

Phylogenetic Relationships of Brown Algae Based on Protein-Coding Plastid *rbcL*, *psaA*, *psbA*, and *psbC* Region Comparisons

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Over the past decade, the study of the evolutionary history and relationships of eukaryotic organisms has been revolutionized by DNA sequence data. Brown algae, the Phaeophyceae, derive their characteristic color from the large amounts of the carotenoid fucoxanthin in their plastids as well as from any phaeophycean tannins that might be present. Brown algae show a great structural diversity, ranging from microscopic filaments to giant kelps of up to 70 meters in length. They together with green and red algae predominate in the intertidal to subtidal coastal regions throughout worldwide, but especially in polar, boreal and temperate latitudes. However, recent progress in molecular systematics show an interesting result that brown algae, despite the structural complexity and benthic life, are more closely related to unicellular planktonic algae and even oomycetes than to red and green algae. Molecular phylogenies based on plastid *rbcL* gene, commonly used in photosynthetic organisms, and nuclear ribosomal DNA large subunit, have proposed major changes in the taxonomy of brown algae. In order to improve our knowledge on the brown algae, we have investigated brown algae using five protein-coding plastid genes: *psaA* (encoding photosystem I P700 apoprotein), *psbA* (encoding photosystem II thylakoid protein D1), *psbC* (encoding photosystem II 43 KDa), and *tufA* (encoding elongation factor Tu) as well as the *rbcL*. The aligned sequences were 1467 bp in *rbcL*, 1488 bp in *psaA*, 885 bp in *psbA*, and 1290 bp in *psbC*. The concatenated 5130 bp from about 40 representatives covering all orders was used in reconstruction of phylogenetic trees. Despite the different characteristics of each of the five protein-coding genes analyzed here, the combined data improved phylogenetic resolution, compared to individual data sets. Bayesian trees of the whole data set support the monophyly of the brown algae, while do not support the long-held concept of an ancestral Ectocarpales and derived Fucales. The early diverging brown algae have apical growth and pyrenoidless discoid plastids as morphological symplesiomorphy. The distribution of living taxa of these basal groups is speculated to have originated in tropical waters during a geographical period, whereas most of brown algae occur along the cold waters.