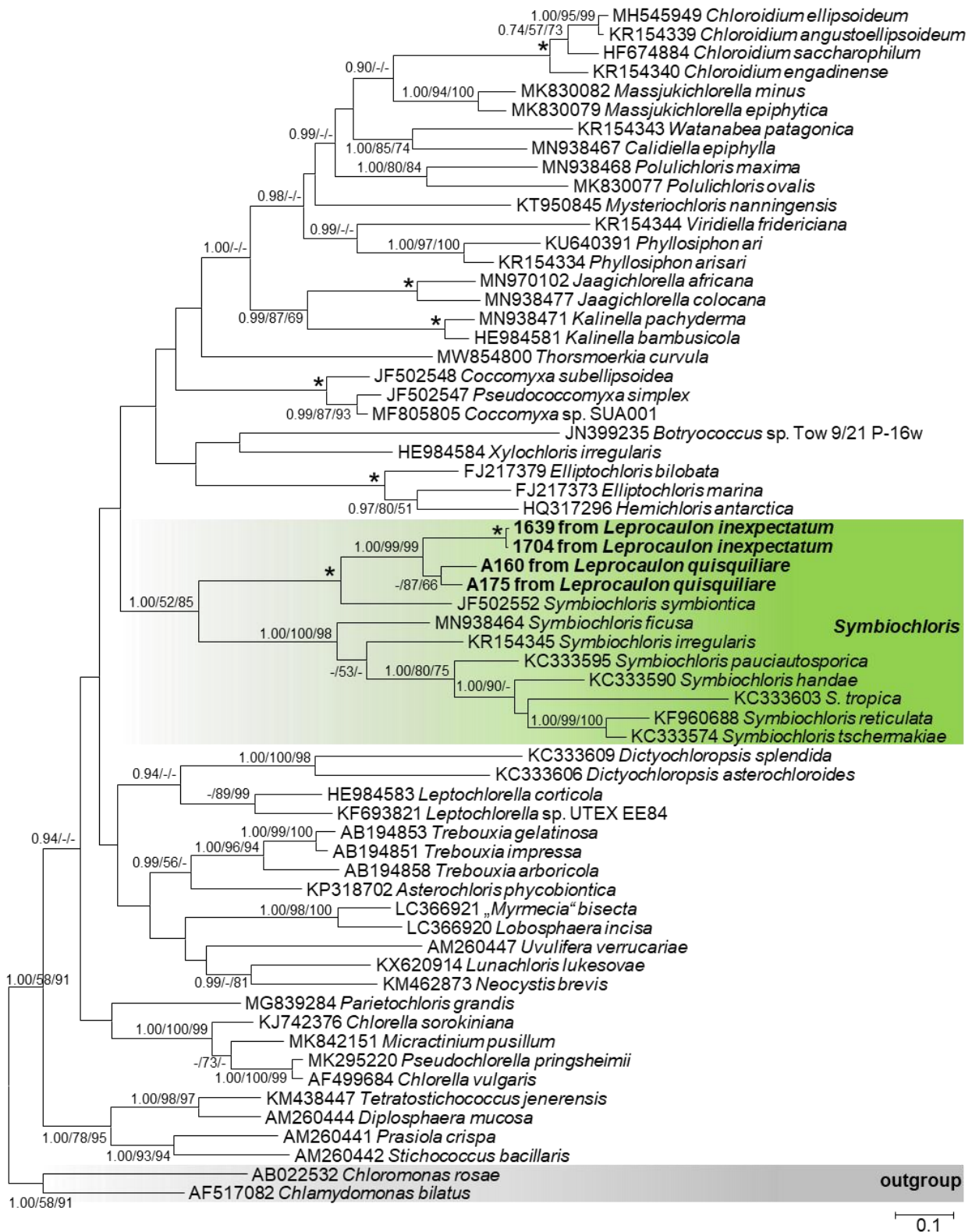


## SUPPLEMENTARY MATERIALS



**Figure S1.** Phylogenetic hypothesis of class *Trebouxiophyceae* resulting from the Bayesian analysis of *rbcL* sequences. Sequences of *Chlamydomonas bilatus* and *Chloromonas rosae* were selected as an outgroup. Values at the nodes indicate the statistical supports of Bayesian posterior probability (left), maximum-likelihood bootstrap (middle) and maximum parsimony bootstrap (right). Fully supported branches (1.0/100/100) are marked with an asterisk. Scale bar shows the estimated number of substitutions per site. Newly obtained sequences are marked in bold.

**Table S1.** Substitution models selected using the Bayesian information criterion (BIC) as implemented in MEGA7 (Kumar *et al.* 2016).

Marker/partition	Photobiont	Mycobiont
ITS (ITS1-5.8S-ITS2) rDNA	TN92 + $\Gamma$ ( $\alpha=1.06$ ) + I	
ITS1 rDNA		K2 + $\Gamma$ ( $\alpha=0.42$ )
5.8S rDNA		K2
ITS2 rDNA		K2 + $\Gamma$ ( $\alpha=0.84$ )
18S rDNA	TN93 + $\Gamma$ ( $\alpha=0.52$ ) + I	
<i>rbcL</i> 1st position	GTR + $\Gamma$ ( $\alpha=0.65$ ) + I	
<i>rbcL</i> 2nd position	JC + $\Gamma$ ( $\alpha=0.06$ )	
<i>rbcL</i> 3rd position	GTR + $\Gamma$ ( $\alpha=3.47$ ) + I	

### Reference

Kumar S, Stecher G and Tamura K (2016) MEGA7: Molecular Evolutionary Genetics Analysis Version 7.0 for Bigger Datasets. *Molecular Biology and Evolution* 33, 1870–1874.