% of the genome of the bacterium, *Thermotoga maritime,* originated from archaea (Nelson *et al.*, 1999).

Despite a pervasive number of examples of horizontal gene transfer in bacteria much less is known about gene transfer among eukaryotes. Three cases of interchange of mitochondrial genes have been documented in species of higher plants (Andersson, 2005). In two of these, the mechanisms of transfer remain unknown but viruses have been implicated (Bergthorsson *et al.*, 2003, Won & Renner, 2003). In the third, an intermediary vector is thought not to be required because of prolonged contact between the donor and host (Davis & Wurdack, 2004). The mixotroph, *Bigelowiella natans*, contains a chloroplast derived from secondary endosymbiosis of a green alga, but roughly 20% of it's 78 plastid targeted proteins have been acquired from foreign sources other than the green alga symbiont (Archibald *et al.*, 2003). For the most part, examples of horizontal gene transfer in protists can be traced to a phagocytic event (Doolittle, 1998). It should be noted that although some modern day photosynthetic organisms lack phagocytic ability, at one time their ancestors must have been phagocytic to acquire the chloroplast. Lack of phagocytic ability does not exclude the possibility of recent lateral gene transfer by non-phagocytic protists by other mechanisms such as viral vectors that have been observed to carry photosynthetic genes (Zeidner *et al.*, 2005). Neither do domain boundaries seem to hinder lateral transfer of genes into eukaryotes. Several cases of horizontal gene transfer from prokaryote to eukaryote have been postulated, including the transfer of 3-hydroxy-3-methylgutaryl-coenzyme A class 2 reductase found in *Giardia* (Loftus *et al.*, 2005), iron hydrogenase in *Nyctotherus* and the fungal catalases (Hall *et al.*, 2005).

Endosymbiotic gene transfer and subsequent vertical inheritance has largely determined an organism's trace metal requirement (Quigg et al., 2003). Contemporary photosynthetic eukaryotes are composed of two separate evolutionary lineages that diverged following the primary photosynthetic endosymbiosis. Member of these lineages use unique combinations of chlorophyll molecules and extrinsic proteins associated with the oxygen evolving center (De Las Rivas *et al.*, 2004). The "green" lineage uses chlorophyll a and chlorophyll b while the "red" lineage uses chlorophyll a and chlorophyll c. The endosymbiont (plastid) within these photosynthetic eukaryotes underwent gene reduction and transfer of genes to the host nucleus. Each lineage has inherited a unique composition of cellular proteins which has largely determined its trace metal requirements. The red supergroup preferentially using Cd, Co and Mn metalloproteins, and the green supergroup Cu, Zn and Fe metalloproteins (Quigg et al., 2003). These trace metal requirements have in turn affected the distribution and activity of those photoautotrophs in the sea.

The acquisition of genes encoding proteins that function in the mitochondria or chloroplast requires a signal peptide to target the protein to the location of function. In the chloroplast of chlorophyll a/b-containing organisms this necessitates an encoded, translated and attached peptide to the protein of function (Morse & Nassoury, 2005). In chlorophyll a/c-containing organisms, greater complexities exist because of the presence of one or two additional membranes surrounding the chloroplast; a result of secondary or tertiary endosymbosis. The presence of a signal peptide allows for the proper translocation of the protein through these additional membranes.

Determination of inheritance

Inheritance of specific genes through vertical or horizontal gene transmission can be determined using an established set of criteria. The evidence of horizontal transfer lies in the signal or marker of the event verses the event itself. Codon composition difference in organisms also allows us to detect a horizontal gene transfer event (Palenik *et al.*, 2006). Codon composition of different strains and of different species may vary (Rocap *et al.*, 2003). Provided that the sequence between donor and recipient organisms differ in their codon bias, transferred genes may be delineated by the difference. For example, the oceanic cyanobacteria, *Synechococcus* (WH 8501) possess genomic regions encoding metal-related genes that have atypical GC content compared to the rest of it's genome but are absent from its sequenced coastal cognate, *Synechococcus* (CC 9331) (Palenik et al., 2006). Although straightforward, this criterion is limited and more difficult to apply or evaluate due to the high quantity of sequence data that is needed.

Another criterion to identify transferred genes can be the unusual distribution of the gene. In a particular species the presence of a gene that is otherwise found in distant relatives but not close relatives may be an indicator (Brown, 2003). Clearly, this criterion alone is insufficient to determine lateral gene transfer because gene loss can also create such a pattern. The unusual distribution of glutamate dehydrogenase genes has been used as evidence of lateral gene transfer within and between prokaryotes and eukaryotes (Andersson & Rogers, 2003).

A third common criterion for lateral gene transfer is the appearance of unexpected gene homologies (Campbell, 2000). Structural and sequence homology has been used to

suggest lateral gene transfer of dermonecrotic toxin between spiders and bacteria (Cordes & Binford, 2006). Programs such as Basic Local Alignment Search Tool (BLAST) (Altschul *et al.*, 1997) provide a quick way to screen for putative genes that may have been transferred through other sources. Finally, the strongest indicator for putative horizontal gene transfer event may be the discordant relationship between the gene sequence or encoded protein (Avise, 2004, Syvanen, 1994) and other phylogenetic markers between species. Incongruence of the phylogenetic tree for two Archeal genes in *Thermotoga maritime*, together with gene structure and distribution data, has been used to identify multiple lateral transfers between Achaea and Bacteria (Nesbø *et al.*, 2001).

In general, both the gene tree and the species tree reach greater accuracy as the number of characters (genes and species, respectively) and size of the character (nucleotide sequence length) increases (Harrison & Langdale, 2006). Datasets may be analyzed using several different methods such as maximum likelihood, maximum parsimony, neighbour-joining and Bayesian analysis. These methods vary in the algorithms they employ (Holder & Lewis, 2003), and each has its own strengths and weaknesses.

No single phylogenetic method performs well under all conditions (Li, 1997). Some of the methods make explicit assumptions about the pattern and rate of character substitution while others make some and others none at all. A method that makes no assumptions is not necessarily better than ones that do. The performance and usefulness of a particular method is dependent on the assumptions and also the computational procedure and optimality criterion used. These issues are considered below.

The maximum likelihood (ML) searches for the maximum likelihood value for the observed character states for each possible tree and chooses the tree that results with the larges ML value (Felsenstein, 2005). It makes explicit assumptions about the rate of evolution and pattern of substitution of characters and hence allows for the choice of different probabilistic models. In general, ML methods are considered to be consistent, but inconsistency can occur if the substitution model that is chosen is unrealistic or if the rate of evolution is assumed to be uniform although it is not.

On the other hand, maximum parsimony (MP) inference makes no explicit assumptions at all and searches for the tree that requires the smallest number of evolutionary changes to explain the observed character states of the outer taxonomic units (Salemi, 2003). Minimizing the number of substitutions also conversely minimizes the number of homeoplastic events and hence this approach does not work well for sequences that have had a large number of parallel, convergent or back reversal substitutions. When the degree of divergence becomes so large that homeoplasys are common, this method may result in misleading inferences.

Neighbour-joining methods seek to find neighbouring outer taxonomic units (OTU) sequentially such that the total length of all the branches forming the tree is minimized. This method, like MP, does not assume a rate constancy but assumes that the effects of unequal rates among branches can be corrected from the distances established in the distance matrix used to construct it (Salemi, 2003). Hence, the accuracy of the distance matrix will affect the accuracy of the NJ inference. If the lengths of the sequences are short then large statistical errors will occur in the distance matrix and the accuracy of this inference will be affected.

A concern with all three of these methods is that when a sufficiently large number of OTUs are used, these methods will use heuristic algorithms, finding the best solution to a subset of sequences, and then sequentially adding branches to that subset to find the best inferred tree. However, this approach does not fully appraise the sample space that incorporates all trees and may result in the inference of a tree that is the best local solution but not global. The use of Bayesian analysis minimizes the probability of this occurring (Holder & Lewis, 2003).

Bayesian analysis (Ronquist & Huelsenbeck, 2005) uses a method based on the Bayes theorem. This type of analysis starts with a random tree typology with random branch lengths and random likelihood parameters and slight changes to the parameter that are either accepted or rejected depending on the posterior probability. After a significant number of cycles the trees generated by Markov sampling start to converge around a posterior probability maxima. A posterior probability can be best described as a probability that the deduced tree fits the observations, in our case, sequence data. The deduced posterior probability may be either the best local posterior probability or the best global posterior probability. To ensure that the tree converged upon is the tree with the highest posterior probability the program uses Metropolis couple Markov chain Monte Carlo to create heated chains to ensure that the resultant tree is indeed the correct one.

Depending on the results of these types of analysis we can infer the relationship of a specific sequence to homologous sequences present in other organisms, thus allowing us to deduce the possible source of our sequence. To explain why a specific gene has been acquired we can examine current ecological data, such as the distribution of the organisms that posses it, as well as, make inferences from geo-historical information.

Thesis Objectives

Recently, an oceanic diatom, *T. oceanica* (CCMP 1005), isolated from a Fe-limited region of the sea was found to have drastically reduced Fe requirements. Differential spectroscopy identified a small soluble blue copper protein that had a high degree of sequence similarity to plastocyanin (Peers and Price, 2006), a Cu-containing photosynthetic electron transport protein.

In the following body of work I have isolated the gene for plastocyanin from chlorophyll a/c-containing diatom, *T. oceanica* (CCMP 1005), an organism that has been found to be especially adapted to low Fe environments. Until now, plastocyanin has been observed to be restricted to the chlorophyll a/b-containing lineage of photosynthetic organisms (Sandmann, 1986, Sandmann *et al.*, 1983, Sigfridsson, 1998). Using the sequence of the plastocyanin gene I have evaluated its phylogenetic relationship to other plastocyanins and have speculated on the possible reason for such an acquisition. The occurrence of the plastocyanin gene in other chlorophyll a/c-containing diatoms was investigated.

References

Altschul, S. F., Madden, T. L., Schaffer, A. A., Zhang, J. H., Zhang, Z., Miller, W. & Lipman, D. J. 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Research* **25**:3389-402.

Andersson, J. 2005. Lateral gene transfer in eukaryotes. *CLMS Cell Mol. Life Sci.* **62**:1189-97.

Andersson, J. O. & Rogers, A. J. 2003. Evolution of glutamate deyhdrogenase genes: evidence for lateral gene transfer within and between prokaryotes and eukaryotes. *BMC Evol. Biology* **3**.

Archibald, J. M., Rogers, M. B., Toop, M., Ishida, K. & Keeling, P. 2003. Lateral gene transfer and the evolution of plastid-targeting proteins in the secondary plastid-containing alga *Bigelowiella natans. Proc. Natl. Acad. Science USA* **100**:429-40.

Avise, J. C. 2004. *Molecular Markers, Natural History, and Evolution, Second Edition.* Sinauer Associates, Sunderland, MA,

Bergthorsson, U., Adams, K. L., Tomason, B. & Palmder, J. D. 2003. Widespread horizontal transfer of mitochondrial genes in flowering plants. *Nature* **424**:197-201.

Boyd, P. W., Watson, A. J., Law, C. S., Abraham, E. R., Trull, T., Murdoch, R., Bakker, D. C. E., Bowie, A. R., K.O., B., Chang, H., Charette, M., Croot, P. & Downing, K. 2000. A mesoscale phytoplankton bloom in the polar Southern Ocean stimulated by iron fertilization. *Nature* **407**:695-702.

Brown, J. R. 2003. Ancient horizontal gene transfer. *Nat Rev Genet* **4**:121-32.

Campbell, A. M. 2000. Lateral gene transfers in prokaryotes. *Theoretical Population Biology* **57**:71-77.

Canadell, J. G., Raupach, M. R., Field, C. B., Buitenhuis, E. T., Ciais, P., Conway, T. J., Gillett, N. P., Houghton, R. A. & Marland, G. 2007. Contributions to accelerating atmospheric CO_2 growth from economic activity, carbon intensity, and efficiency of natural sinks. *Proceedings of the National Academy of Sciences* **104**:18866-70.

Castruita, M., Saito, M., Schottel, P. C., Elmegreen, L. A., Myneni, S., Stiefel, E. I. & Morel, F. M. M. 2006. Overexpression and characterization of an iron storage and DNA-binding Dps protein from *Trichodesmium erythraeum*. *Appl. Environ. Microbiol.* **72**:2918-24.

Coale, K. H., Johnson, K. S., Fitzwater, S. E., Gordon, R. M., Tanner, S. & Chavez, F. P. 1996. A massive phytoplankton bloom induced by an ecosystem-scale iron fertilization experiment in the equatorial Pacific Ocean. *Nature* **383**:513-17.

Cordes, M. H. J. & Binford, G. J. 2006. Lateral gene transfer of a dermonecrotic toxin between spiders and bacteria. *Bioinformatics* **22**:264-68.

Da Silva, J. & Williams, R. 1991. *The Biological Chemistry of the Elements: The Inorganic Chemistry of Life.* Oxford University Press, New York, 600p.

Davis, C. C. & Wurdack, K. J. 2004. Host-to-parasite gene transfer in the flowering plants: phylogenetic evidence from *Malipighiales*. *Science* **305**:676-78.

De Las Rivas, J., Balsera, M. & Barber, J. 2004. Evolution of oxygenic photosynthesis: genome-wide analysis of the OEC extrinsic proteins. *Trends in Plant Science* **9**:18-25.

Doolittle, W. F. 1998. You are what you eat: a gene transfer ratchet could account for bacterial genes in eukaryotic nuclear genomes. *Trends in Genetics* **14**:307-11.

Erdner, D. L. & Anderson, D. M. 1999. Ferrdoxin and flavodoxin as biochemical indicators of iron limitation during open-ocean iron enrichment. *Limnology and Oceanography* **44**:1609-15.

Erdner, D. L., Price, N. M., Doucette, G. J., Pelato, M. & Anderson, D. M. 1999. Characterization of ferredoxin and flavodoxin as markers of iron limitation in marine phytoplankton. *Marine Ecology Progress Series* **184**: 43-53.

Falkowski, P., Scholes, R., Boyle, E., Canadell, J., Canfield, D., Elser, J., Gruber, N., Hibbard, K., Högberg, P., Linder, S., Mackenzie, F., Moore, B., Pedersen, T., Rosenthal, Y., Seitzinger, S., Smetacek, V. & Steffen, W. 2000. The global carbon cycle: A test of our knowledge of earth as a system *Science* **290**:291-96.

Falkowski, P. G., Katz, M. E., Knoll, A. H., Quigg, A., Raven, J. A., Schofield, O. & Taylor, F. J. R. 2004. The evolution of modern eukayotic phytoplankton. *Science* **305**:354-60.

Felsenstein, J. 2005. PHYLIP (Phylogeny Inference Package) version 3.6. Distributed by the author. Department of Genome Sciences, Univewrsity of Washington, Seattle.

.

Hall, C., Brachat, S. & Dietrich, F. S. 2005. Contribution of Horizontal Gene Transfer to the Evolution of *Saccharomyces cerevisiae*. *Eukaryotic Cell* **4**:1102-15.

Harrison, C. J. & Langdale, J. A. 2006. A step by step guide to phylogeny reconstruction. *The Plant Journal* **45**:561-72.

Holder, M. & Lewis, P. O. 2003. Phylogeny estimation: traditional and Bayesian approaches. *Nat Rev Genet* **4**:275-84.

Hudson, R. J. M. 2005. Trace metal uptake, natural organic matter and the free-ion model. *Journal of Phycology* **41**:1-6.

Hurtt, G. C., Pacala, S., Moorcroft, P., Caspersen, J., Shevliakova, E., Houghton, R. & Moore, B. 2002. Projecting the future of the U.S. carbon sink. *Proc Natl Acad Sci U S A* **99**:1389-94.

Jain, R., RIvera, M. C. & Lake, J. A. 1999. Horizontal gene transfer among genomes: The complexity hypothesis. *Proc. Natl. Acad. Science USA* **96**:3801-06.

Kerfeld, C. A. & Krogmann, D. W. 1998. Photosynthetic cytochromes c in cyanobacteria, algae, and plants. *Annual Review of Plant Physiology and Plant Molecular Biology* **49**:397-425.

LaRoche, J., Boyd, P. W., McKay, R. M. L. & Geider, R. J. 1996. Flavodoxin as an in situ marker for iron stress in phytoplankton. *Nature* **382**:802-05.

Li, H. H., Quinn, J., Culler, D., GirardBascou, J. & Merchant, S. 1996. Molecular genetic analysis of plastocyanin biosynthesis in *Chlamydomonas reinhardtii*. *Journal of Biological Chemistry* **271**:31283-89.

Li, W.-H. 1997. *Molecular Evolution.* Sinauer and Associates, Sunderland, MA,

Loftus, B., Anderson, I., Davies, R., Alsmark, U. C. M., Samuelson, J., Amedeo, P., Roncaglia, P., Berriman, M., Hirt, R. P., Mann, B. J., Nozaki, T., Suh, B., Pop, M., Duchene, M., Ackers, J., Tannich, E., Leippe, M., Hofer, M., Bruchhaus, I., Willhoeft, U., Bhattacharya, A., Chillingworth, T., Churcher, C., Hance, Z., Harris, B., Harris, D., Jagels, K., Moule, S., Mungall, K., Ormond, D., Squares,

R., Whitehead, S., Quail, M. A., Rabbinowitsch, E., Norbertczak, H., Price, C., Wang, Z., Guillen, N., Gilchrist, C., Stroup, S. E., Bhattacharya, S., Lohia, A., Foster, P. G., Sicheritz-Ponten, T., Weber, C., Singh, U., Mukherjee, C., El-Sayed, N. M., Petri, W. A., Clark, C. G., Embley, T. M., Barrell, B., Fraser, C. M. & Hall, N. 2005. The genome of the protist parasite *Entamoeba histolytica*. *Nature* **433**:865-68.

Maldonado, M. T. & Price, N. M. 1999. Utilization of iron bound to strong organic ligands by plankton communities in the subarctic Pacific Ocean. *Deep-Sea Research II* **46**.

Maldonado, M. T. & Price, N. M. 2001. Reduction and transport of organically bound iron by *Thalassiosira oceanica* (Bacillariophyceae). *Journal of Phycology* **37**:298-309.

Marchetti, A., Maldonado, M. T., Lane, E. S. & Harrison, P. J. 2006. Iron requirements of the pennate diatom *Pseudo-nitzschia*: Comparison of oceanic (high-nitrate, low-chlorophyll waters) and coastal species. *Limnology and Oceanography* **51**:2092-101.

Moeck, G. S. & Coulton, J. W. 1998. TonB-dependent iron acquisition: mechanisms of siderophore-mediated active transport. *Molecular Microbiology* **28**:675-81.

Morel, F. M. M., Hudson, R. J. M. & Price, N. M. 1991. Limitation of productivity by trace metals in the sea. *Limnology and Oceanography* **36**:1742-55.

Morse, D. & Nassoury, N. 2005. Protein targeting to the chloroplast of photosynthetic eukaryotes: getting there is half the fun. *Biochimica et Biophysica Acta* **1743**:5-19.

Nelson, K. E., Clayton, R. A., Gill, S. R., Gwinn, M. L., Dodson, R. J., Haft, D. H., Hickey, E. K., Peterson, J. D., Nelson, W. C., Ketchum, K. A., McDonald, L., Utterback, T. R., Malek, J. A., Linher, K. D., Garrett, M. M., Stewart, A. M., Cotton, M. D., Pratt, M. S., Phillips, C. A., Richardson, D., Heidelberg, J., Sutton, G. G., Fleischmann, R. D., Eisen, J. A., White, O., Salzberg, S. L., Smith, H. O., Venter, J. C. & Fraser, C. M. 1999. Evidence for lateral gene transfer between Archaea and Bacteria from genome sequence of *Thermotoga maritima*. *Nature* **399**:323-29.

Nesbø, C., L'Haridon, S., Stetter, K. & Doolittle, W. 2001. Phylogenetic analysis of two 'archaeal' genes in *Thermotoga maritima* revealmultiple transfers between Archaea and Bacteria. *Mol Biol Evol* **18**:362-75.

Nodwell, L. M. & Price, N. M. 2001. Direct use of inorganic colloidal iron by marine mixotropic phytoplankton. *Limnology and Oceanography* **46**.

Palenik, B., Ren, Q., Dupont, C. L., Myers, G. S., Heidelberg, J. F., Badger, J. H., Madupu, R., Nelson, W. C., Brinkac, L. M., Dodson, R. J., Durkin, A. S., Daugherty, S. C., Sullivan, S. A., Khouri, H., Mohamoud, Y., Halpin, R. & Paulsen, I. T. 2006. Genome sequence of *Synechococcus* CC9311: Insights into adaptation to a coastal environment. *Proceedings of the National Academy of Sciences* **103**:13555-59.

Peers, G. & Price, N. M. 2006. Copper-containing plastocyanin used for electron transport by an oceanic diatom. *Nature* **441**:340-44.

Peers, G., Quesnel, S.-A. & Price, N. M. 2005. Copper requirements for iron acquisition and growth of coastal and oceanic diatoms. *Limnology and Oceanography* **50**:1149-58.

Posey, J. E. & Gherardini, F. C. 2000. Lack of a role for iron in the lyme disease pathogen. *Science* **288**:1651-53.

Price, N. M. 2005. The elemental stoichiometry and composition of an iron-limited diatom. *Limnology and Oceanography* **50**:1159-71.

Quigg, A., Finkel, Z. V., Irwin, A. J., Rosenthal, Y., Ho, T.-Y., Reinfelder, J. R., Schofield, O., Morel, F. M. M. & Falkowski, P. G. 2003. The evolutionary inheritance of elemental stoichiometry in marine phytoplankton. *Nature* **425**:291-94.

Raven, J. A., Evans, M. C. W. & Korb, R. E. 1999. The role of trace metals in photosynthetic electron transport in O_2-evolving organisms. *Photosynthesis Research* **60**:111-49.

Raven, J. A. & Falkowski, P. 2002. Oceanic sinks for atmospheric CO_2. *Plant, Cell & Environment* **22**:741-55.

Rocap, G., Larimer, F. W., Lamerdin, J., Malfatti, S., Chain, P., Ahlgren, N. A., Arellano, A., Coleman, M., Hauser, L., Hess, W. R., Johnson, Z. I., Land, M., Lindell, D., Post, A. F., Regala, W., Shah, M., Shaw, S. L., Steglich, C., Sullivan, M. B., Ting, C. S., Tolonen, A., Webb, E. A., Zinser, E. R. & Chisholm, S. W. 2003. Genome divergence in two *Prochlorococcus* ecotypes reflects oceanic niche differentiation. *Nature* **424**:1042-47.

Rogers, M., Patron, N. & Keeling, P. 2007. Horizontal transfer of a eukaryotic plastid-targeted protein gene to cyanobacteria. *BMC Biology* **5**:26.

Ronquist, F. & Huelsenbeck, J. P. 2005. Mr Bayes: Bayesian inference of phylogenetic trees. *Bioinformatics* **17**:754-55.

Ryther, J. H. & Kramer, D. D. 1961. Relative iron requirement of some coastal and offshore plankton algae. *Ecology* **42**:444-46.

Salemi, M. 2003. *The Phylogenetic Handbook: A practical approach to DNA and protein phylogeny.* Cambridge University Press, Cambridge, United Kingdom,

Sandmann, G. 1986. Formation of plastocyanin and cytochrome c-553 in different species of blue-green algae. *Archives of Microbiology* **145**:76-79.

Sandmann, G., Reck, H., Kessler, E. & Boger, P. 1983. Distribution of plastocyanin and soluble plastidic cytochrome c in various classes of algae. *Archives of Microbiology* **134**:23-27.

Sigfridsson, K. 1998. Plastocyanin, an electron-transfer protein. *Photosynthetic Research* **57**:1-28.

Strzepek, R. F. & Harrison, P. J. 2004. Photosynthetic acrhitecture differs in coastal and oceanic diatoms. *Nature* **431**:689-92.

Sunda, W. G. & Huntsman, S. A. 1995. Iron uptake and growth limitation in oceanica and coastal phytoplankton. *Marine Chemistry* **50**:189-206.

Syvanen, M. 1994. Horizontal gene transfer: evidence and possible consequences. *Annual Review of Genetics* **28**:237-61.

Trick, C. G., Anderson, R. J., Price, N. M., Gillam, A. & Harrison, P. J. 1983. Examination of hydroxamate-siderophore production by neritic eukaryotic marine phytoplankton. *Marine Biology* **75**:9-17.

Tsunda, A., Takeda, S., Saito, H., Nishioka, J., Nojiri, Y., Kudo, I.,Kiyosawa, H., Shiomoto, A., Imai, K., Tsuneo, O., Simamoto, A., Tsumune, D., Yoshimura, T., Aono, T., Hiuma, A., Kinugasa, M., Suzuki, K., Sohrun, Y., Nori, Y., Tani, H., Deguchi, Y., Tsurushima, N., Ogawa, H., Fukami, K., Kuma, K. & Saino, T. 2003. A mesoscale iron enrichment in the western Subarctic Pacific induces a large centric diatom bloom. *Science* **300**.

Won, H. and Renner, S. S. 2003. Horizontal gene transfer from flowering plants to *Gentum*. *Proc. Natl. Acad. Science USA* **100**:10824-29.

Zeidner, G., Bielawski, J. P., Shmoish, M., Scanlan, D. J., Sabehi, G. & Beja, O. 2005. Potential photosynthsis gene recombination between *Prochlorococcus* and *Synechococcus* via viral intermediates. *Environmental Microbiology* **7**:1505-13.

Chapter 2. Nucleotide sequence and phylogeny of a plastocyanin gene in the marine diatom, *Thalassiosira oceanica*.

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Abstract

Diatoms are thought to have acquired an Fe-containing cytochrome (cyt) c_6 to transfer electrons between cyt b_6f and photosystem (PS) I of the photosynthetic apparatus like other chlorophyll a/c-containing phytoplankton. Here we report the isolation and cloning of a plastocyanin gene from *Thalassiosira oceanica* (CCMP 1005). The gene encoded a Cu-containing protein that is known in other organisms to functionally replace the Fe-containing cyt c_6. The inferred protein sequence had the highest identity with the green haptophyte, *Emiliania huxleyi,* and possessed many of the globular properties necessary for function and interaction with upstream and downstream partners. Eleven strains of oceanic and coastal diatoms were screened for the presence of the plastocyanin gene using degenerate primers: one other species was observed to contain the gene; *T. oceanica* (CCMP 1006). Phylogenetic analysis of the 5.8 rRNA gene of these species showed that both *T. oceanica* strains with plastocyanin were closely related to each other. The cloned sequence of T. oceanica (CCMP 1006) contained greater than 80% of the protein-coding region and shared 99% nucleotide identity and 100% conserved unique intronic region. The inferred protein sequence of this species had 100% identity with the inferred protein sequence of *T. oceanica* (CCMP 1005).

Résumé

Durant l'évolution de la photosynthèse, il est pensé que les diatomées ont acquis cytochrome (cyt) c6, une protéine contenant un atome de Fe, pour le transfert des électrons entre le complexe cyt b6f et le photosystème (PS) I de l'appareil photosynthetique, comme d'autres phytoplanctons ayant les chlorophyll a/c. Ici, nous rapportons l'isolement et clonage du gène de plastocyanin du diatomée Thalassiosira oceanica (CCMP 1005). Le gene codait une protéine contenant un atome de Cu qui est connue de remplacer fonctionellement cyt c6 (contenant un atome de Fe). La sequence inférée de la proteine montrait la plus grande identité avec Emiliania huxleyi, un haptophyte vert (green haptophyte), et possèdait de nombreuses propriétés globulaires nécessaires aux fonctions et intérections avec les protéines partenaires en amont et en aval. Onze espèces de diatomées océanique et côtières ont été examinées pour la présence du gène codant pour plastocyanin en utilisant les amorces dégénérées (degenerate primers): une autre espèce a révélé la présence du gène de plastocyanin; T. ocenica (CCMP 1006). L'analyse phylogénétique des gènes 5.8 rRNA de cet espèce a démontré que la souche de T. oceanica possèdant le plastocyanin sont étroitement reliées entre elles. Les séquences clônées de T. oceanica (CCMP 1006) recelaient plus de 80% de la région cryptant la protéine et partageaient 99% des nucléotides et 100% des régions introniques uniques. La séquence de protéine inférée de ces espèces de phytoplanctons ont démontré 100% d'identité avec celle inférée pour T. oceanica (CCMP 1005).

Introduction

Oxygenic photosynthesis evolved within an ancestral prokaryote (cyanobacterium) and subsequently spread to eukaryotes through primary, secondary and tertiary endosymbiosis. Its essential features include a manganese-containing oxygen evolving center, two photosystems with light-harvesting chlorophyll pigments, and electron carriers that participate in cyclic and non-cyclic electron flow (Nelson & Ben-Shem, 2005). Although differences are found in the types of accessory pigments used to capture light energy and in the extrinsic proteins of the oxygen evolving center (De Las Rivas et al., 2004), most components of the light reaction of photosynthesis have remained conserved among eukaryotes with two notable exceptions. First, in algae, flavodoxin and ferrodoxin are functionally interchangeable redox proteins that transfer electrons to NADP+. When Fe is in short supply flavodoxin can replace ferrodoxin (a heme -containing protein) (Erdner *et al.*, 1999), but some higher plants can only use ferrodoxin (Arabidopsis Genome Initiative, 2000). Second, in some cyanobacteria and unicellular green algae cytochrome c_6 or plastocyanin can be used in electron transport depending on environmental conditions (Inda & Pelato, 2002, Merchant & Bogorad, 1986). Cytochrome c_6 in absent from higher plants and plastocyanin is used constitutively (De la Rosa *et al.*, 2002). Unicellular algae with red algal-derived plastids are thought to use only cytochrome c_6 and to lack plastocyanin (Sandmann, 1986, Sandmann et al., 1983).

Cytochrome c_6 and plastocyanin are soluble metalloproteins in the thylakoid lumen that transfer electrons between cytochrome b_6f complex and photosystem I

(Nelson & Ben-Shem, 2005, Nugent, 1996). Plastocyanin is a 10,000-12,000 kDa Cu-containing protein that has been extensively studied and well characterized (Sigfridsson, 1998). All plastocyanins exhibit a characteristic oxidized-minus-reduced spectrum and contain several conserved amino acids crucial to Cu binding (Nersissian & Shipp, 2002). Cytochrome c_6 is a low molecular weight soluble redox carrier typically comprised of 83-90 amino acids and a single haem group (Howe *et al.*, 2006). Both proteins have similar isoelectric points and midpoint redox potentials (De la Rosa et al., 2002). As far as it is known, there is little reason to use one protein over the other (Raven et al., 1999), except if the necessary metal co-factor is unavailable.

In cyanobacteria and certain unicellular green algae, plastocyanin expression is regulated by the availability of copper. *Chlamydomonas reinhardtii*, for example, synthesizes plastocyanin preferentially in the presence of Cu in adequate amounts required for photosynthesis (Merchant & Bogorad, 1986). When Cu is limiting, plastocyanin production ceases and the heme-containing cytochrome c_6 is induced as a substitute (Li *et al.*, 1996). In the green alga *Scendesmus vacuolatus*, cytochrome c_6 concentrations increases when Fe concentration increases (Peleato *et al.*, 2003). When one of these proteins is absent and insufficient amounts of the metal co-factor is available for synthesis of the other, growth is inhibited.

The distribution of plastocyanin and cytochrome c_6 among photosynthetic eukaryotes is believed to be determined by evolutionary history (Sandmann, 1986, Sandmann *et al.*, 1983). Both proteins existed in oxygenic photosynthetic bacteria that eventually became plastids of green algae and higher plants. Depending on gene loss, living cyanobacteria may posses both plastocyanin and cytochrome c_6. Unicellular

chlorophyll a/b-containing organisms, such as the unicellular green alga, *Chlamydomonas reinhardtii*, may use either protein to transport electrons from cytochrome b_6f to PSI (Merchant & Bogorad, 1986). The lineage that gave rise to higher plants appears to have lost cytochrome c_6 (De la Rosa et al., 2002) which only use plastocyanin. A cytochrome c_6-like protein has been identified in *Arabidopsis* (Gupta *et al.*, 2002), but it contains an additional 12 amino acid loop that alters the surface properties of the protein and is not believed to be a functional cytochrome c_6 (Howe et al., 2006). Chlorophyll a/c-containing organisms, derived from secondary endosymbiosis of a red alga, are thought to have only cytochrome c_6 (Sandmann, 1986, Sandmann et al., 1983).

The presence of cytochrome c_6 and absence of plastocyanin in algae with chlorophyll a/c was originally established by spectroscopic analysis (Sandmann, 1986, Sandmann et al., 1983). In eight species of chromophyte algae that were examined the oxidized-minus-reduced spectra lacked the diagnostic absorption maxima at 597 nm for a type-1 copper protein (Sandmann et al., 1983). Since this work, many more classes and species of algae have been obtained in culture and are available for study. Very recent results challenge the pattern of distribution of plastocyanin and cytochrome c_6 originally established. Plastocyanin sequences have now been identified from expressed sequence tags (EST) of *Emiliania huxleyi* (haptophyte) (Nosenko *et al.*, 2006) and *Karenia brevis* (dinoflagellate) (Nosenko et al., 2006) and the nucleotide database of *Karlodinium micrum* (dinoflagellate) (Patron *et al.*, 2006). Peers and Price (2006) purified a plastocyanin from *Thalassiosira oceanica* (CCMP1005) and showed that it had a high similarity to plastocyanin from cyanobacteria. Reduced-minus-oxidized spectra indicate

that *T. oceanica* (CCMP1005) has reduced amounts of cytochrome b_6f, as compared to its coastal cognate, *Thalassiosira weissflogii* (CCMP 1335), and non-detectable amounts of cytochrome c_6 even in Fe-replete media (Strzepek & Harrison, 2004).

The distribution of plastocyanin in *Karenia brevis* is thought to have occurred through tertiary endosymbiosis of a haptophyte ancestor that itself acquired the plastocyanin from either a green alga or cyanobacterium (Nosenko et al., 2006). *Karlodinium micrum*, like *Karenia brevis*, is also capable of phagocytosis and may have acquired plastocyanin in a similar manner. Phylogenetic inference indicates that plastocyanin in these organisms diverged from plastocyanin from the green lineage (Nosenko et al., 2006). Acquisition of plastocyanin through phagocytosis is unlikely in a diatom because of its rigid outer Si frustule.

In this paper we used published protein sequence data for primer design to isolate a fragment of the gene encoding plastocyanin in *T. oceanica* (CCMP 1005). We subsequently cloned and sequenced the complete mature protein coding sequence and used phylogenetic analysis to infer the origin of this gene in *T. oceanica* (CCMP 1005). Using our deduced protein sequence we screened 10 other strains of chlorophyll a/c-containing diatoms for the presence of the plastocyanin gene.

Materials and Methods

Algal Material used. Different species and strains of coastal and oceanic *Thalassiosira* were chosen to represent the branches of the maximum-likelihood phylogenetic tree inferred from 5.8 rRNA sequences. *Minutocellus spp.* was selected as an outgroup. Phytoplankton were obtained from the Culture Collection of Marine Phytoplankton (CCMP), Bigelow Laboratories for Ocean Sciences (West Boothbay Harbor, ME, USA) and maintained in f/2 media. Filter sterilized nutrients were added to 0.22 μm filtered natural seawater according to protocol (Guillard, 1975), autoclaved and filtered again. *Thalassiosira oceanica* (CCMP 1005, CCMP 1006, CCMP 999); *T. rotula* (CCMP 1647); *T. pseudonana* (CCMP 1015, CCMP1335); *T. weissflogii* (CCMP 1336); *Minutocellus polymorphous* (CCMP 497) and *Minutocellus* sp. (CCMP 1701) were grown under continuous light with an irradiance of 180 μmol quanta $m^{-2}s^{-1}$ at 22°C. *Thalassiosira guillardii* (CCMP 988) and *T. pseudonana* (CCMP 1014) were grown under a 13:11 light: dark cycle with an irradiance of 100 μmol quanta $m^{-2}s^{-1}$. Cultures used for degenerate PCR were grown in 10L volumes of f/2 media in clear polycarbonate carboys (Nalgene, Rochester, NY, USA), harvested by filtration onto 2 μm polycarbonate filters (GE Osmotics, Minnetonka, MN, USA), snap frozen in liquid nitrogen and stored at –80°C.

Extraction of nucleic acids. Genomic DNA was extracted using DNeasy Mini-Prep Kit (Qiagen, Mississauga, ON, CAN) according the manufacture's protocol and further purified by ethanol precipitation (Sambrook & Russell, 2004). The quality of the DNA

was determined by performing a full spectrum (220-750 nm) scan using a NanoDrop ND-1000 spectrometer (NanoDrop Technologies Inc., Wilmington, DE, USA). Only DNA samples with a 260 nm/280 nm ratio greater than 1.8 and a 260/230 ratio greater than 2.2 were used. Purified DNA was stored at -20^{o}C until use. Total RNA was extracted using RNeasy (Qiagen) according to the manufacture's instructions. RNA was stored at -80^{o}C. RNA integrity was verified by comparing the 28s and 18s rRNA Swedberg peaks on an Agilent 2100 Bioanalyzer (Genome Quebec, Montreal, QC, CAN).

Plastocyanin isolation, cloning and annotation. Two degenerate primers, NTERM forward and IPTERP reverse, were manually designed to the plastocyanin's N-terminal sequence AQTVEVKM and a conserved amino acid sequence, PHNVVFDEDNIP, of plastocyanin (Table 1). PCR amplification was performed using 0.5 μM of primers with 2.5 *U* TAQ DNA polymerase (Qiagen) and 1.5 mM $MgCl_2$, 10 mM dNTP and 250 ng of *T. oceanica* (CCMP 1005) DNA in a 50 μL reaction volume. The PCR cycling condition used was: 94^{o}C for 10 min followed by 35 cycles of 94^{o}C for 1 min, 42^{o}C for 1 min and 72^{o}C for 1 min with a final elongation step at 72^{o}C for 10 min. PCR products were visualized on a 1% high purity agarose gel (Invitrogen, Burlington, ON, CAN), excised and extracted with the QIAquick PCR Purification kit (Qiagen). Fragments were ligated into the linearized pCR2.1 vector with TA overhangs and covalently bound Topoisomerase (Invitrogen). The resultant plasmids were subsequently used to transform chemically competent *Escherichia coli* DH5α cells (Invitrogen). Transformed cells were grown on LB agar containing 50 μg/ml kanamycin. Ten clones were subsequently chosen randomly and grown in liquid LB with 50 μg/ml kanamycin. Plasmids were isolated from

the bacterial cells using a QIAprep Spin Miniprep kit (Qiagen). Plasmids were sequenced by Genome Quebec using a 3730xl DNA Analyzer system (Applied Biosystems, Foster City, CA, USA) using M13 primers. Identities of the sequences were checked by BLASTX? searches of the National Center for Biotechnology Information's (NCBI) non-redundant database (Altschul et al. 1990) using default parameters. A sequence of high homology to plastocyanin was identified and used to design a 3' internal forward primer for 3' Restriction Ligase Mediated Rapid Amplification of DNA ends (Ambion, Palo Alta, CA, USA) (Table 1). A 5' internal reverse primer (Table 1) was designed to the original internal genomic fragment and 5'RACE was completed using a 5'SMART RACE cDNA Amplification Kit (BD Biosciences, Mississauga, ON Canada). Ten products were cloned using TOPO-pCR2.1 vector as described above. The complete coding sequence was determined by overlapping fragments and blasted against the NCBI non-redundant database using the BLASTX ?program with default parameters.

Comparative Modeling. Using the previously determined N-terminal sequence (Peers & Price, 2006) to identify the proper reading frame, the mature protein sequence was deduced and blasted against the protein database. The primary amino acid sequence was then threaded to a number of best templates using the first approach option of the SwissModel program (Schwede *et al.*, 2003). PyMol (DeLano, 2004) was then used to generate a 3-D representation and identify hydrophobic, acidic and basic patches on the protein's surface.

Sequence analysis of plastocyanin and rRNA sequences from photosynthetic organisms and phylogenetic inference. The protein sequence was used to search the NCBI non-

redundant proteins sequence database (Altschul *et al.*, 1990). Protein sequences with an expected score greater than 6.0e-4 were retrieved. The accession numbers of the sequences and the species used for phylogenetic analysis are listed (Table 2).

Conserved blocks of sequences were constructed using the Block Maker program (http://blocks.fhcrc.org/blockmkr/make_blocks.html) (Henikoff *et al.*, 1995) and concatenated. A multiple alignment was created with ClustalW using the default settings and manually edited with BioEdit. This procedure resulted in a 26-taxon dataset with 86 amino acids. A substitution matrix was chosen using the best BIC and AIC values as calculated by PROTTEST (http://darwin.uvigo.es/software/prottest_server.html). Protein maximum likelihood phylogenies were inferred using PHYML with a Whelan and Goldman (WAG) substitution matrix and with the assumption of both invariant residuals and variable rates of evolution. The alpha values were calculated using 8 rate categories. Using TREE-PUZZLE (http://www.tree-puzzle.de) a second protein maximum likelihood tree was constructed using branch swamping and a WAG substitution model with an eight-model discrete-gamma model. Both trees resulted in identical typologies. Each maximum likelihood inference was bootstrapped 200 times. For all other methods, the assumption was made that rate of evolution was constant between amino acid residuals. The same multiple alignment was used in subsequent analysis. Neighbour-joining tree was produced with the NJ program from the PHYLIP package (http://evolution.genetics.washington.edu/phylip) using 200 replicates and the Jones-Taylor-Thornton matrix assuming invariant sites and 8-category rate of substitution. Consensus tree was created using CONSENSUS from the PHYLIP package and

visualized with TREEVIEW (http://taxonomy.zoology.gla.ac.uk/rod/treeview) for each analysis.

Bayesian analysis was performed using Mr. Bayes (Ronquist & Huelsenbeck, 2005) with a WAG substitution matrix. Every 100 generations were sampled and the analysis was terminated when convergence was reached (2,500,000 generations). Deviation between posterior probabilities was 0.005837. Four thousand generations were burnt at the end of the run and the potential scale factor equalled one. TREEVIEW was used to create a graphic representation.

Phylogenetic analysis of species used for degenerate PCR was performed with Mr. Bayes, as described above. The accession numbers of 5.8S rRNA sequences used for this analysis are listed (Table 3).

Degenerate PCR. Degenerate PCR was used to amplify a portion of the sequence encoding plastocyanin using 2.5*U* TAQ DNA polymerase (Qiagen) and 1.5 mM $MgCl_2$, 10 mM dNTP and 250 ng of genomic DNA in a 50 µl reaction volume. BLOCKB forward and BLOCKC reverse, designed to the conserved regions of plastocyanin, CEPHQGAG and PHNVVF, and degenerate NTERM forward and CEPH reverse primers were used (Table 1). For each species a variety of PCR conditions were tested. Primer concentration varied from 0.1 µM to 1 µM, melting temperatures varied from 32^{o}C to 47^{o}C and cycle durations varied from 1 to 3 min, genomic DNA quantity ranged from 100 ng to 1µg. In some samples, DMSO was used to reduce the possibility of inhibition by secondary structures. The following PCR reaction conditions were found to

amplify plastocyanin: 94^{o}C for 3 min followed by 35 cycles of 94^{o}C for 1 min, 45^{o}C for 1 min, 72^{o}C for 1 min and with final 10 min extension step at 72^{o}C. Products were visualized on a 1% gel and were excised, cloned and sequenced as described above.

Results

Gene Cloning. A 395 nucleotide gene fragment was isolated from *Thalassiosira oceanica* (CCMP 1005) using degenerate primers to the N-terminus of plastocyanin (NTERM forward) (Peers & Price, 2006) and the conserved motif, CEPHQGAG Block C reverse (Table 1). The conserved region was identified by a multiple alignment of 25 plastocyanin sequences from the NCBI database. The isolated gene fragment encoded for an amino acid sequence, PHNVVDEDIP, common to most plastocyanins, and included one of the two histidines (H) required for Cu-binding by the mature protein. It also encoded a portion of the N-terminal sequence determined from protein sequencing (Peers & Price, 2006).

The gene fragment possessed a 95 nucleotide intron that had no appreciable similarity to any sequence in the NCBI database. Nucleotides surrounding the 5' splice site, nucleotide 95 to 96, were similar to the canonical AGGT(A/G)AGT sequence (Shapiro & Senapathy, 1987, Mount, 1982) except thymidine replaced adenine at nucleotide position 93. Such substitution occurs in 17% of eukaryotic splice sites (Shapiro & Senapathy, 1987). Translation of the gene sequence and alignment with known plastocyanin protein sequences also identified these residuals as a splice site. An automated exon intron detection program, GENESCAN (Burge & Karline, 1998), predicted with 98.5% probability that this sequence was a splice site. The 3' splice site, nucleotides 192 to 193, followed canonical rules and corresponded exactly to conserved 3' splice site signal (Shapiro & Senapathy, 1987). The intron contained a polypyrimidine track of less than 11 nucleotides (nt 175-85) and a branch point similar to that highly

conserved in yeast and *Giardia lamblia* (Nixon et al., 2002a). Results from the 3' RACE showed that the putative intron was missing in amplified cDNA.

Rapid amplification of 3' and 5' cDNA ends successfully amplified the remaining nucleotides upstream and downstream of the original primers (and as well those nucleotides bound by the original degenerate primers). The inferred protein sequence was found to possess Cys-X (2)-His-X (4)-Met and an upstream His residue necessary for the binding of the Cu^{2+} co-factor (Sigfridsson, 1998, Nersissian & Shipp, 2002). This motif is a hallmark of the family of type I blue copper proteins, of which plastocyanin is a member. The presence of such a motif further confirms the gene sequence identification as plastocyanin. The beginning of the coding region was determined by the presence of a start codon and the amino acid sequence information from the N-terminus (Peers & Price, 2006). The presence of a stop codon and the poly-A tail of our transcript determined the end of the codon regions. The complete gene sequence encoded for a protein of 100 amino acids in length with a molecular mass of 11.1 kDa (Fig. 1). Sequence comparison of the inferred protein showed the highest similarity with plastocyanin of S*cenedesmus obliquus* (71%) and highest identity with plastocyanin of *Emiliania huxleyi* (57%).

Comparative Modeling. Comparative modeling of the plastocyanin sequence demonstrated the inferred product possessed the structural elements and correct globular properties needed for interaction with upstream and downstream partners (Fig. 2). The protein model identified a single hydrophobic patch containing His-82, a residual involved in coordinated covalent bonding of the Cu co-factor. This hydrophobic patch is a common property of all blue copper proteins (Sigfridsson, 1998). Tyrosine-78 was

located in an acidic patch known to play a role in electron transfer. The presence of these patches and their orientation with respect to each other, the hydrophobic patch on the northern side and the acidic patch on the eastern side, are consistent with other plastocyanins and needed for proper functioning and interaction (De Rienzo *et al.*, 2000) . The structure and surface typology of plastocyanin from *Chlamydomonas reinhardtii* has been well studied (Redinbo *et al.*, 1993) and is included for comparison (Fig. 2).

Sequence analysis of plastocyanin and rRNA sequences from photosynthetic organisms and phylogenetic inference. Phylogenetic analysis of the inferred protein sequence was performed using Bayesian analysis (Ronquist & Huelsenbeck, 2005), neighbour-joining (Felsenstein, 2005) and maximum likelihood (Guindon & Gascuel, 2003) methods. Shown in Figure 3 is a Bayesian inferred tree with posterior probability and the bootstrap support values from maximum likelihood and neighbour joining at each node. All phylogenetic methods produced similar superclade typologies. The twenty-six sequences in the analysis were divided into a monophyletic and a polyphyletic group. A monophyletic group contained the eukaryote plastocyanins; including the green algae, chromophytes and higher plants. The cyanobacterial sequences of plastocyanin formed a polyphyletic group. The relationship between gene sequences differed depending on the phylogenetic method of analysis, but the overall structure of the tree was maintained. Within the green algal clade, low bootstrap value for maximum likelihood analysis occurred at the node separating red algal sequences from green algal and higher plant sequences. This made the relationship between the red green algal sequences uncertain. However, all phylogenetic inference methods placed *T. oceanica's* sequence into a clade closely related to green algal ancestral plastocyanins, suggesting that the group of red

algal sequences is indeed closely related to green algal sequences. Maximum likelihood, neighbour-joining and Bayesian analyses inferred *T. oceanica's* plastocyanin to be monophyletic with green algae and those plastocyanin sequences found in dinoflagellates, separate from cyanobacterial sequences. Sequence analysis of the complete inferred protein sequence for plastocyanin indicated that it was most similar to *Scenedesmus obliquus*, a green (chlorophyll a/b) chloroplast -containing alga.

Using published sequences of 5.8s rRNA and 18s rRNA, we inferred the relationship of *T. oceanica* (CCMP 1005) to other species of *Thalassiosira* to ensure that its classification within this genus was justified by genetic relatedness in addition to observed morphological similarities (Round *et al.*, 1990). Phylogenetic analysis using either 18s rRNA (supplemental) or 5.8s rRNA (Fig. 4) showed that *T. oceanica* (CCMP 1005) was closely related to *T. weissflogii* and distantly related to the sequenced diatom, *T. pseudonana* (CCMP 1335), but firmly within the *Thalassiosira* clade, a red chloroplast -containing algal group.

Degenerate PCR. We tested other diatoms for the presence of a plastocyanin gene using degenerate primers designed to conserve regions. Two combinations of primers were used: BLOCKB forward and BLOCKC reverse, as well as, NTERM forward and BLOCKC reverse. These primers successfully amplified products from *Arabidopsis thaliana*, a higher plant containing plastocyanin (results not shown). *Thalassiosira oceanica* (CCMP 1005) was used as a positive control in the experiments. Degenerate PCR products were cloned as described above. A sequence with homology to plastocyanin was found in *T. oceanica* (CCMP 1006) (Figure 4). The sequenced product,

including intronic and exonic regions, had 99% nucleotide identity to plastocyanin from *T. oceanica* (CCMP 1005). The inferred protein sequence had 100% protein identity.

Discussion

The pathway of electron flow in the light reactions of oxygenic photosynthesis has been largely delineated in model organisms (e.g. *Chlorella*) and extrapolated to other photoautotrophs. Significant differences in the types of accessory and primary photosynthetic pigments were recognized early on as one of the distinguishing features of different alga taxa (Fott, 1974).Those algae possessing chlorophyll c or chlorophyll b, recently referred to as the red and green plastid lines (Falkowski & Raven, 1997), not only possessed different pigments but a number of other biochemical and cytological features that were used to classify algae into their respective groups.

Plastocyanin and cytochrome c_6 are interchangeable redox proteins that transfer electrons from cytochrome b_6f to PSI. Although many photosynthetic organisms contain both proteins, many do not. Indeed, plastocyanin is the only carrier in higher plants, and some green algae and cyanobacteria (Weigel *et al.*, 2003, Merchant & Bogorad, 1986, Ho & Krogmann, 1984). One of the unique characteristics of chlorophyll c-containing phytoplankton was thought to be their exclusive use of cytochrome c_6 (Raven et al., 1999). This conclusion (paradigm) was established in the mid 1980's by studies that examined only a few representative species in the red plastid lineage (Sandmann, 1986, Sandmann *et al.*, 1983). The method of analysis at that time was difference spectroscopy which was used to identify the characteristic absorption maximum of plastocyanin at 597 nm in partially-purified protein extracts. It remains one of the key methods to quantify plastocyanin. Recent efforts to sequence whole genomes of a wide diversity of protists and the creation of expressed sequence tag (EST) databases have provided an alternative

means to look at the taxonomic distribution of plastocyanin and cytochrome c_6. Sequence search of the genomes of chlorophyll c-containing organisms, including the hot spring alga *Cyanidioschyzon merolae,* the thermophile *Galdieria sulphuraria* and the EST and genome databases of the diatoms, *T. pseudonana* (CCMP 1335) and *Phaeodactylum tricornutum* (CAPP1051/1, CCMP 632) are in agreement with the original results (Sandmann et al., 1983). These organisms lack plastocyanin and instead contain cytochrome c_6. The molecular results are in agreement with the original survey of the *Chrysophyceae*, *Xanthophyceae*, *Phaeophyceae* and *Rhodophyceae* that were unable to detect plastocyanin in these chlorophyll c-containing organisms (Sandmann et al., 1983).

The results presented here confirm that the red algal derived diatom, *Thalassiosira oceanica* (CCMP 1005), contains a plastocyanin gene. The inferred mature protein sequence had the highest identity with *Emiliania huxleyi* and similarity with *Scenedesmus obliquus*. The necessary motifs for function were present and comparative modeling illustrated the presence of structural elements and globular properties needed for interaction with upstream and downstream partners, as well as for function. These molecular data supports biochemical and physiological data from our lab that identified this protein and its role in photosynthetic electron flow in *T. oceanica* (CCMP 1005) (Peers & Price, 2006).

Using published sequences of 5.8s and 18s rRNA gene, we inferred the relationship of *T. oceanica* (CCMP 1005) to other *Thalassiosira* species. Phylogenetic analysis using either gene showed that *T. oceanica* (CCMP 1005) was closely related to

other *Thalassiosira* species (Supplemental Fig. 2; Fig. 5). Thus, this oceanic strain appears to be correctly assigned to the *Thalassiosira* genus, belonging to the red (chlorophyll a/c) plastid lineage. Previous work supports the relatedness of the Thalassiosiraceae (Hoppenrath *et al.*, 2007, Kaczmarska *et al.*, 2006). *Thalassiosira oceanica* (CCMP 1005) was not analyzed in these published data, however, our results show that it is closely related to *T. weissflogii* (CCMP 1336) and distantly related to *T. pseudonana* (CCMP 1335), the sequenced diatom (Armbrust *et al.*, 2004). Our 18s rRNA data show that two of the *T. oceanica* species studied here (CCMP 1001 and 1005) are more closely related to coastal species than to each other (Supplemental Fig. 2). The inclusion of CCMP 1001 in a clade with *T. pseudonana* was strongly supported by Kaczmaraska et al. (2007).

Species within the same genus may possess vastly different physiologies (Marchetti et al., 2006, Peers et al., 2005, Dupont *et al.*, 2006, Rocap et al., 2003, Palenik et al., 2006). A good example of this is the tolerance of closely related diatoms to Fe limitation. *Thalassiosira oceanica* (CCMP 1005) and *T. weissflogii* (CCMP 1336) are genetically similar yet the former species, isolated from metal poor waters of the open ocean, is able to grow at near maximum rates with 1/10 of the amount to Fe as its coastal congener. This is possible because of specific adaptations that reduce the cellular requirements for the limiting metal, including the use of alternative biochemical pathways (Archibald, 1983, Posey & Gherardini, 2000, Erdner *et al.*, 1999), up-regulation of resource scavengers (Trick et al., 1983), and changes in the stoichiometry of nutrient requiring cellular components (Strzepek & Harrison, 2004).

Under Fe limitation, Fe-containing proteins are replaced with alternative proteins with non-Fe metal cofactors (Kunert *et al.*, 1976, Wood, 1978, Merchant & Bogorad, 1986, Sandmann, 1986, Erdner et al., 1999, Peers & Price, 2004). Such replacements include increased use of a Mn-superoxide dismutase (SOD) for a Fe-SOD (Peers & Price, 2004), loss of Fe requiring secretary products (Posey & Gherardini, 2000) or the total replacement of all pathways requiring Fe (Archibald, 1983). Most trace metals in *Thalassiosira* are used in the light reactions of photosynthesis (Raven et al., 1999). Under Fe-limitation, a decrease in PSI (which contains 12 Fe atoms) and a reduction Fe-containing cytochrome b_6f occurs in *T. oceanica* (Strzepek & Harrison, 2004). The Fe-containing electron transport protein ferrodoxin is also replaced by an non-Fe -containing flavodoxin (LaRoche et al., 1996), further economizing on Fe. Collectively, these adaptations account for a 3-fold reduction in the cellular Fe requirements of the oceanic compared to the coastal isolate. Similarly, the substitution of plastocyanin for it's Fe containing homologue would further decrease Fe requirements by 10% (Peers & Price, 2006), although it would increase by 10-fold the need for Cu. Given the greater relative abundance of Cu than of Fe in the sea, this trade off may be advantageous. Importantly, such a substitution would possibly maintain electron transport from PSII to PSI and production of ATP in situations where Fe is limiting (Peers & Price, 2006).

The loss of the electron carrier between PSII and PSI in autotrophs contributes to excessive superoxide radical formation (Tognetti *et al.*, 2006) and decreased growth (Tognetti *et al.*, 2007). In the absence of Cu or Fe or impaired electron transport on the donor side of PSI, a decrease in autotrophic growth is observed (Peers & Price, 2006). Organisms that possess both cytochrome c_6 and plastocyanin may use either protein to

transfer electrons between PSII and PSI, depending on the availability of the metal co-factors, Cu and Fe. For example, in copper deficient cells of the cyanobacteria, Synechocystis, (Zhang *et al.*, 1992) and the green algae, *Chlamydomonas reinhardtii* (Li *et al.*, 1996, Eriksson *et al.*, 2004), plastocyanin is decreased and cytochrome c_6 production is induced. However, in many marine phytoplankton, cytochrome c_6 has been the only observed primary electron carrier to PSI. The presence of the Fe-containing cytochrome c_6 may have been beneficial during the evolution of the red plastid lineage since the availability of Fe in the early ocean was greater than it is now (Anbar & Knoll, 2002). As the ocean became increasingly Fe-poor, growth of species that were able to use other redox proteins would have been selected for with strong selection on organisms using a Cu-containing plastocyanin in regions where Fe was limited.

Our PCR method amplified a plastocyanin gene in two strains of diatoms. These strains (*T. oceanica* (CCMP 1006 and 1005)) were of oceanic provenance and had low Fe requirements for growth (Peers et al., 2005). Plastocyanin was not detected in cultures isolated from coastal regions, even in closely related species (e.g. *T. oceanica* (CCMP 999) and *T. weissflogii* (CCMP 1336)). Physiological experiments in our lab have demonstrated different physiological reactions under low trace metal concentrations. Both diatoms, *T. oceanica* (CCMP 1005) and *T. oceanica* (CCMP 1006) are able to persist at iron concentrations that are non permissive to coastal diatoms such as CCMP 1335 and 1336 (Peers & Price, 2004). So as argued above, it is not surprising that both CCMP 1005 and 1006 were found to have plastocyanin while the coastal diatoms, *T. pseudonana* (CCMP 1335 and 1336), did not. We note that we are unable at this time to evaluate the phylogenic relationship between the two oceanic strains to determine if they

are truly different species. Nor can we explain why plastocyanin was not detected in some of the other oceanic strains (CCMP 1014, CCMP 497). For one of these species, *Thalassiosira pseudonana* (CCMP 1014), however, the lack of plastocyanin was consistent with its unusually high Fe requirements for growth compared to other open ocean isolates. This species possesses a more coastal-like physiology than other oceanic diatoms and may be an ephemeral resident of the Pacific gyre that is only intermittently supplied to offshore waters by coastal jets and eddies that transport water away from the coast.

One possible explanation for the occurrence of plastocyanin in these diatom species may be horizontal gene transfer (HGT). Other than that of plastid acquisition and symbiosis, lateral gene transfer into oceanic plankton from an exogenous source is not surprising. Although most examples of horizontal gene transfer occur between prokaryotes themselves or between the chloroplast and the nucleus of photosynthetic organism, intra and inter domain transfer between other kingdoms have occurred (Pollack *et al.*, 2005, Waller *et al.*, 2006, Archibald et al., 2003) and may be a major driving force in eukaryotic algae evolution (Archibald et al., 2003). Many individual genes such as thymidine kinase (White *et al.*, 2005), NADH oxidase (Nixon *et al.*, 2002b), and flavohemoglobin (Anderson et al. 2003) have been acquired in some protists by HGT. However, sequence analysis suggest that since the initial acquisition, plastocyanin has been vertically inherited – an observation that doesn't not exclude the possibility of gene transfer through the acquisition of a new symbiont as previously suggested for the green dinoflagellate (Nosenko et al., 2006).

Sequence analysis of the complete inferred protein sequence for plastocyanin indicated that it shared the highest identity with the haptophyte *E. huxleyi* and highest similarity with the unicellular green alga *Scenedesmus obliquus* and not to cyanobacteria, as suggested by N-terminal sequence analysis (Peers & Price, 2006). Analysis of the plastocyanin sequence of *T. oceanica* (CCMP 1005) using NJ, ML, MP (supplemental) and Bayesian analyses (Figure 3), placed it in a monophyletic clade with the dinoflagellates and the haptophyte. This branch was closely related to the sequences of chlorophyll b-containing algae, relative to those sequences from cyanobacteria. Early branching of the plastocyanin sequences in the chlorophyll c-containing species is consistent with the early separation of the red algal lineage from cyanobacteria and green algae. The grouping of the dinoflagellate, haptophyte, and now, diatom sequences with each other suggests a common source and vertical inheritance since the acquisition of the gene.

The trace metal requirements of photosynthetic protists are thought to reflect the ancestral condition of the original plastid prior to endosymbiosis and to be transferred by vertical inheritance to subsequent generations (Quigg et al., 2003). A schism gave rise to different clades of photosynthetic eukaryotes to create the "green" lineage (chlorophyll a/b) and the "red" lineage (chlorophyll a/c) of photosynthetic organisms. Two competing hypotheses exist to explain the origin of the wide diversity of organisms with a red algal plastid. The chromalveolate hypothesis, supported by morphological, biogeochemical and shared-derived characteristics suggests that a single secondary endosymbiotic event occurred to give rise to this lineage containing dinoflagellates, heterokonts (including diatoms), and haptophytes (including coccolithophores) (Cavalier-Smith, 2002a). The

competing hypothesis proposes that the diverse number of extant organisms serving as hosts to secondary red plastids acquired a red plastid in separate independent endosymbiotic events and do not share a recent common ancestor (Grzebyk *et al.*, 2003). If plastocyanin were acquired by the endosymbiont before the initial secondary endosymbiotic event, then we would expect to see a more frequent distribution of the gene among extant red algal derived species than currently observed. This distribution would be determined by the extent of gene loss by the plastid before and after endosymbiosis (portable hypothesis) or after (chromalveolate hypothesis). Plastocyanin has been found within the red plastid -containing protist, *Karenia brevis*, and blast searches for the plastocyanin sequence have identified it in *Karlodinium micrum* and the haptophyte*, E. huxleyi.* Both dinoflagellates, *Karlodinium micrum* and *Karenia brevis,* have been examined and it has been suggested that the secondary plastid in these organisms has been replaced by a tertiary plastid of haptophyte origin (Yoon *et al.*, 2002, Tengs *et al.*, 2000, Nosenko et al., 2006). The plastid-encoded plastocyanin of *Karenia brevis* has been examined in detail and distribution and phylogenetic evidence (Patron *et al.*, 2006) indicates that a haptophyte ancestor that became the tertiary endosymbiont most likely acquired the plastocyanin gene from a green alga. Because all eukaryotic photosynthetic organisms were phagotrophic, at one point in their evolution, it is quite possible that the gene may have been horizontally transferred from an organism of green algal lineage. Our analysis supports this scenario since all our phylogenetic inferences resulted in the grouping of the red plastocyanin sequences with those of the green lineage.

The acquisition and utilization of plastocyanin by the common ancestor of the coccolithophores, diatoms and dinoflagellates would have been beneficial during

changing habitat conditions. Estimates based on the evolution of ribosomal genes and the molecular clock theory indicate that diatoms originated as much as 251 million years ago (Falkowski et al., 2004). Iron concentrations were decreasing at this time while Cu was becoming progressively more available as the ocean changed from anoxic to oxic (Saito *et al.*, 2003). Responding, and thus adapting, to such a changing environment would have been necessary for ecological success. Selection of specific chemical elements would have depended on abundance, availability and utility in biochemical reactions (Da Silva & Williams, 1991). Utilizing elements that would be less costly in terms of energy would therefore be beneficial. Hence acquiring the use of a Cu based protein, an element that was increasingly becoming more abundant, and replacing the use of a functional equivalent costlier Fe based protein was advantageous. This advantage would be increasingly important as red algae came to dominate the ocean over those of green origin during the next 250 million years (Falkowski et al., 2004). Indeed, *E. huxleyi*, a member of the coccolithophore, a group of phytoplankton possessing chlorophyll c, but in steady decline over the last 55 million years, is present and abundant in the world's ocean (Falkowski et al., 2004). Diatoms, such as the *T. oceanica,* radiated about 125 million years ago and potentially proliferated as late as 33 million years ago were undoubtedly under similar selection pressures. Those processing this adaptation would have an advantage over others and may have given rise to extant species. Those species possessing plastocyanin, but inhabiting relatively Fe rich environments, would have eventually lost the gene.

The maintenance and use of plastocyanin in diatoms today may provide a distinct ecological advantage over other species that reply on Fe-containing cytochrome. We

hypothesize that the ancestral plastid (the endosymbiont) contained plastocyanin and that selective pressure maintained it in some *Thalassiosira* species but that others lost it or no longer express it. The acquisition of this gene coupled with the need for diatoms to reduce their iron requirements may have provided a necessary condition for diatoms to inhabit Fe-limiting environments. The presence of plastocyanin in oceanic diatoms may thus be an example of an ecologically relevant gene acquisition.

References

Altschul, S. F., GIsh, W., Miller, W., Myers, E. W. & Lipman, D. J. 1990. Basic Local Alignment Search Tool. *Journal of Molecular Biology* **215**:403-10.

Anbar, A. D. & Knoll, A. H. 2002. Proterozoic ocean chemistry and evolution: A bioinorganic bridge? *Science* **297**:1137-42.

Archibald, F. 1983. *Lactobacillus-plantarum*, an organism not requiring iron. *FEMS Microbiology Letters* **19**:29-32.

Archibald, J. M., Rogers, M. B., Toop, M., Ishida, K. & Keeling, P. 2003. Lateral gene transfer and the evolution of plastid-targeting proteins in the secondary plastid-containing alga *Bigelowiella natans*. *Proc. Natl. Acad. Science USA* **100**:429-40.

Armbrust, E. V., Berges, J. A., Bowler, C., Green, B. R., Martinez, D., Putnam, N. H., Zhou, S. G., Allen, A. E., Apt, K. E., Bechner, M., Brzezinski, M. A., Chaal, B. K., Chiovitti, A., Davis, A. K., Demarest, M. S., Detter, J. C., Glavina, T., Goodstein, D., Hadi, M. Z., Hellsten, U., Hildebrand, M., Jenkins, B. D., Jurka, J., Kapitonov, V. V., Kroger, N., Lau, W. W. Y., Lane, T. W., Larimer, F. W., Lippmeier, J. C., Lucas, S., Medina, M., Montsant, A., Obornik, M., Parker, M. S., Palenik, B., Pazour, G. J., Richardson, P. M., Rynearson, T. A., Saito, M. A., Schwartz, D. C., Thamatrakoln, K., Valentin, K., Vardi, A., Wilkerson, F. P. & Rokhsar, D. S. 2004. The genome of the diatom *Thalassiosira pseudonana*: Ecology, evolution, and metabolism. *Science* **306**:79-86.

Arabidopsis Genome Initiative. 2000. Analysis of the genome sequence of the flowering plant *Arabidopsis thaliana*. *Nature* **408**:796-815.

Bruland, K. W., Rue, E. L. & Smith, G. J. 2001. Iron and macronutrients in California coastal upwelling regimes: Implications for diatom blooms. *Limnology and Oceanography* **46**:1661-74.

Burge, C. & Karline, S. 1998. Find the genes in genomic DNA. *Current Opinion in Structural Biology* **8**:346-54.

Cavalier-Smith, T. 2002. The neomuran origin of archaebacteria, the negibacterial root of the universal tree and bacterial megaclassification. *International Journal of Systematic and Evolutionary Microbiology* **52**:7-76.

Da Silva, J. & Williams, R. 1991. *The Biological Chemistry of the Elements: The Inorganic Chemistry of Life.* Oxford University Press, New York, 600.

De la Rosa, M., Navarro, J., Diaz-Quintana, A., De la Cerda, B., Molina_hereda, F., Balme, A., Murdoch, P. d. S., Diaz-Moreno, I., Duran, R. V. & Hervas, M. 2002. An evolutionary analysis of the reaction mechanisms of photosystem I reduction by cytochrome c_6 and plastocyanin. *Bioelectrochemsitry* **55**:41-45.

De Las Rivas, J., Balsera, M. & Barber, J. 2004. Evolution of oxygenic photosynthesis: genome-wide analysis of the OEC extrinsic proteins. *TRENDS in Plant Science* **9**:18-25.

De Rienzo, F., Gabdoulline, R. R., Menziani, M. C. & Wade, R. C. 2000. Blue copper proteins: A comparative analysis of their molecular interaction properties. *Protein Science* **9**:1439-54.

DeLano, W. L. 2004. Use of PyMol as a communications tool for molecular science. *Abstracts of Papers of the American Chemical Society* **228**:U313-U14.

Dupont, C. L., Yang, S., Palenik, B. & Bourne, P. E. 2006. Modern proteomes contain putative imprints of ancient shifts in trace metal geochemistry. *Proc. Natl. Acad. Science USA* **103**:17822-27.

Erdner, D. L., Price, N. M., Doucette, G. J., Pelato, M. & Anderson, D. M. 1999. Characterization of ferredoxin and flavodoxin as markers of iron limitation in marine phytoplankton. *Marine Ecology Progress Series* **184**:43-53..

Eriksson, M., Moseley, J. L., Tottey, S., del Campo, J. A., Quinn, J., Kim, Y. & Merchant, S. 2004. Genetic dissection of nutritional copper signalling in *Chlamydomonas* distinguishes regulatory and target genes. *Genetics* **168**:795-807.

Falkowski, P. & Raven, J. A. 1997. *Aquatic Photosynthesis.* Blackwell, Malden, MA,

Falkowski, P. G., Katz, M. E., Knoll, A. H., Quigg, A., Raven, J. A., Schofield, O. & Taylor, F. J. R. 2004. The evolution of modern eukayotic phytoplankton. *Science* **305**:354-60.

Felsenstein, J. 2005. PHYLIP (Phylogeny Inference Package) version 3.6. Distributed by the author. Department of Genome Sciences, Univewrsity of Washington, Seattle.

Fott, B. 1974. The phylogeny of eucaryotic algae. *Taxon* **23**:449-61.

Grzebyk, D., Schofield, O., Vetriani, C. & Falkowski, P. 2003. The mesozoic radiation of eukaryotic algae: The portable plastid hypothesis. *Journal of Phycology* **39**:259-67.

Guillard, R. R. L. 1975. Culture of phytoplankton for feeding marine invertebrates. *In*: Smith, W. L. & M.H, C. [Eds.] *Culture of Marine Invertebrate Animals.* Plenum Press, New York.

Guindon, S. & Gascuel, O. 2003. PhyML - A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood.*Systematic Biology* **52**:696-704.

Gupta, R., He, Z. & Luan, S. 2002. Functional relationship of cytochrome c_6 and plastocyanin in *Arabidopsis*. *Nature* **417**:567-71.

Henikoff, S., Henikoff, J. G., Alford, W. J. & Pietrokovski, S. 1995. Automated construction and graphical presentation of protein blocks from unaligned sequences. *GeneVOLUME*:17-26.

Ho, K. K. & Krogmann, D. W. 1984. Electron-donors to P700 in cyanobacteria and algae - an instance of unusual genetic-variability. *Biochimica et Biophysica Acta* **766**:310-16.

Hoppenrath, M., Beszteri, B., Gerhard Drebes, G., Hannelore Halliger, H., Van Beusekom, J., Janisch, S. & Wiltshire, K. 2007. *Thalassiosira* species (Bacillariophyceae, Thalassiosirales) in the North Sea at Helgoland (German Bight) and Sylt (North Frisian Wadden Sea) – a first approach to assessing diversity. *European Journal of Phycology* **42**:271-88.

Howe, C. J., Schlarb-Ridley, B. G., Wastl, J., Purton, S. & Bendall, D. S. 2006. The novel cytochrome c6 of chloroplasts: a case of evolutionary bricolage? *Journal of Experimental Botany* **57**:13-22.

Inda, L. & Pelato, M. 2002. Immunoquantification of flavodoxin and ferrodoxin from *Scendesmus vacuolatus* (Chlorophta) as iron-stress molecular markers. *European Journal of Phycology* **37**:579-86.

Kaczmarska, I., Beaton, M., Benoit, A. & Medlin, L. 2006. Molecular phylogeny of selected members of the order *Thalassiosirales* (Bacillaryiophyta) and evolution of the fultoportula. *Journal of Phycology* **42**:121-38.

Kunert, K. J., Bohme, H. & Boger, P. 1976. Reactions of plastocyanin and cytochrome 553 with photosystem I of *Scenedesmus*. *Biochimica et Biophysica Acta* **449**:541-53.

LaRoche, J., Boyd, P. W., McKay, R. M. L. & Geider, R. J. 1996. Flavodoxin as an in situ marker for iron stress in phytoplankton. *Nature* **382**:802-05.

Li, H. H., Quinn, J., Culler, D., GirardBascou, J. & Merchant, S. 1996. Molecular genetic analysis of plastocyanin biosynthesis in *Chlamydomonas reinhardtii*. *Journal of Biological Chemistry* **271**:31283-89.

Marchetti, A., Maldonado, M. T., Lane, E. S. & Harrison, P. J. 2006. Iron requirements of the pennate diatom *Pseudo-nitzschia*: Comparison of oceanic (high-nitrate, low-chlorophyll waters) and coastal species. *Limnology and Oceanography* **51**:2092-101.

Merchant, S. & Bogorad, L. 1986. Regulation by copper of the expression of plastocyanin and cytochrome c552 in *Chlamydomonas reinhardtii*. *Mol. Cell. Biol.* **6**:462-69.

Mount, S. M. 1982. A catalogue of splice junction sequences. *Nucleic Acids Research* **10**:459-72.

Nelson, N. & Ben-Shem, A. 2005. The structure of photosystem I and evolution of photosynthesis. *BioEssays* **27**:914-22.

Nersissian, A. M. & Shipp, E. L. 2002. Blue copper-binding domains. In: Valentine J.S., Gralla E.B., editors. *Copper-Containing Proteins.* New York, NY, USA: Academic Press; 2002. pp. 271-340.

Nixon, J. E., Wang, A., Morrison, H. G., McArthur, A. G., Sogin, M. L., Loftus, B. & Samuelson, J. 2002a. A splicosomal intron in *Giardia lamblia*. *Proc. Natl. Acad. Science USA* **99**:3701-05.

Nixon, J. E. J., Wang, A., Field, J., Morrison, H. G., McArthur, A. G., Sogin, M. L., Loftus, B. J. & Samuelson, J. 2002b. Evidence for lateral transfer of genes encoding ferredoxins, nitroreductases, NADH oxidase, and alcohol dehydrogenase 3 from anaerobic prokaryotes to *Giardia lamblia* and *Entamoeba histolytica*. *Eukaryotic Cell* **1**:181-90.

Nosenko, T., Lidie, K. L., Van Dolah, F. M., Lindquist, E., Cheng, J. F. & Bhattacharya, D. 2006. Chimeric plastid proteome in the florida "red tide" dinoflagellate *Karenia brevis*. *Molecular Biology and Evolution* **23**:2026-38.

Nugent, J. H. 1996. Oxygenic photosynthesis. *European Journal of Biochemistry* **237**:519-31.

Palenik, B., Ren, Q., Dupont, C. L., Myers, G. S., Heidelberg, J. F., Badger, J. H., Madupu, R., Nelson, W. C., Brinkac, L. M., Dodson, R. J., Durkin, A. S., Daugherty, S. C., Sullivan, S. A., Khouri, H., Mohamoud, Y., Halpin, R. & Paulsen, I. T. 2006. Genome sequence of *Synechococcus* CC9311: Insights into adaptation to a coastal environment. *Proceedings of the National Academy of Sciences* USA **103**:13555-59.

Patron, N. J., Waller, R. F. & Keeling, P. J. 2006. A tertiary plastid uses genes from two endosymbionts. *Journal of Molecular Biology* **357**:1373-82.

Peers, G. & Price, N. M. 2004. A role for manganese in superoxide dismutases and growth of iron-deficient diatoms. *Limnology and Oceanography* **49**:1774-83.

Peers, G. & Price, N. M. 2006. Copper-containing plastocyanin used for electron transport by an oceanic diatom. *Nature* **441**:340-44.

Peers, G., Quesnel, S.-A. & Price, N. M. 2005. Copper requirements for iron acquisition and growth of coastal and oceanic diatoms. *Limnology and Oceanography* **50**:1149-58.

Peleato, M. L., Saraiva, L., Inda, L. & Miramar, D. M. 2003. Plastocyanin/cytochrome c_6 interchange in *Scenedesmus vacuolatus*. *Journal of Plant Physiology* **160**:1483-86.

Pollack, J. D., Li, Q. Q. & Pearl, D. K. 2005. Taxonomic utility of a phylogenetic analysis of phosphoglycerate kinase proteins of Archaea, Bacteria, and Eukaryota: Insights by Bayesian analyses. *Molecular Phylogenetics and Evolution* **35**:420-30.

Posey, J. E. & Gherardini, F. C. 2000. Lack of a role for iron in the lyme disease pathogen. *Science* **288**:1651-53.

Quigg, A., Finkel, Z. V., Irwin, A. J., Rosenthal, Y., Ho, T.-Y., Reinfelder, J. R., Schofield, O., Morel, F. M. M. & Falkowski, P. G. 2003. The evolutionary inheritance of elemental stoichiometry in marine phytoplankton. *Nature* **425**:291-94.

Raven, J. A., Evans, M. C. W. & Korb, R. E. 1999. The role of trace metals in photosynthetic electron transport in O_2-evolving organisms. *Photosynthesis Research* **60**:111-49.

Redinbo, M., Cascio, D., Choukair, M., Rice, D., Merchant, S. & Yeates, T. 1993. The 1.5-A crystal structure of plastocyanin from the green alga *Chlamydomonas reinhardtii*. *Biochemistry* **32**.

Rocap, G., Larimer, F. W., Lamerdin, J., Malfatti, S., Chain, P., Ahlgren, N. A., Arellano, A., Coleman, M., Hauser, L., Hess, W. R., Johnson, Z. I., Land, M., Lindell, D., Post, A. F., Regala, W., Shah, M., Shaw, S. L., Steglich, C., Sullivan, M. B., Ting, C. S., Tolonen, A., Webb, E. A., Zinser, E. R. & Chisholm, S. W. 2003. Genome divergence in two *Prochlorococcus* ecotypes reflects oceanic niche differentiation. *Nature* **424**:1042-47.

Ronquist, F. & Huelsenbeck, J. P. 2005. Mr Bayes: Bayesian inference of phylogenetic trees. *Bioinformatics* **17**:754-55.

Round, E., Crawford, R. & Mann, D. 1990. *The diatoms. Biology and morphology of the genera.* Cambridge University Press, Cambridge, UK,

Saito, M., Sigman, D. M. & Morel, F. M. M. 2003. The bioinorganic chemistry of the ancient ocean: the co-evolution of cyanobacterial metal requirements and the biogeochemical cycles at the Archean-Proterozic boundary? *Inorganica Chemica Acta* **356**:308-18.

Sambrook, J. & Russell, D. 2004. *Molecular Cloning: A Laboratory Manual.* Cold Spring Harbor Laboratory Press, New York,

Sandmann, G. 1986. Formation of plastocyanin and cytochrome c-553 in different species of blue-green algae. *Archives of Microbiology* **145**:76-79.

Sandmann, G., Reck, H., Kessler, E. & Boger, P. 1983. Distribution of plastocyanin and soluble plastidic cytochrome c in various classes of algae. *Archives of Microbiology* **134**:23-27.

Schwede, T., Kopp, J., Guex, N. & Peitsch, M. C. 2003. Swiss-model: an automated protein homology-modeling server. *Nucleic Acids Research* **31**:3381-85.

Shapiro, M. & Senapathy, P. 1987. RNA splice junction of different classes of eukaryotes: sequence statistics and functional implications in gene expressions. *Nucleic Acids Research* **15**:7155-74.

Sigfridsson, K. 1998. Plastocyanin, an electron-transfer protein. *Photosynthetic Research* **57**:1-28.

Strzepek, R. F. & Harrison, P. J. 2004. Photosynthetic architecture differs in coastal and oceanic diatoms. *Nature* **431**:689-92.

Tengs, T., Dahlberg, O. J., Salchian-Tabrizi, K., LKlavness, D., Rudi, K., Delwiche, C. F. & Jakobsen, K. S. 2000. Phylogenetic analyses indicate that the 19' hexanoyloxy-fucoxanthine-containing dinoflagellates have tertiary plastids of haptophyte origin. *Mol. Biol. Evol.* **17**.

Tognetti, V. B., Palatnik, J. F., Fillat, M. F., Melzer, M., Hajirezaei, M.-R., Valle, E. M. & Carrillo, N. 2006. Functional replacement of ferredoxin by a cyanobacterial flavodoxin in tobacco confers broad-range stress tolerance. *Plant Cell* **18**:2035-50.

Tognetti, V. B., Zurbriggen, M., Morandi, E., Filliat, M., Valle, E., Hajirezaei, M. & Carrillo, N. 2007. Enhanced plant tolerance to iron starvation by functional substitution of chloroplast ferredoxin with a bacterial flavodoxin. *Proc. Natl. Acad. Science USA* **104**:11495-500.

Trick, C. G., Anderson, R. J., Price, N. M., Gillam, A. & Harrison, P. J. 1983. Examination of hydroxamate-siderophore production by neritic eukaryotic marine phytoplankton. *Marine Biology* **75**:9-17.

Waller, R. F., Slamovits, C. H. & Keeling, P. J. 2006. Lateral gene transfer of a multigene region from cyanobacteria to dinoflagellates resulting in a novel plastid-targeted fusion protein. *Molecular Biology and Evolution* **23**:1437-43.

Weigel, M., Varotto, C., Pesaresi, P., Finazzi, G., Rappaport, F., Salamini, F. & Leister, D. 2003. Plastocyanin is indispensable for photosynthetic electron flow in *Arabidopsis thaliana*. *Journal of Biological Chemistry* **278**:31286-89.

White, M. W., Jerome, M. E., Vaishnava, S., Guerini, M., Behnke, M. & Striepen, B. 2005. Genetic rescue of a *Toxoplasma gondii* conditional cell cycle mutant. *Molecular Microbiology* **55**:1060-71.

Wood, P. M. 1978. Interchangeable copper and iron proteins in algal photosynthesis - studies on plastocyanin and cytochrome c552 in *Chlamydomonas*. *European Journal of Biochemistry* **87**:9-19.

Yoon, H. S., Hacket, J. D. & Battacharya, D. 2002. A single origin of the peridinin- and fucoxanthin-containing plastids in dinoflagellates through tertiary endosymbiosis. *Proc. Natl. Acad. Science USA* **99**.

Zhang, L., McSpadden, B., Pakrasi, H. B. & Whitmarsh, J. 1992. Copper-mediated regulation of cytochrome-c553 and plastocyanin in the cyanobacterium *Synechocystis*-6803. *Journal of Biological Chemistry* **267**:19054-59.

Table 1. Primers and probes used to identify and isolate the plastocyanin gene in Thalassiosira oceanica (CCMP 1005) using 5' and 3' RACE and degenerate PCR. The NTERM forward primer was designed to the amino acids, LVFEPAK, of the N-terminal region of the protein (Peers & Price, 2006) and the IPTERP reverse primer was designed to the conserved amino acid residuals, PHNVVFDEDNIP. Both of these primers were used for the initial isolation and identification of plastocyanin and for subsequent probing and blotting. The 5' internal reverse and the 3' internal forward primers were designed to a genomic fragment from T. oceanica (CCMP 1005) and were used in 5' and 3' RACE procedures. The BLOCK C reverse primer was designed to the amino acids, CEPHQGAG. The BLOCK B forward primer was designed to the motif PHNVVF and used for degenerate PCR. Primer sequences are listed using IUPAC nomenclature where Y = C or T, R = A or G and N = A, G, T or C. Inosine (I) was used instead of a nucleotide base at some positions.

Primers / Probe	Target	Sequence
NTERM forward	QTVEVKM	5′-CYC ARA CYG TYG ARG TYA ARA TGG G-3′
IPTERP reverse	PHNVVFDEDNIP	5′-GGI ATR TTR TCY TCR TCR TCC ACC ACR TTR TGN GG-3′
Block B forward	PHNVVF	5′-CCI CAY AAY GTN GTN TTY-3′
Block C reverse	CEPHQGAG	5′-CCI GCI CCY TGR TGI GGY TCR CA-3′
3’ internal forward		5′-CTC CGG ACT TCT TGT CTT CG-3′
5’ internal reverse		5′-AAG GAG CGT TGA GCG ATC CCC TCC A-3′

Table 2. List of species and accession numbers of plastocyanin protein sequences used for phylogenetic analysis.

Species	Supergroup [$]/Division*	Class*, [Φ]	Accession Number
Crocosphaera watsonii WH 8501	Cyanobacteria	Chroobacteria	ZP_00517105
Phormidium laminosum	Cyanobacteria	Chroobacteria	Q51883
Prochlorococcus marinus CCMP 1375	Cyanobacteria	Chroobacteria	NP_875473
Synechococcus sp. WH 8102	Cyanobacteria	Chroobacteria	NP_897590
Synechocystis sp. PCC 6803	Cyanobacteria	Chroobacteria	NP_442157
Trichodesmium erythraeum IMS101	Cyanobacteria	Chroobacteria	Q111R2
Gloeobacter violaceus PCC 7421	Cyanobacteria	Gloeobacteria	Q7NIA7
Nostoc punctiforme PCC 73102	Cyanobacteria	Hormogoneae	B2IVD7
Karenia brevis	Protozoa	Dinophyceae	DQ531587
Karlodinium micrum	Protozoa	Dinophyceae	Q2IA53
Emiliania huxleyi	Protozoa	Prymnesiophyceae	GM1.2200045
Physcomitrella patens	Plantae	Bryopsida	Q9SXW9
Chlamydomonas reinhardtii	Plantae	Chlorophyceae	XP_001702952
Chlorella vulgaris	Plantae	Chlorophyceae	P00300
Pediastrum boryanum	Plantae	Chlorophyceae	AB017810
Pediastrum duplex	Plantae	Chlorophyceae	BAE00064
Scenedesmus obliquus	Plantae	Chlorophyceae	P26956
Hordeum vulgare	Plantae	Lilopsida	P08248
Oryza sativa	Plantae	Lilopsida	A2Y886
Zea mays	Plantae	Lilopsida	P16002
Arabidopsis thaliana	Plantae	Magnoliopsida	Q8LD06
Nicotiana tabacum	Plantae	Magnoliopsida	P35476
Pisum sativum	Plantae	Magnoliopsida	P16002
Solanum crispum	Plantae	Magnoliopsida	P00297
Scherffelia dubia	Plantae	Prasinophytae	AJ919618

[$](Cavalier-Smith, 2002a)

*(Cavalier-Smith, 2002b)

[Φ] (Adl *et al.*, 2005)

Table 3. Species, clones, collection sites and accession numbers of 5.8s rRNA gene sequences of diatoms screened for plastocyanin by degenerate PCR. The provenance of each clone was determined according to its collection site reported in the CCMP database.

Species	Strain Number	Collection Site	5.8s rRNA accession number	Provenance
Thalassiosira guillardii	CCMP 988	North Atlantic, Continental Shelf 39.6000N 70.1000W	EF208788	Uncertain*
T. oceanica	CCMP 999	North Atlantic, Continental Slope 39.0833N 71.9333W	EF134953	Uncertain *
T. oceanica	CCMP 1005	Sargasso Sea 33.1833N 65.2500W	EF362630	Oceanic
T. oceanica	CCMP 1006	Sargasso Sea 32.3000N 64.8400W	EF362631	Oceanic
T. pseudonana	CCMP 1014	North Pacific Gyre 28.000N 155.0000W	EF208791	Oceanic
T. pseudonana	CCMP 1015	San Juan Island, Washington State, USA 48.5440N 123.0100W	EF208792	Coastal
T. pseudonana	CCMP1335	Moriches Bay, New York, USA 40.7560N 72.8200W	EF208793	Coastal
T. rotula	CCMP 1647	Gulf of Naples, Italy 40.7500N 14.3300E	EF208798	Coastal
T. weissflogii	CCMP 1336	Gardiners Island New York, USA 41.1100N 72.1000W	DQ469927	Coastal
Minutocellus polymorphus	CCMP 497	Sargasso Sea 32.0000N 64.0000W	N/A	Oceanic
Minutocellus sp.	CCMP 1701	Gulf of Oman, Arabian Sea 23.5643N 58.8530E	N/A	Coastal

*These species were isolated from warm core eddies over the continental shelf and slope and are most likely of oceanic origin, but they could also be coastal species that were transported into the eddy.

Figure 1. Genomic structure of plastocyanin and the inferred protein sequence for *Thalassiosira oceanica* (CCMP 1005). The top and bottom rows of each line represent the genomic coding sequence and the deduced amino acid sequence, respectively. The gap between amino acid residuals, nucleotides 95 to 191, indicates an intronic region identified by classical intronic excision signals.

```
  1 - GCCCAAACTGTCGAGGTTAAGATGGGAGCCGACTCCGGACTT   - 42
  1 -  A  Q  T  V  E  V  K  M  G  A  D  S  G  L   - 14

 43 - CTTGTCTTCGAGCCTGCCAAGGTCACTGTCTGCAAGGGAGAC   - 84
 15 -  L  V  F  E  P  A  K  V  T  V  C  K  G  D   - 28

 85 – ACTGTCAAGTGGTAAGTTTTGATTCTCCTGATTTTTTCTGCA   - 126
 29 -  T  V  K  W                                 - 42

127 – CATGGACCACGAATGGACGAGCTGACTAACTCACAAAACCGG   - 168
 43 -                                             - 56

169 – ATGACGAATCGATTCGTCTCAGGATCAACAACAAGGCTGGAC   - 210
 57 -                        I  N  N  K  A  G     - 70

211 - CCCACAACGTGGTGGACGACGAGGATAACATCCCTGATGGCG   - 252
 71 - P  H  N  V  V  D  D  E  D  N  I  P  D  G    - 84

253 - TCGATCAGGAGAAGATTTCCATGGACGACCAGCTCGGCGAGC   - 294
 85 - V  D  Q  E  K  I  S  M  D  D  Q  L  G  E    - 98

295 - CGGGAGACACCTTCGAAATGAAATTCGATACCGCCGGAACCT   - 336
 99 - P  G  D  T  F  E  M  K  F  D  T  A  G  T    - 112

337 - ATGGTTACTACTGCGAACCTCACCGCGGTGCCGGCATGCAGG   - 378
113 - Y  G  Y  Y  C  E  P  H  R  G  A  G  M  Q    - 126

379 - CCACCCTTGTTGTTCAG                           - 395
127 - A  T  L  V  V  Q                           - 132
```

Figure 2. Modeled globular surface images of the tertiary plastocyanin protein structure using the inferred protein sequence of *Thalassiosira oceanica* (CCMP 1005) (A, B) and the plastocyanin protein sequence of C*hlamydomonas reinhardtii* (C, D). C*hlamydomonas reinhardtii* protein sequence was deduced from the gene sequence (Merchant *et al.*, 1990) and the structure determined by crystallography (Redinbo et al., 1993). The right hand image (eastern side) is rotated 90 degrees to the left relative to the left hand image (northern side). Shades of red coloration indicate the degree of acidic residuals in a region; shades of blue coloration indicate the degree of basic residuals in a region and white area represent hydrophobic regions of the protein. PyMOL was used to generate this figure.

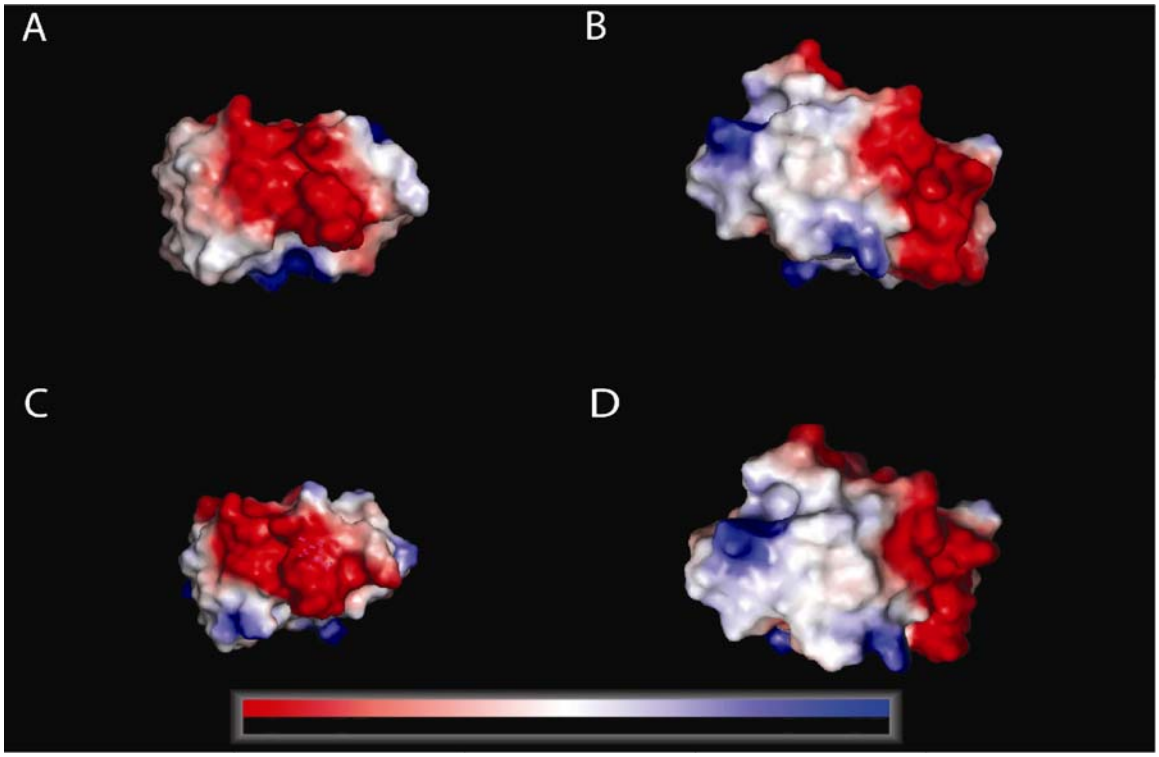

A
B
C
D

Figure 3. Phylogenetic analysis of plastocyanin from *Thalassiosira oceanica* (CCMP 1005). Values at nodes represent maximum likelihood bootstrap values, Bayesian analysis posterior probabilities and neighbour-joining bootstrap values, respectively. Dashes indicate situations where a bootstrap value was not possible. The tree was constructed using the inferred mature protein sequence of plastocyanin for each organism represented. Green lettering denotes chlorophyll a/b-containing organisms, blue lettering indicates cyanobacteria and red lettering indicates chlorophyll a/c-containing organisms.

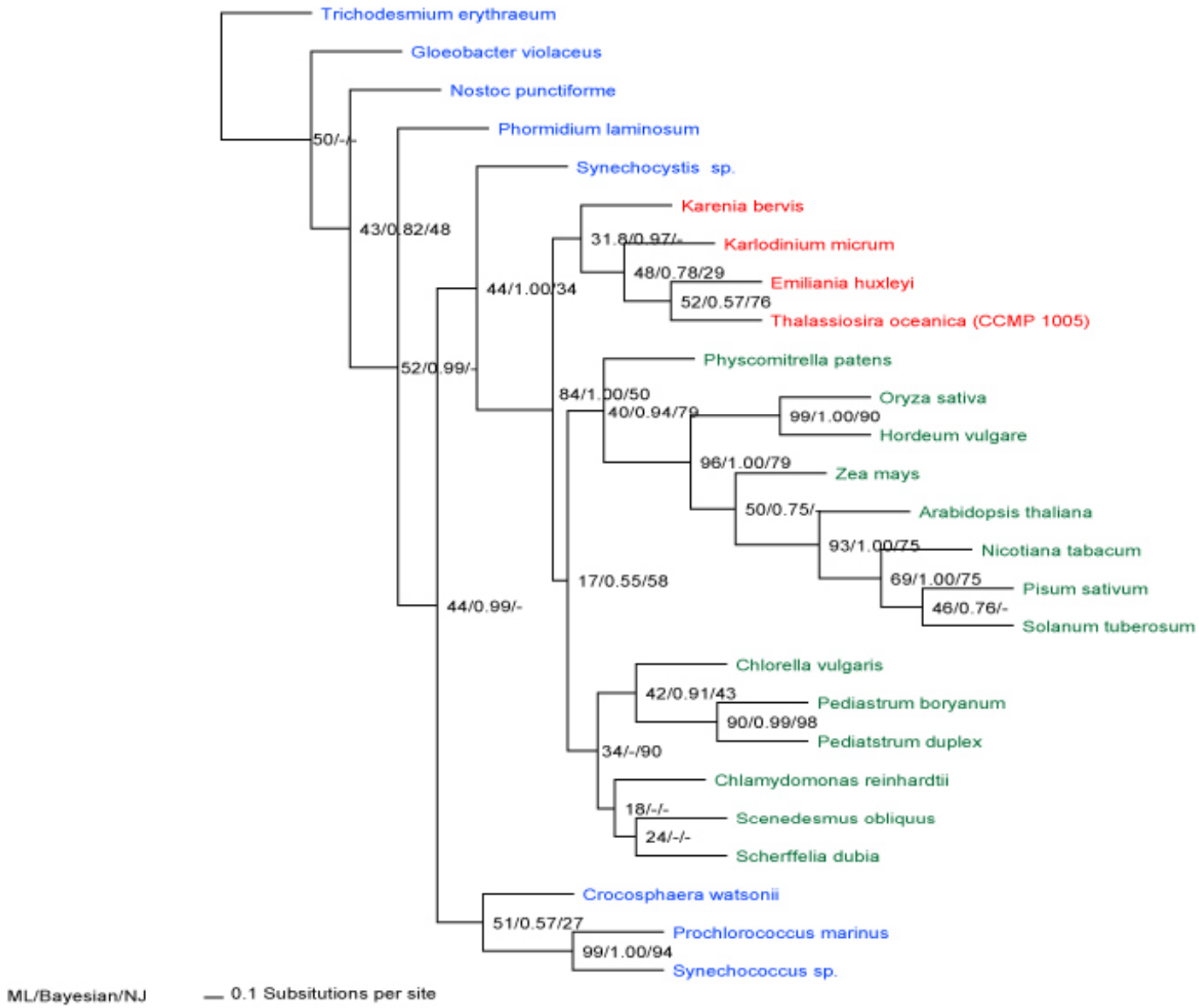

Trichodesmium erythraeum
Gloeobacter violaceus
Nostoc punctiforme
Phormidium laminosum
50/-/-
Synechocystis sp.
Karenia bervis
43/0.82/48
31.8/0.97/-
Karlodinium micrum
48/0.78/29
Emiliania huxleyi
44/1.00/34
52/0.57/76
Thalassiosira oceanica (CCMP 1005)
Physcomitrella patens
52/0.99/-
84/1.00/50
Oryza sativa
40/0.94/79
99/1.00/90
Hordeum vulgare
96/1.00/79
Zea mays
50/0.75/-
Arabidopsis thaliana
93/1.00/75
Nicotiana tabacum
69/1.00/75
Pisum sativum
17/0.55/58
46/0.76/-
Solanum tuberosum
44/0.99/-
Chlorella vulgaris
42/0.91/43
Pediastrum boryanum
90/0.99/98
Pediatstrum duplex
34/-/90
Chlamydomonas reinhardtii
18/-/-
Scenedesmus obliquus
24/-/-
Scherffelia dubia
Crocosphaera watsonii
51/0.57/27
Prochlorococcus marinus
99/1.00/94
Synechococcus sp.
ML/Bayesian/NJ
0.1 Subsitutions per site

Figure 4. Phylogenetic tree of *Thalassiosira* spp. inferred by Bayesian analysis using 5.8s rRNA sequences. The green algae, *Chlamydomonas reinhardtii*, was used as the outgroup. Oceanic species are marked with an asterisk. Values at the nodes indicate posterior probabilities.

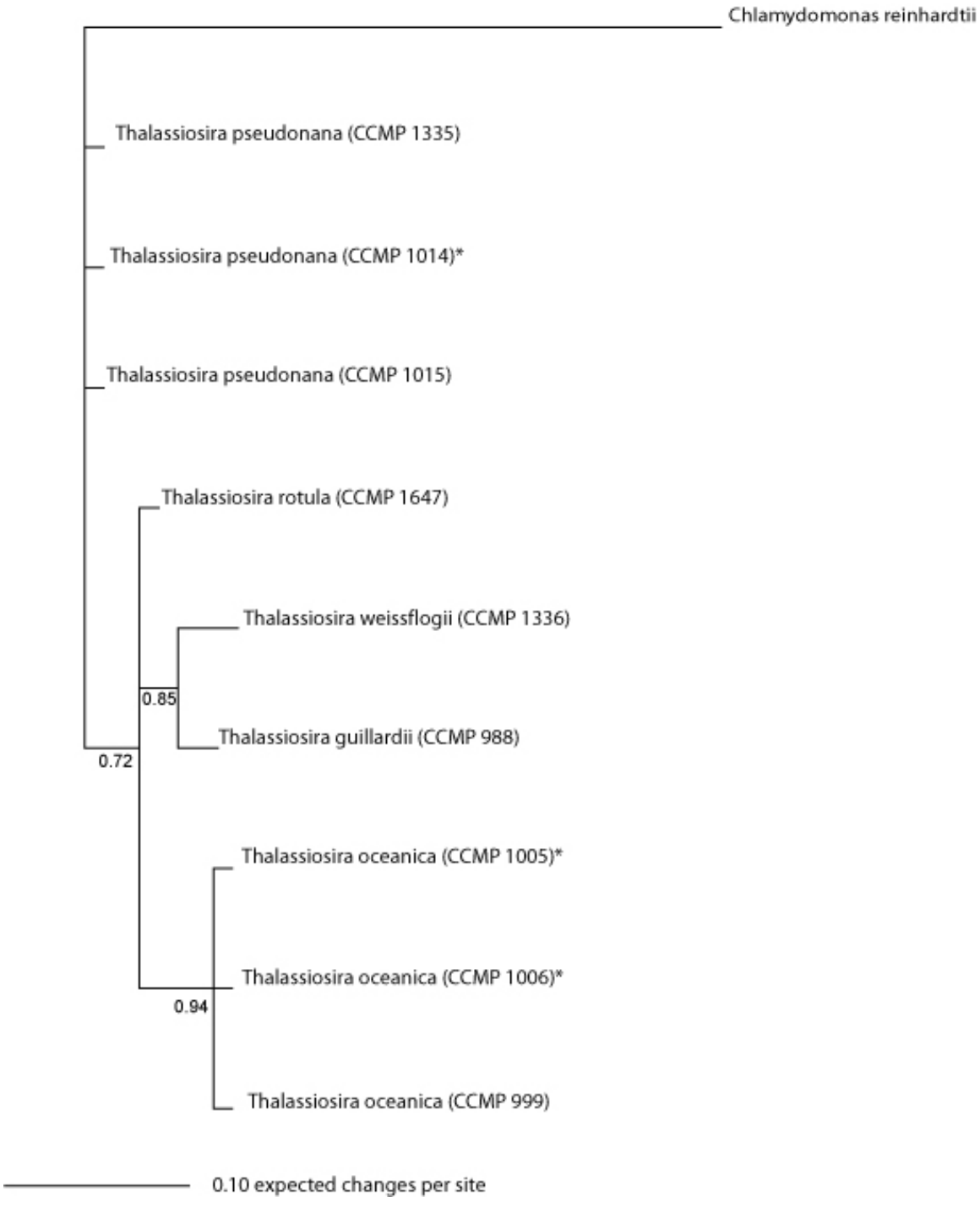

Chlamydomonas reinhardtii
Thalassiosira pseudonana (CCMP 1335)
Thalassiosira pseudonana (CCMP 1014)*
Thalassiosira pseudonana (CCMP 1015)
Thalassiosira rotula (CCMP 1647)
Thalassiosira weissflogii (CCMP 1336)
0.85
Thalassiosira guillardii (CCMP 988)
0.72
Thalassiosira oceanica (CCMP 1005)*
Thalassiosira oceanica (CCMP 1006)*
0.94
Thalassiosira oceanica (CCMP 999)
0.10 expected changes per site

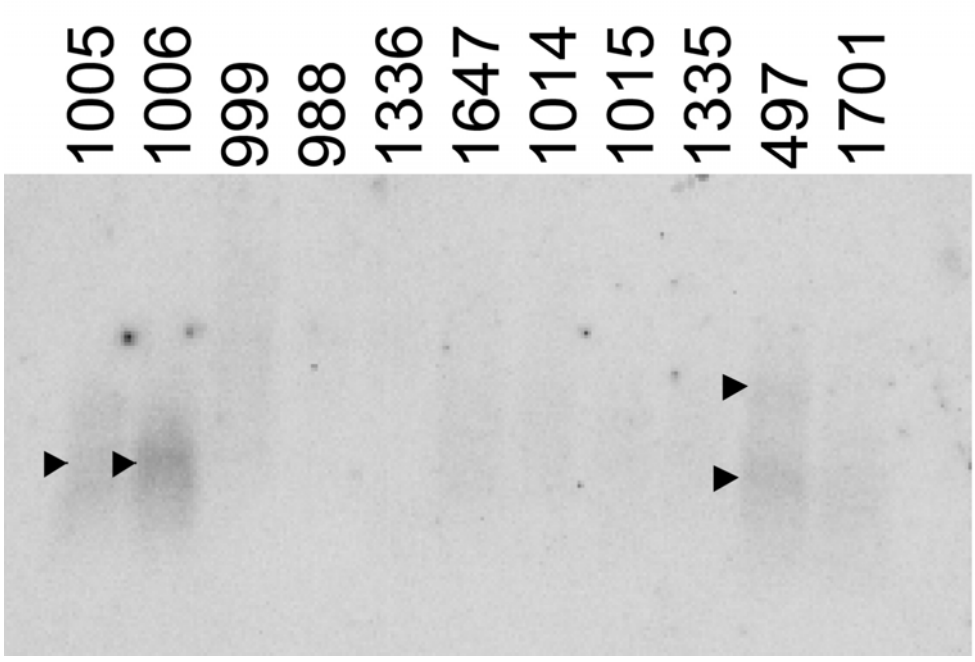
Figure 5. Aligned sequences of plastocyanin from *Thalassiosira oceanica* (CCMP 1005) and *Thalassiosira oceanica* (CCMP 1006). Italicized nucleotides represent primer sequences; asterisks indicate variable nucleotides.

```
                              20                  40
CCMP1005 : GCCCAAACTGTCGAGGTTAAGATGGGAGCCGACTCCGGACTTCTTGTCTT :  50
CCMP1006 : GCACAAACAGTGGAAGTAAAGATGGGAGCCGACTCCGGACTTCTTGTCTT :  50


                    60                  80                  100
CCMP1005 : CGAGCCTGCCAAGGTCACTGTCTGCAAGGGAGACACTGTCAAGTGGTAAG : 100
CCMP1006 : CGAGCCTGCCAAGGTCACTGTCTGCAAGGGAGACACTGCCAAGTGGTAAG : 100
                                                *

                           120                 140
CCMP1005 : TTTTGATTCTCCTGATTTTTTCTGCACATGGACCACGAATGGACGAGCTG : 150
CCMP1006 : TTTTGATTCTCCTGATTTTTTCTGCACATGGACCACGAATGGACGAGCTG : 150


                  160                 180                 200
CCMP1005 : ACTAACTCACAAAACCGGATGACGAATCGATTCGTCTCAGGATCAACAAC : 200
CCMP1006 : ACTAACTCACAAAACCGGATGACGAATCGATTCGTCTCAGGATCAGCAAC : 200
                                                      *

                           220                 240
CCMP1005 : AAGGCTGGACCCCCACAACGTGGTGGACGACGAGGATAACATCCC : 244
CCMP1006 : AAGGCTGGACCTCACAATGTCGTGGACGACGAGGACAACATCCC : 244
```

Supplemental Figure 1. Southern blot analysis of coastal and oceanic species of phytoplankton using probes designed to plastocyanin from *Thalassiosira oceanica* (CCMP 1005).

Numbers above blot represent clone numbers of *Thalassiosira oceanica* (CCMP 1005, CCMP 1006, CCMP 999); *T. guillardii* (CCMP 988); *T. weissflogii* (CCMP 1336); *T. rotula* (CCMP 1647); *T. pseudonana* (CCMP 1014, CCMP 1015, CCMP1335); *Minutocellus polymorphus* (CCMP 497), and *Minutocellus* sp. (CCMP 1701). A fully degenerate probe was designed to the conserved plastocyanin sequence CEPHQGAG (Table 1) using the CODEHOP program(Rose *et al.*, 1998) with all plastocyanin protein sequences from the protein database, InterPro (http://www.ebi.ac.uk/interpro/). Fifteen micrograms of genomic DNA was digested to completion as indicted by complete co-digestion of 0.25µg of pBR355 plasmid DNA (Invitrogen) using 35U/µg ALU1 (New England Biolabs, Ipswich, MA, USA), and loaded onto a 1% agarose, 0.5X TBE (Tris Borate EDTA) gel. Transfer of nucleic acids from the gel to a solid support for southern blotting was done using upward capillary action using alkaline transfer (Sambrook & Russell, 2004) onto Hybond XL nylon (Amersham, Piscataway, NJ, USA) overnight. Probes were labeled using the 5'-[γ -^{32}P] ATP T4 terminal labeling kit (Amersham) and purified using a G25 Sephadex column (GE Illustra, Piscataway, NJ, USA). To confirm 5'-[γ -^{32}P] ATP labelling of the probe, the probe was run on a 6% urea PAGE gel and assessed for the presence of proper labelled product and exposed overnight. Hybridization was performed at 42^{o}C and washes were performed as follows: 5X SSC (sodium chloride sodium citrate), 0.1% SDS (sodium dodecyl sulfate), 2 X 5 minutes at 21^{o}C; 1X SSC, 0.1% SDS, 15 minutes at 42^{o}C, 0.5X SSC, 0.1% SDS 20 minutes at 42^{o}C.

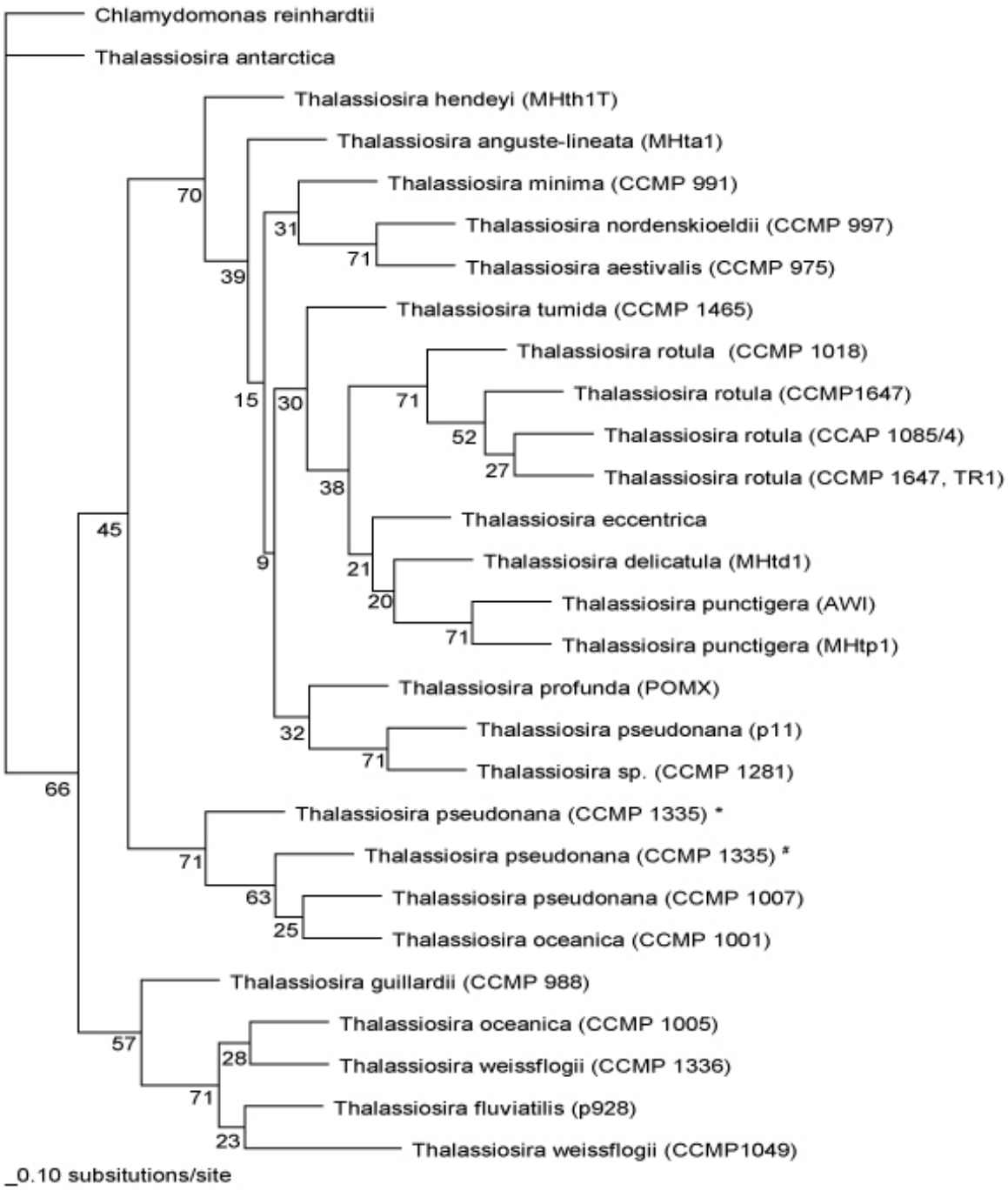
An alkaline phosphate screen was exposed for 24, 48 and 64 hours and visualized using a Phosphoimager. Film and conventional autoradiography was used.


1005
1006
999
988
1336
1647
1014
1015
1335
497
1701

Supplemental Figure 2. Maximum likelihood analysis of 18s rRNA gene sequences of *Thalassiosira* species. Sequences were aligned using the Clustal W program and the alignment was manually corrected to exclude gaps and ambiguously coded regions. The PHYLIP suite of programs, including SEQBOOT, PROML, CONSENSUS was used to analyze and compare the sequences. PROML was used to construct ML tree with the Dayhoff substitution matrix. The analysis was bootstrapped 100 times using SEQBOOT. A consensus tree was created with CONSENSUS using the majority rule. The tree was visualized using TREEVIEW (http://taxonomy.zoology.gla.ac.uk/rod/treeview.html). The sequences used in this analysis can be found in the GenBank (http://www.ncbi.nlm.nih.gov/Genbank/) database under the following accession numbers: AM235383.1, *Thalassiosira profunda* (POMX); DQ093369.1, *Thalassiosira aestivalis* (CCMP 975); DQ093368.1, *Thalassiosira tumida* (CCMP 1465); AF374481.2, *Thalassiosira pseudonana* (CCMP 1335)*, DQ093367.1, (CCMP 1007), AY485452.1 (CCMP 1335)#, AJ535169.1 (p11); DQ093366.1, *Thalassiosira minima* (CCMP 991); DQ093365.1, *Thalassiosira nordenskioeldii* (CCMP 997); AM050629.1, *Thalassiosira hendeyi (*MHth1T); AJ810854.1, *Thalassiosira anguste-lineata* (Mhta1); AJ810856.1, *Thalassiosira punctigera* (MHtp1), AY485526.1 (AWI)*;* AJ810855.1, *Thalassiosira delicatula* (MHtd1); AF374477.2, *Thalassiosira weissflogii,* AY485445.1 (CCMP1049); AJ535171.1, *Thalassiosira sp.* (CCMP 1281); AJ535170.1, *Thalassiosira fluviatilis* (clone p928); AF374482.2, *Thalassiosira antarctica*; AF374479.2, *Thalassiosira oceanica* (CCMP 1005), DQ093364.1 (CCMP 1001); AF374478.2, *Thalassiosira guillardii*; AF374480.2, *Thalassiosira rotula*, AF462059.1 (CCMP1018), AF462058.1

(CCMP1647), X85397.1 (CCAP 1085/4); X85396.1,*Thalassiosira.eccentrica*;

AY665727.1, *Chlamydomonas reinhardtii*.


Chlamydomonas reinhardtii
Thalassiosira antarctica
Thalassiosira hendeyi (MHth1T)
Thalassiosira anguste-lineata (MHta1)
Thalassiosira minima (CCMP 991)
Thalassiosira nordenskioeldii (CCMP 997)
Thalassiosira aestivalis (CCMP 975)
Thalassiosira tumida (CCMP 1465)
Thalassiosira rotula (CCMP 1018)
Thalassiosira rotula (CCMP1647)
Thalassiosira rotula (CCAP 1085/4)
Thalassiosira rotula (CCMP 1647, TR1)
Thalassiosira eccentrica
Thalassiosira delicatula (MHtd1)
Thalassiosira punctigera (AWI)
Thalassiosira punctigera (MHtp1)
Thalassiosira profunda (POMX)
Thalassiosira pseudonana (p11)
Thalassiosira sp. (CCMP 1281)
Thalassiosira pseudonana (CCMP 1335) *
Thalassiosira pseudonana (CCMP 1335) #
Thalassiosira pseudonana (CCMP 1007)
Thalassiosira oceanica (CCMP 1001)
Thalassiosira guillardii (CCMP 988)
Thalassiosira oceanica (CCMP 1005)
Thalassiosira weissflogii (CCMP 1336)
Thalassiosira fluviatilis (p928)
Thalassiosira weissflogii (CCMP1049)
70
31
71
39
15
30
71
52
27
38
45
9
21
20
71
66
32
71
71
63
25
57
28
71
23
_0.10 subsitutions/site

Supplemental Figure 3. Distribution of cytochrome c_6 and plastocyanin in photosynthetic organisms containing chlorophyll c.

Class	Species	Cytochrome c_6 identified (Yes/No)	Plastocyanin identified (Yes/No)	Point of Isolation	Type of Evidence
Bacillariophyceae	Phaeodactylum tricornutum (1090-1b)[a]	Yes	No	Coastal	Differential Spectroscopy Genomic Sequencing
Coscinodiscophyceae	Skeletonema costatum (LB 1077/1, C)[a]	Yes	No	Coastal	Differential Spectroscopy
	Thalassiosira oceanica (CCMP 999)[b]	-	No	Uncertain	Degenerate PCR / Southern blot
	Thalassiosira guillardii (CCMP 988)[b]	-	No	Uncertain	Degenerate PCR / Southern blot
	Thalassiosira.weissflogii (CCMP 1336)[b,d]	Yes	No	Coastal	Degenerate PCR / Southern blot
	Thalassiosira rotula (CCMP 1647)[b]	-	No	Coastal	Degenerate PCR / Southern blot
	Thalassiosira pseudonana (CCMP 1335)[b]	Yes	No	Coastal	Degenerate PCR / Southern blot Genomic Sequencing
	T. minuscula (CCMP 1036)[c]	-	No	Coastal	Physiological
	Thalassiosira oceanica (CCMP 1003)[c, d]	-	Yes	Oceanic	Physiological
	Thalassiosira oceanica (CCMP 1006)[c]	No	Yes	Oceanic	Degenerate PCR / Southern blot Physiological
	Thalassiosira oceanica (CCMP 1005)[b, c, e]	No	Yes	Oceanic	Degenerate PCR / Southern blot Physiological
	Thalassiosira pseudonana (CCMP 1015)[b]	-	Yes	Coastal	Degenerate PCR / Southern blot
	Minutocellus sp. (CCMP 1701)[b]	-	No	Coastal	Degenerate PCR / Southern blot
	Minutocellus polymorphus (CCMP 497)[b]	-	No	Oceanic	Degenerate PCR / Southern blot
	Thalassiosira pseudonana (CCMP 1014)[b]	-	No	Oceanic	Degenerate PCR / Southern blot
Xanothophyceae	Bumilleriopsis filiformis (Konstanz stock)[a]	Yes	No	Coastal	Differential Spectroscopy
	Vischeria stellata (887-2, G)[a]	Yes	No	Coastal	Differential Spectroscopy
	Tribonema aequale (880-1, G)[a]	Yes	No	Coastal	Differential Spectroscopy
	Bumilleria sicula	Yes	No	Coastal	Differential Spectroscopy
Phaeophyceae	Ectocarpus siliculosus (Konstanz)[a]	Yes	No	Coastal	Differential Spectroscopy
	Cutleria multifida[a]	Yes	No	n.a.	Differential Spectroscopy
Rhodophyceae	Cyanidium caldarium (RK-1)[a]	Yes	No	Coastal	Differential Spectroscopy
	Phorphyridium cruentum (1380-1a, G)[a]	Yes	No	Coastal	Differential Spectroscopy
	Phorphyridium aerugineum (1380-2, G)[a]	Yes	No	Coastal	Differential Spectroscopy
	Polysiphonia sp.[a]	Yes	No	n.a.	Differential Spectroscopy
Dinophyceae	Karenia brevis (CCMP 718)[f]	-	Yes	Coastal	EST database
	Karlodinium micrum (CCMP 415)[g]	Yes	Yes	Coastal	EST database
Prymnesiophyceae	Emiliania huxleyi (CCMP 371)[f]	-	Yes	Oceanic	EST database

[a] Sandmann et al. 1983; [b] own result; [c] Peers, Quesnel and Price 2005; [d] Strzepek and Harrison 2004; [e] Peers and Price 2006; [f] Nosenko et al 2006; [g] Patron et al. 2006