

ABSTRACT

PHYLOGENETIC ANALYSES OF THE CAULERPALES (ULVOPHYCEAE, CHLOROPHYTA) BASED ON RUBISCO LARGE SUBUNIT GENE SEQUENCES

In a review of caulerpalean taxonomy, Hillis-Colinvaux recognized two suborders, the Bryopsidineae and Halimedineae. Phylogenetic analyses based on 18S rRNA sequence data supported the hypothesis of two monophyletic suborders within the Caulerpales. However, analyses of morphological characters inferred monophyly in only the Halimedineae. These results prompted the current reanalysis of this diverse group of green algae based on plastid encoded RUBISCO large subunit (*rbcL*) gene sequences. Thirty-two caulerpalean ingroup taxa were analyzed via maximum parsimony (MP), maximum likelihood (ML) and Bayesian inference (BI). Results of all analyses suggest that the Halimedineae and Bryopsidineae form separate monophyletic assemblages. The phylogenetic position of taxa with uncertain affinity, such as *Dichotomosiphon tuberosus* and *Pseudocodium floridanum* were also resolved with *rbcL* sequence data. Molecular evolutionary analyses detected no evidence of positive selection for the *rbcL* gene among caulerpalean taxa.

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