S3 Fig. A. Maximum-Likelihood tree inferred from mitochondrial *nad1* of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. B. Maximum-Likelihood tree inferred from mitochondrial *nad2* of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig.  C. Maximum-Likelihood tree inferred from mitochondrial nad3 of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. D. Maximum-Likelihood tree inferred from mitochondrial *nad4* of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. E. Maximum-Likelihood tree inferred from mitochondrial nad4L of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. F. Maximum-Likelihood tree inferred from mitochondrial nad5 of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. G. Maximum-Likelihood tree inferred from mitochondrial \textit{nad}6 of algal taxa in Table 1 using a GTR+\Gamma+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. H. Maximum-Likelihood tree inferred from mitochondrial *cox2* of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. I. Maximum-Likelihood tree inferred from mitochondrial *cox3* of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. J. Maximum-Likelihood tree inferred from mitochondrial *atp6* of algal taxa in Table 1 using a GTR+$\Gamma$+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. K. Maximum-Likelihood tree inferred from mitochondrial atp9 of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. L. Maximum-Likelihood tree inferred from plastid atpA of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. M. Maximum-Likelihood tree inferred from plastid *atpB* of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. N. Maximum-Likelihood tree inferred from plastid *atpE* of algal taxa in Table 1 using a GTR+$\Gamma$+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. O. Maximum-Likelihood tree inferred from plastid atpF of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. P. Maximum-Likelihood tree inferred from plastid *atpH* of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. Q. Maximum-Likelihood tree inferred from plastid petA of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. R Maximum-Likelihood tree inferred from plastid \textit{psaA} of algal taxa in Table 1 using a GTR+$\Gamma$+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. S. Maximum-Likelihood tree inferred from plastid *psaB* of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. T. Maximum-Likelihood tree inferred from plastid psaC of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. U. Maximum-Likelihood tree inferred from plastid psbB of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. V. Maximum-Likelihood tree inferred from plastid psbC of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. W. Maximum-Likelihood tree inferred from plastid *psbD* of algal taxa in Table 1 using a GTR+$\Gamma$+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. X. Maximum-Likelihood tree inferred from plastid psbE of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. Y. Maximum-Likelihood tree inferred from plastid psbH of algal taxa in Table 1 using a GTR+\Gamma+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. Z. Maximum-Likelihood tree inferred from plastid *psbN* of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AA. Maximum-Likelihood tree inferred from plastid *psbZ* of algal taxa in Table 1 using a GTR+\(\Gamma\)+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AB. Maximum-Likelihood tree inferred from plastid rpl2 of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AC. Maximum-Likelihood tree inferred from plastid rpl5 of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AD. Maximum-Likelihood tree inferred from plastid *rpl14* of algal taxa in Table 1 using a GTR+$\Gamma$+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AE. Maximum-Likelihood tree inferred from plastid rpl16 of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AF. Maximum-Likelihood tree inferred from plastid *rpl20* of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AG. Maximum-Likelihood tree inferred from plastid *rps2* of algal taxa in Table 1 using a GTR+$\Gamma$+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AH. Maximum-Likelihood tree inferred from plastid *rps3* of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AI. Maximum-Likelihood tree inferred from plastid rps4 of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AJ. Maximum-Likelihood tree inferred from plastid rps7 of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AK. Maximum-Likelihood tree inferred from plastid \textit{rps8} of algal taxa in Table 1 using a GTR+$\Gamma$+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AL. Maximum-Likelihood tree inferred from plastid \( rps11 \) of algal taxa in Table 1 using a GTR+\( \Gamma \)+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AM. Maximum-Likelihood tree inferred from plastid *rps12* of algal taxa in Table 1 using a GTR+\( \Gamma \)+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AN. Maximum-Likelihood tree inferred from plastid rps14 of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AO. Maximum-Likelihood tree inferred from plastid *rps18* of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AP. Maximum-Likelihood tree inferred from plastid rps19 of algal taxa in Table 1 using a GTR+$\Gamma$+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AQ. Maximum-Likelihood tree inferred from plastid ycf3 of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AR. Maximum-Likelihood tree inferred from plastid clpP of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AS. Maximum-Likelihood tree inferred from plastid rbcL of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AT. Maximum-Likelihood tree inferred from mitochondrial cob of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AU. Maximum-Likelihood tree inferred from mitochondrial cox1 of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AV. Maximum-Likelihood tree inferred from plastid petB of algal taxa in Table 1 using a GTR+$\Gamma$+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AW. Maximum-Likelihood tree inferred from plastid petG of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AX. Maximum-Likelihood tree inferred from plastid *psbA* of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AY. Maximum-Likelihood tree inferred from plastid psbF of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. AZ. Maximum-Likelihood tree inferred from plastid *psbI* of algal taxa in Table 1 using a GTR+\(\Gamma\)+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. BA. Maximum-Likelihood tree inferred from plastid psbJ of algal taxa in Table 1 using a GTR+$\Gamma$+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. BB. Maximum-Likelihood tree inferred from plastid *psbK* of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. BC. Maximum-Likelihood tree inferred from plastid psbL of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. BD. Maximum-Likelihood tree inferred from plastid psbT of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. BE. Maximum-Likelihood tree inferred from plastid rpl36 of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. BF. Maximum-Likelihood tree inferred from plastid ycf12 of algal taxa in Table 1 using a GTR+Γ+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.
S3 Fig. BG. Maximum-Likelihood tree inferred from 2 rDNA sequences (rrnL and rrs) of algal taxa in Table 1 using a GTR+I+I nucleotide substitution model. Bootstrap value from ML and posterior probability from Bayesian inference are shown at the node. The scale bar represents the estimated number of nucleotide substitution per site.