Supplementary Materials

Algae 2023, 38(4): 241-252
https://doi.org/10.4490/algae.2023.38.11.30

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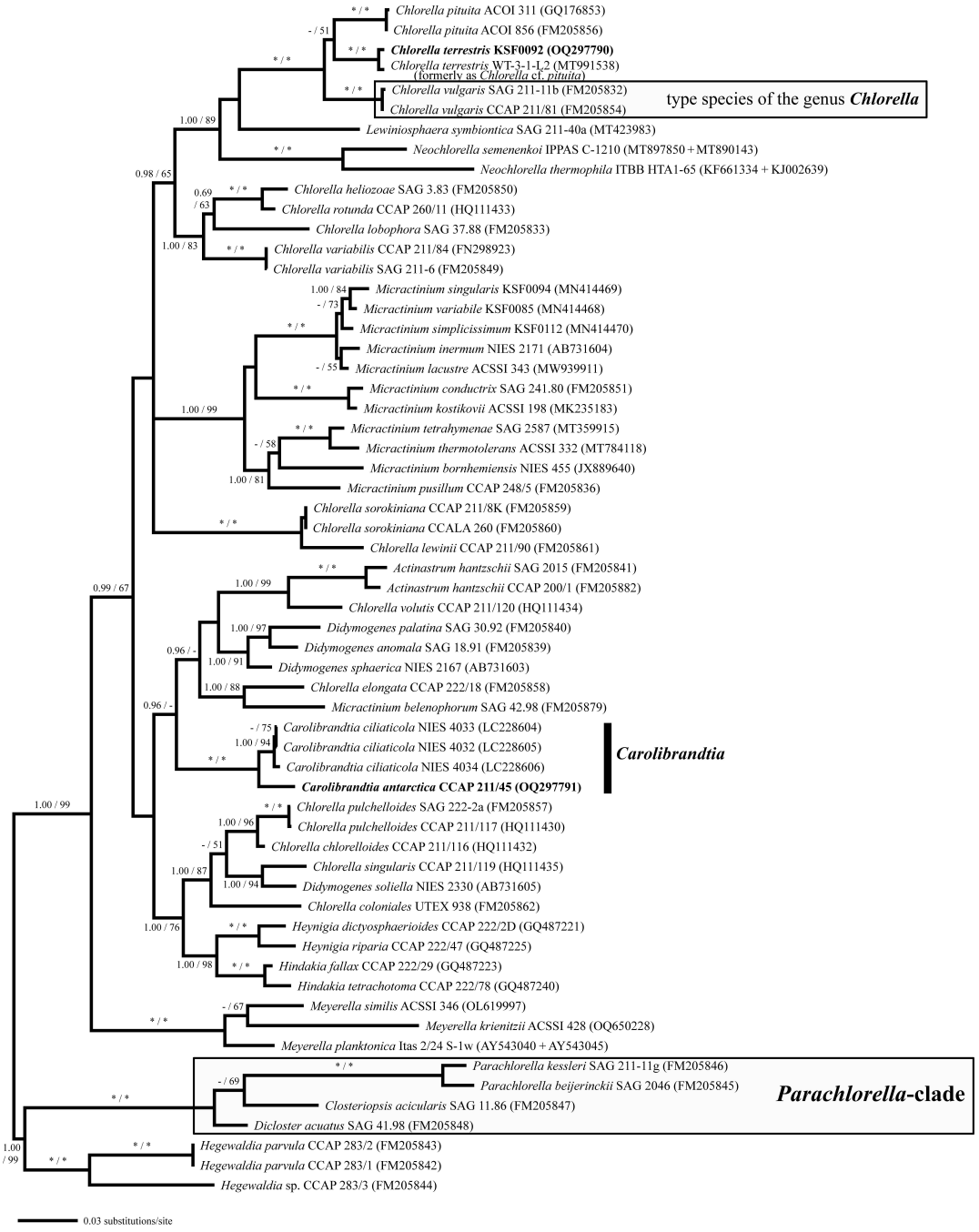

Supplementary Fig. S1. Bayesian phylogenetic tree constructed from small subunit, internal transcribed spacer 1, 5.8S, and internal transcribed spacer 2 ribosomal DNA sequences. The phylogenetic tree shown was inferred based on the aligned dataset in BioEdit 7.0.5.3 using the ClustalW algorithm. Numbers at each node are Bayesian probability (>0.95, left) and Maximum likeli-hood (>50%, right). * / * at each node indicates Bayesian probability 1.00 and Maximum likelihood 100%. The new sequences are in bold font.

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http://e-algae.org pISSN: 1226-2617 eISSN: 2093-0860