

Organelle inheritance and genome architecture variation in isogamous and anisogamous brown algae

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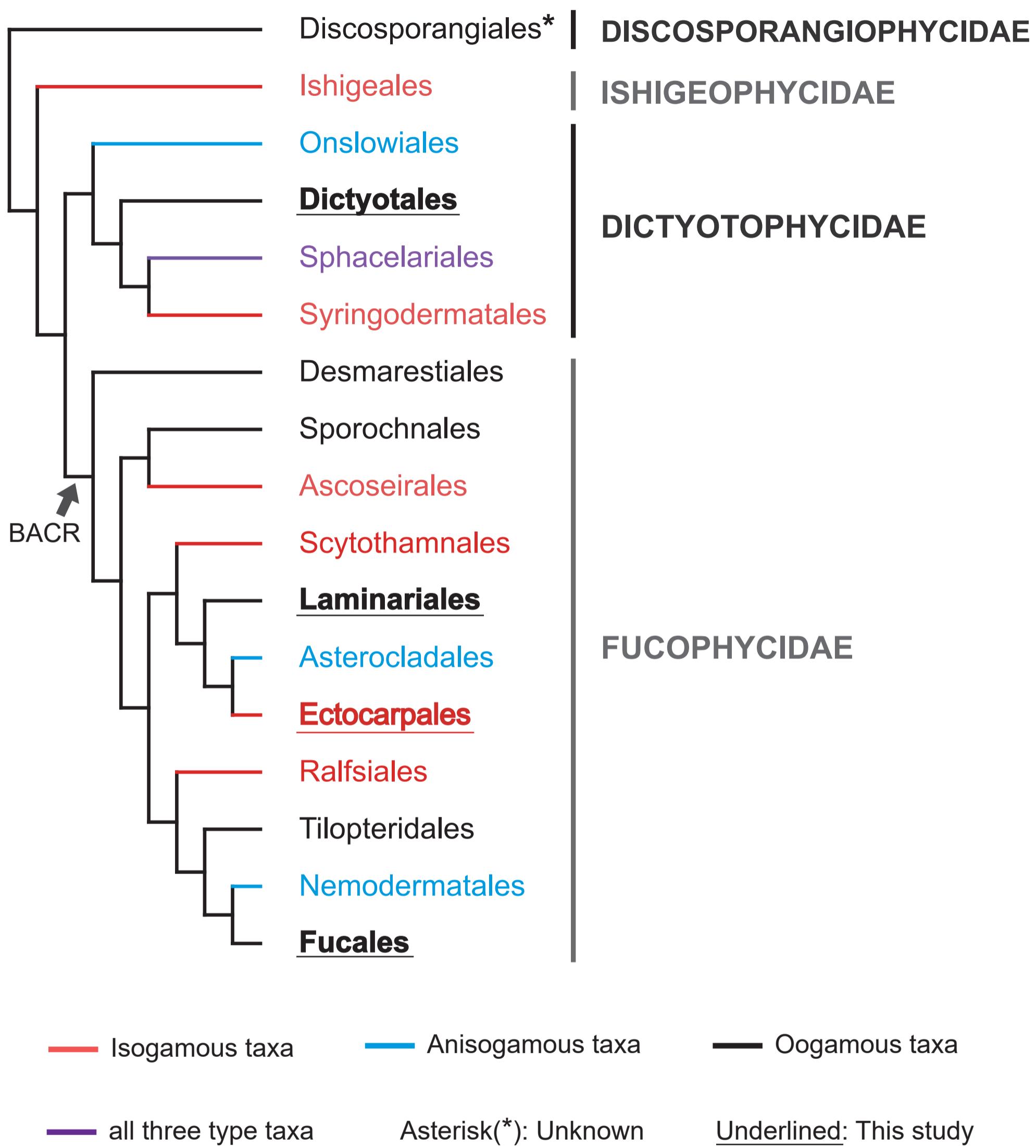


Fig. S1. Classification of four subclasses of Phaeophyceae and the type of fertilization at the order level.
(BACR: Brown algal crown radiation)

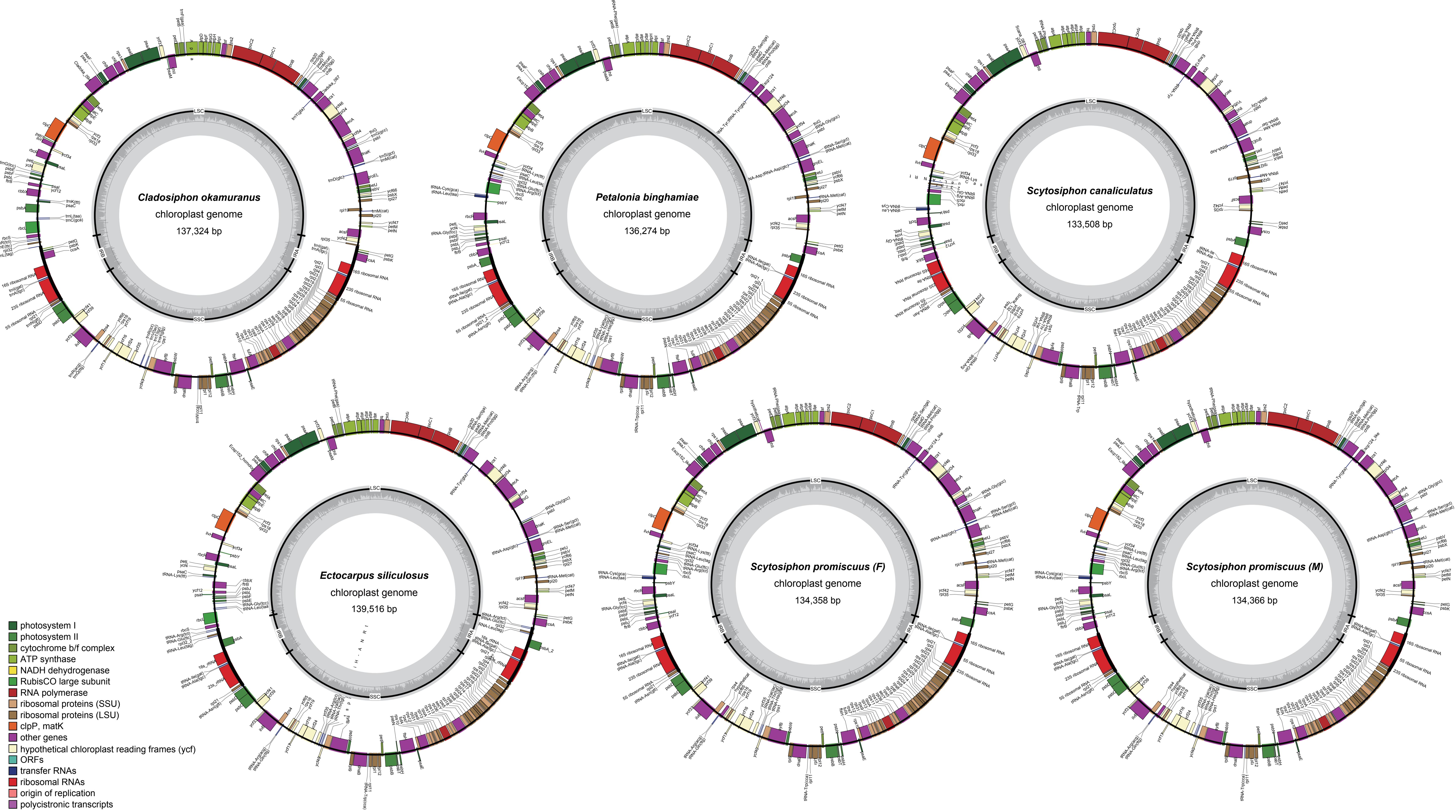


Fig. S2. Circular maps of the plastid genomes of four Ectocarpales species.

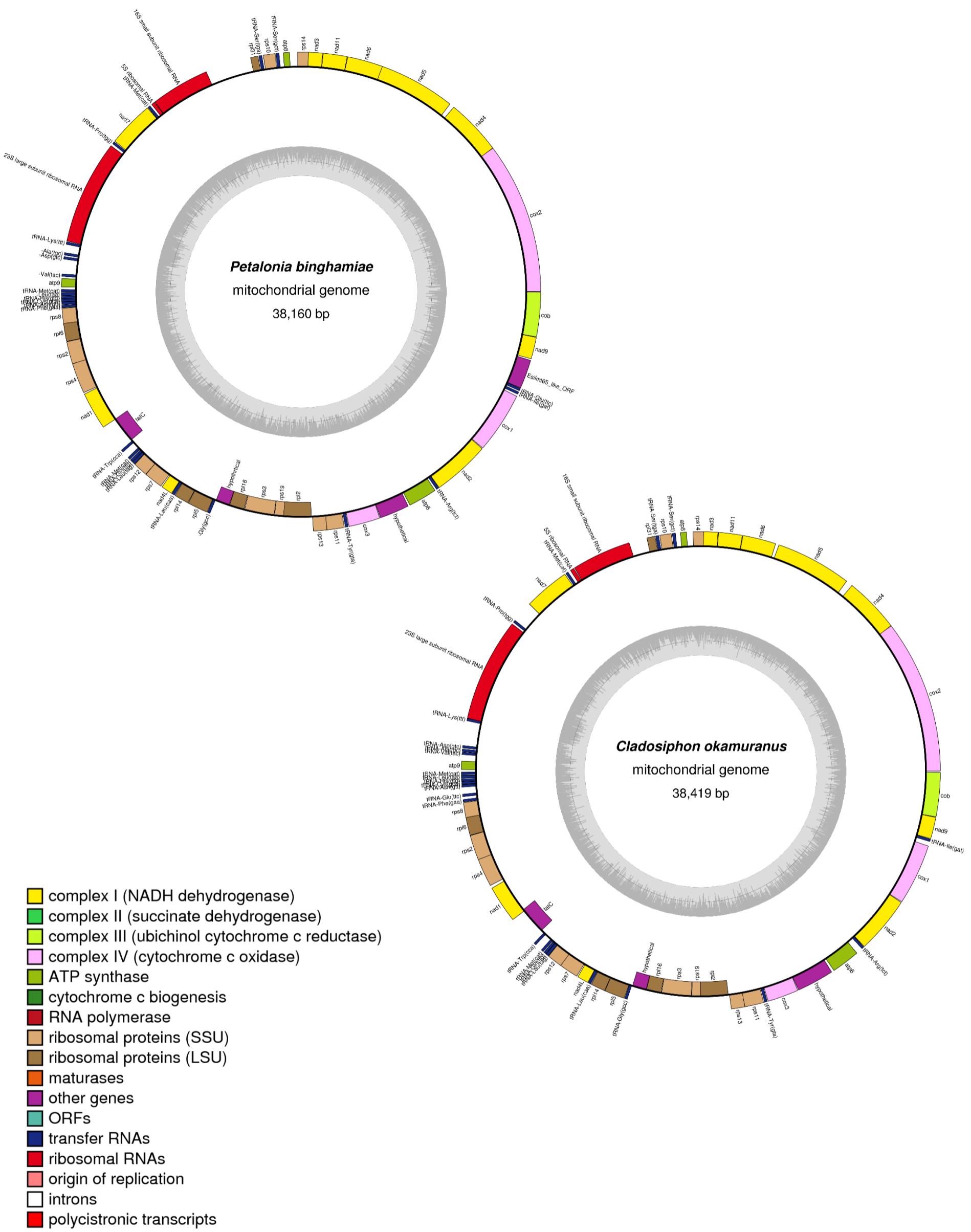


Fig. S3. Circular maps of the mitochondrial genomes of two Ectocarpales species.

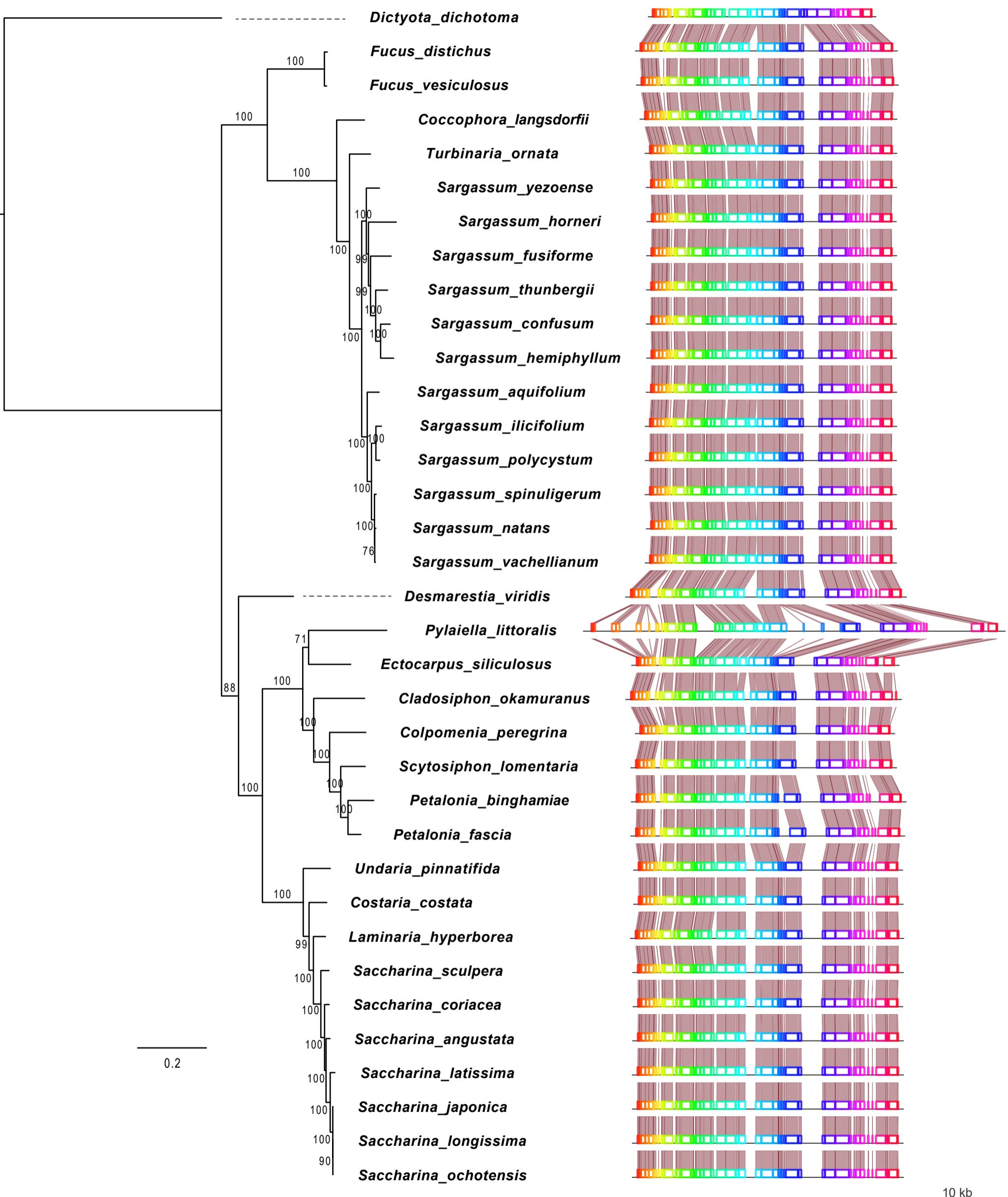


Fig. S4. Co-linear alignment and phylogeny-based clustering of mtDNAs of 32 brown algal species

Table. S1. Plastid genome sequencing statistics

	<i>Scytoniphon canaliculatus</i>	<i>Scytoniphon promiscuus</i> (♂)	<i>Scytoniphon promiscuus</i> (♀)	<i>Petalonia binghamiae</i>	<i>Ectocarpus siliculosus</i> (♂)	<i>Cladosiphon okamuranus</i> ¹
NGS Platform	Ion PGM	Ion PGM	Ion PGM	Ion PGM	Ion PGM	Illumina
No. reads	4,066,433	4,511,276	7,604,996	4,232,288	7,659,092	46,686,028
Total length (Mb)	1,137	1,375	2,781	1,028	2,752	13,916
N50 contig (bp) ²	2,478	4,860	1,829	3,533	8,679	21,705
Average coverage	193.5	371.2	494.8	470.9	159.9	99.4
Reference	This study	This study	This study	This study	This study	Nishitsuji et al. and this study

¹The whole genome sequencing of *Cladosiphon okamuranus* was conducted in Nishitsuji et al. (2016).

²The N50 value was calculated from the merged all assemblies

Table S2. Protein coding gene contents of plastid genomes used in the phylogenomic analysis. Presence of genes are indicated as filled boxes in each species (Duplicated genes are filled darker). Genes are categorized by their functions. Unidentified open reading frames (orf) are excluded. A 137 core genes are written in red.

Table S2. continued

