

Plastid genome sequences of *Gymnochlora stellata*, *Lotharella vacuolata*, and *Partenskyella glossopodia* reveal remarkable structural conservation among chlorarachniophyte species

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Online Resource 1

List of the plastid genomes that we used in the comparative analyses

Classification	Species	Accession NO.	
Ulvoephyceae	<i>Oltmannsiellopsis viridis</i>	DQ291132.1	
	<i>Pseudodoclonium akinetum</i>	AY835431.1	
	<i>Ulva</i> sp. UNAO0071828	KP720616.1	
	<i>Bryopsis hypnoides</i>	GQ892829.1	
	<i>Bryopsis plumosa</i>	LN810504.1	
	<i>Tydemania expeditiones</i>	LN810505.1	
Chlorophyceae	<i>Acutodesmus obliquus</i>	DQ396875.1	
	<i>Chlamydomonas reinhardtii</i>	BK000554.2	
	<i>Dunaliella salina</i>	GQ250046.1	
	<i>Volvox carter*</i>	GU084820.1	
	<i>Floydiella terrestris</i>	GU196268.1	
	<i>Oedogonium cardiacum</i>	EU677193.1	
	<i>Schizomeris leibleinii</i>	HQ700713.1	
	<i>Stigeoclonium helveticum</i>	DQ630521.1	
	Trebouxiophyceae	<i>Coccomyxa subellipsoidea</i>	HQ693844.1
		<i>Leptosira terrestris</i>	EF506945.1
<i>Oocystis solitaria</i>		FJ968739.1	
<i>Geminella minor</i>		KM462883.1	
<i>Gloeotilopsis sterilis</i>		KM462877.1	
<i>Planctonema lauterbornii</i>		KM462880.1	
<i>Ettlia pseudoalveolaris</i>		KM462869.1	
<i>Fusochloris perforata</i>		KM462882.1	
<i>Microthamnion kuetzingianum</i>		KM462876.1	
<i>Xylochloris irregularis</i>		KM462872.1	
<i>Neocystis brevis</i>		KM462873.1	
<i>Pabia signiensis</i>		KM462866.1	
<i>Koliella longiseta</i>		KM462868.1	
<i>Stichococcus bacillaris</i>		KM462864.1	
<i>Prasiolopsis</i> sp. SAG 84.81		KM462862.1	
" <i>Chlorella</i> " <i>mirabilis</i>		KM462865.1	
<i>Chlorosarcina brevispinosa</i>		KM462875.1	
<i>Myrmecia israelensis</i>		KM462861.1	
<i>Lobosphaera incisa</i>		KM821265.1	
<i>Dictyochloropsis reticulata</i>		KM462860.1	
<i>Watanabea reniformis</i>		KM462863.1	
<i>Botryococcus braunii</i>		KM462884.1	
<i>Choricystis minor</i>		KM462878.1	
<i>Elliptochloris bilobata</i>		KM462887.1	
Trebouxiophyceae sp. MX-AZ01		JX402620.1	
		<i>Paradoxia multiseta</i>	KM462879.1
Chlorodendrophyceae		<i>Tetraselmis subcordiformis*</i>	GANN00000000.1
Pedinophyceae		<i>Pedinomonas minor</i>	FJ968740.1
		<i>Pedinomonas tuberculata</i>	KM462867.1
		<i>Marsupiomonas</i> sp. NIES 1824	KM462870.1
Chlorellales		<i>Chlorella vulgaris</i>	AB001684.1
		<i>Chlorella variabilis</i>	KJ718922.1
	<i>Chlorella sorokiniana</i>	KJ397925.1	
	<i>Chlorella</i> sp. ArM0029B	KF554427.1	
	<i>Parachlorella kessleri</i>	FJ968741.1	
	<i>Dicloster acutus</i>	KM462885.1	
	<i>Pseudochloris wilhelmii</i>	KM462886.1	
	<i>Marvania geminata</i>	KM462888.1	
Prasinophytes	<i>Prasinoderma coloniale</i>	KJ746598.1	
	Prasinophyceae sp. MBIC10622	KJ746602.1	
	<i>Prasinococcus</i> sp. CCMP1194	KJ746597.1	
	<i>Pyramimonas parkeae</i>	FJ493499.1	
	<i>Ostreococcus tauri</i>	CR954199.2	
	<i>Monomastix</i> sp. OKE-1	FJ493497.1	
	<i>Nephroselmis olivacea</i>	AF137379.1	
	<i>Nephroselmis astigmatica</i>	KJ746600.1	
	<i>Pycnococcus provasolii</i>	FJ493498.1	
	<i>Picocystis salinarum</i>	KJ746599.1	
	Prasinophyceae sp. CCMP1205	KJ746601.1	
	Chlorarachniophyceae	<i>Bigeloviella natans</i>	DQ851108.1
		<i>Lotharella oceanica</i>	KF438023.1

*used only by phylogenetic analyses

Online Resource 2

Conserved genes in the plastid genomes of chlorarachniophytes

Function	Conserved genes
ATP synthase	<i>atpA, atpB, atpE, atpF, atpH, atpI</i>
Cytochrome	<i>petA, petB, petD, petG</i>
Photosystem I	<i>psaA, psaB, psaC, psaJ</i>
Photosystem II	<i>psbA, psbB, psbC, psbD, psbE, psbF, psbH, psbI, psbJ, psbK, psbL, psbM, psbN, psbT</i>
RubisCO	<i>rbcL</i>
LSU ribosomal proteins	<i>rpl14, rpl16, rpl19, rpl20, rpl2, rpl23, rpl36, rpl5</i>
SSU ribosomal proteins	<i>rps11, rps12, rps14, rps18, rps19, rps2, rps3, rps4, rps7, rps8, rps9</i>
RNA polymearse	<i>rpoA, rpoB, rpoC1, rpoC2</i>
Miscellaneous	<i>chlI, clpP, tufA, ycf1, ycf3, ycf4, maturase-like^a</i>
rRNAs	<i>rrnS, rrnL, rrn5S</i>
tRNAs	<i>trnA (UGC), trnC (GCA), trnD (GUC), trnE (UUC), trnF (GAA), trnG (GCC)^b, trnG (UCC), trnH (GUG)^b, trnI (GAU), trnK (UUU), trnL (CAA)^c, trnL (UAA), trnL (UAG), trnM (CAU), trnN (GUU), trnP (UGG), trnQ (UUG), trnR (ACG), trnR (UCU), trnS (GCU), trnT (UGU), trnV (UAC), trnW (CCA), trnY (GUA)</i>

^alacking in the plastid genome of *B. natans*.

^blacking in the plastid genome of *L. vacuolata*.

^clacking in the plastid genome of *L. oceanica*.