

Supporting Information

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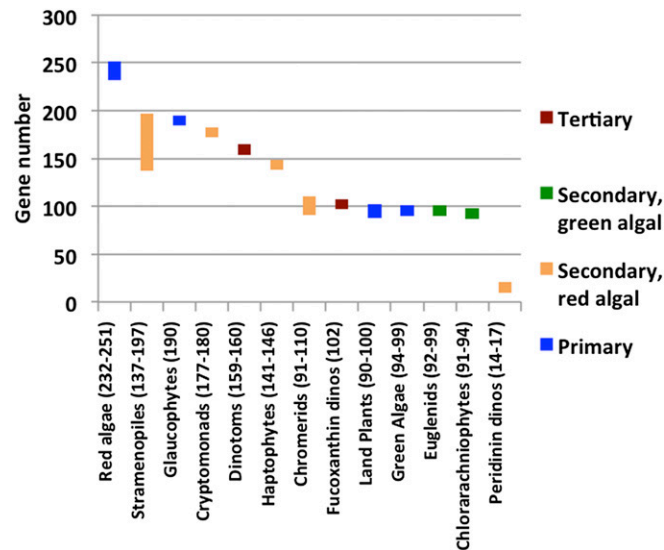


Fig. S1. Genome content of different plastid lineages. This figure shows the gene content of different major plastid lineages, using information compiled from refs. 1–7. This figure shows the gene content of different major plastid lineages. The color of each bar corresponds to the phylogenetic origin of the plastid lineage. The colored bars correspond to the range between the minimum and maximum numbers of genes identified in the plastid genomes of different functionally photosynthetic members of each lineage. Minimum and maximum gene numbers are additionally given in brackets next to each taxon name. Only one plastid genome has been completed from the glaucophytes and the fucoxanthin dinoflagellates; thus, the minimum and maximum gene numbers given in each case are identical.

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2. Hovde BT, et al. (2014) The mitochondrial and chloroplast genomes of the haptophyte *Chrysochromulina tobin* contain unique repeat structures and gene profiles. *BMC Genom* 15:604.
3. Imanian B, Pombert JF, Keeling PJ (2010) The complete plastid genomes of the two 'dinotoms' *Durinskia baltica* and *Kryptoperidinium foliaceum*. *PLoS ONE* 5(5):e10711.
4. Gabrielsen TM, et al. (2011) Genome evolution of a tertiary dinoflagellate plastid. *PLoS ONE* 6(4):e19132.
5. Wiegert KE, Bennett MS, Triemer RE (2013) Tracing patterns of chloroplast evolution in euglenoids: Contributions from *Colacium vesiculosum* and *Strombomonas acuminata* (Euglenophyta). *J Eukaryot Microbiol* 60(2):214–221.
6. Tanifuji G, et al. (2014) Nucleomorph and plastid genome sequences of the chlorarachniophyte *Lotharella oceanica*: Convergent reductive evolution and frequent recombination in nucleomorph-bearing algae. *BMC Genom* 15:374.
7. Mungpakdee S, et al. (2014) Massive gene transfer and extensive RNA editing of a symbiotic dinoflagellate plastid genome. *Genome Biol Evol* 6(6):1408–1422.

Table S1. Editing events in peridinin and fucoxanthin dinoflagellate plastids

Species	Refs.	Editing events
Peridinin species		
<i>Ceratium horridum</i>	(1)	A ↔ G; A ↔ U; C ↔ U; A → C; G → C; U → G
<i>Alexandrium tamarense</i>	(2)	A ↔ G; C ↔ U; A → C; G → C; U → G
<i>Lingulodinium polyedrum</i>	(3)	A ↔ G; C ↔ U; G → C; U → G
<i>Heterocapsa triquetra</i>	(4)	A ↔ G; A ↔ U; C ↔ U; A → C; G → C
<i>Symbiodinium minutum</i>	(5)	A → C; A ↔ G; A → U; C ↔ U; G → C; G → U
Fucoxanthin species		
<i>Karenia mikimotoi</i>	(6)	A ↔ C; A ↔ G; A ↔ U; C ↔ G; C ↔ U; G ↔ U
<i>Karlodinium veneficum</i>	(7, 8)	A ↔ C; A ↔ G; A ↔ U; C ↔ G; C ↔ U; G ↔ U

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- Wang Y, Morse D (2006) Rampant polyuridylylation of plastid gene transcripts in the dinoflagellate *Lingulodinium*. *Nucleic Acids Res* 34(2):613–619.
- Dang Y, Green BR (2009) Substitutional editing of *Heterocapsa triquetra* chloroplast transcripts and a folding model for its divergent chloroplast 16S rRNA. *Gene* 442(1-2):73–80.
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- Dorrell RG, Howe CJ (2012) Functional remodeling of RNA processing in replacement chloroplasts by pathways retained from their predecessors. *Proc Natl Acad Sci USA* 109(46): 18879–18884.
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Table S2. Predicted plastid proteins of peridinin origin in serial dinoflagellates

Sequence	Organism	Refs.	Notes
3-Dehydroquinate synthetase	Fucoxanthin	(1)	Ultimately of proteobacterial origin
Ascorbate peroxidase	Fucoxanthin	(2)	
ATP synthase gamma subunit	Fucoxanthin	(2)	Ultimately of actinobacterial origin
Cysteine synthase	Fucoxanthin	(2)	
Form II NADP-dependent isocitrate dehydrogenase	Fucoxanthin	(3)	Ultimately of proteobacterial origin
Glyceraldehyde-3-phosphate dehydrogenase isoform C1	Fucoxanthin	(4, 5)	
O-methyltransferase	Fucoxanthin	(1)	Ultimately of proteobacterial origin
Phosphoribulokinase	Fucoxanthin	(2)	
Unidentified poly(U) addition/editing factors	Fucoxanthin	(6)	Ultimately of proteobacterial origin
1-Deoxy-D-xylulose 5-phosphate reductoisomerase	<i>Lepidodinium</i>	(7)	
4-Diphosphocytidyl-2C-methyl-D-erythritol kinase	<i>Lepidodinium</i>	(7)	Ultimately of proteobacterial origin
Ferredoxin NADP reductase	<i>Lepidodinium</i>	(7)	
Glyceraldehyde-3-phosphate dehydrogenase isoform C1	<i>Lepidodinium</i>	(5)	

This table lists all of the ESTs identified in dinoflagellates that have undergone serial endosymbiosis events that are predicted to be derived from the ancestral peridinin plastid symbiosis, and encode plastid-targeted proteins. Data in this table are compiled from refs. 1–7.

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- Minge MA, et al. (2010) A phylogenetic mosaic plastid proteome and unusual plastid-targeting signals in the green-colored dinoflagellate *Lepidodinium chlorophorum*. *BMC Evol Biol* 10:191.