

Table S1. General features of the two phaeophyte plastid genomes.

	<i>Ectocarpus siliculosus</i>	<i>Fucus vesiculosus</i>
Genome length (bp)	139,954	124,986
Inverted repeat (IR)	17,230	9,726
Small single-copy region (SSC)	42,714	40,347
Large single-copy region (LSC)	80,010	74,913
G+C content (%)	30.7	28.9
Predicted coding sequence (%)	80.3	85.5
Protein-coding sequences (%)	72.2	76.6
Total predicted genes (located in the IRs)	185 (22)	173 (10)
Protein-coding genes	148 (8)	139
rRNA genes	6 (6)	6 (6)
tRNA genes	31 (8)	28 (4)
Introns	0	1

Table S2. Reversal distance matrix for pairwise comparisons between available heterokont plastid genomes. Gene order and orientation (+/- strand) for genes present were compared, using *E. siliculosus* as reference. Values in the table are minimum numbers of steps in pairwise comparisons necessary to explain the differences (as rearrangements) between genomes.

Species	Esil	Fves	Vlit	Haka	Ptri	Tpse	Osin
Esil	-	16	30	38	37	36	37
Fves		-	30	36	38	39	37
Vlit			-	36	37	36	38
Haka				-	34	38	34
Ptri					-	18	10
Tpse						-	16
Osin							-

Species abbreviations: *Ectocarpus siliculosus* (Esil), *Fucus vesiculosus* (Fves), *Vaucheria litorea* (Vlit), *Heterosigma akashiwo* (Haka), *Phaeodactylum tricornutum* (Ptri), *Thalassiosira pseudonana* (Tpse), *Odontella sinensis* (Osin). See Table S1 for genome accession numbers.

The genome rearrangement analysis was performed using GRIMM ^(*) (<http://nbc.scd.edu/GRIMM/mgr.cgi>). A list of homologous genes present in all the taxa was prepared and genes were coded for order and orientation (+/- strand) relative to *E. siliculosus*. The analysis was performed for circular and signed (+/- orientation) genomes for this list of common genes (losses and/or inter-chromosomal transfers, i.e., plastid to nuclear transfer, cannot be incorporated) to give a matrix of reversal distance between genome pairs, i.e., the minimum number of steps required to rearrange genome 1 into genome 2.

^(*) Tesler G. 2002. GRIMM: genome rearrangements web server. Bioinformatics 18:492-493.

Figure S1.

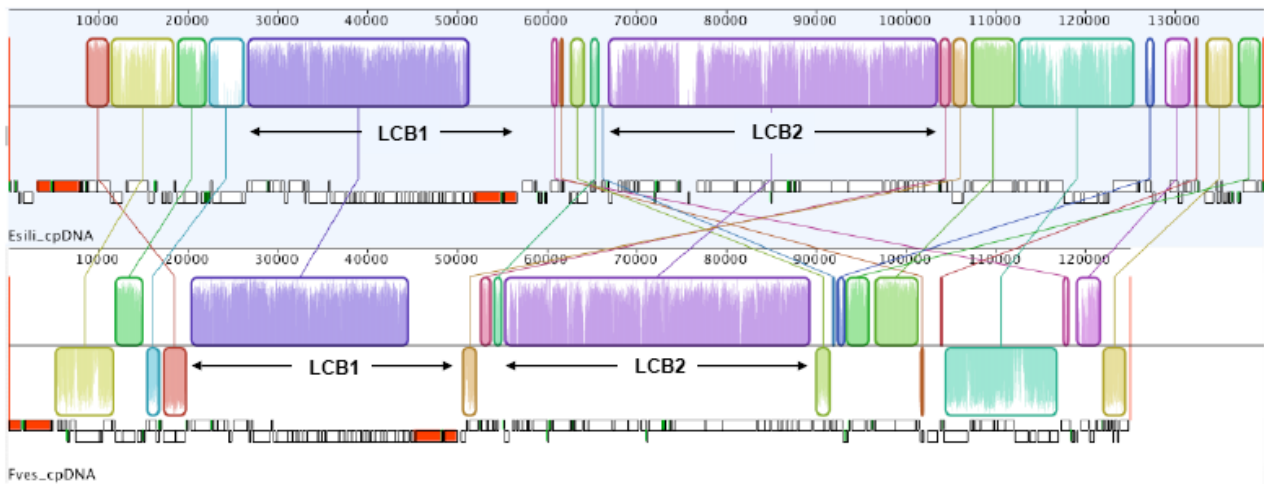


Figure S1. MAUVE genome comparison between *E. siliculosus* (upper, light blue background) and *F. vesiculosus* (lower, white background) plastid genomes.

The (linearized) genomes are represented by small white (protein coding genes) or red (rRNA genes) boxes. Locally collinear blocks (LCBs) identified by MAUVE are colour-coded; links between LCBs are indicated by the thin coloured lines. In the lower portion of the figure, *F. vesiculosus* LCBs lying below the black line have an inverse orientation relative to *E. siliculosus*. The comparison was made using the MauveAligner algorithm with seed weight = 9 and minimum LCB = 50. The MAUVE^(*) genome alignment software package was implemented in Geneious (4.0.3).

The two major syntenic regions, LCB1 and LCB2 are indicated. LCB1 contains 48 genes, from the *rpl9* to *rns_2* genes. An overlap of 8 bases between *rpl4/rpl23* is present in both taxa in LCB1. LCB2 covers 40 (*E. siliculosus*) and 39 genes (*F. vesiculosus*), respectively. The additional gene present in *E. siliculosus*, *Escp117*, encodes a putative protein that has no counterpart in *Fucus*. Numerous smaller regions (from 2 to 13 genes) show strict synteny or identical organisation with an inverted order. Two pairs of same-strand overlapping genes are common to both genomes: *psbC/psbD* with 53 overlapping nucleotides (covering the 17 C-terminal codons of *psbD*) and *ycf16(sufC)/ycf24(sufB)* with 4 nucleotides (overlap between the start and stop codons).

(*) Darling ACE, Mau B, Blatter FR, Perna NT. 2004. Mauve: multiple alignment of conserved genomic sequence with rearrangements. *Genome Res.* 14:1394-1403.