

F201 Phylogenetic analysis of the microalgae by comparing the sequences of the internal transcribed spacers and 5.8S ribosomal DNA

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The nucleotide sequences of internal transcribed spacer (ITS) regions of ribosomal DNA including the 5.8S rRNA gene have been determined for 13 strains of the microalgae in order to analyze phylogenetic relationship. Their sequences were compared and aligned those extracted from the Genbank database for the comparative purpose. These microalgae were divided into four groups based on the similarity of nucleotide sequences and were similar to the taxonomical criterions by the morphological characteristics. The genus of *Pseudonizia* grouped independently Group I compared with other microalgae. *Gymnodinium* and close related taxa, including *Gyrodinium*, *Cocholodinium*, *Prorocentrum*, and *Heterocapsa*, formed Group II. Group III was formed the genus of *Alexandrium*.

F202 Genomic Cloning and Characterization of mitochondrial elongation factor Tu (EF-Tu) gene (*tufM*) from Maize (*Zea mays* L.)

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We have characterized a mitochondrial elongation factor Tu (EF-Tu) gene (*tufM*) in maize. The *tufM* gene encoded a polypeptide of 453 amino acid residues, consisting of a transit peptide of 55 residues and a mature EF-Tu of 398 residues. The coding region was composed of 12 exons and 11 introns that range in length from 76 to 1,953 bp. The deduced amino acid sequence showed 84.9 % and 61.2 % identity with *Arabidopsis thaliana* mitochondria and chloroplast EF-Tu sequence, respectively. The transcription initiation site was determined 165 bp upstream of the AUG initiation codon by primer extension analysis. Southern blot analysis revealed that the cloned EF-Tu gene is encoded by a member of small gene family in maize. This gene does not closely resemble the *Arabidopsis* nuclear *tufA* gene, which encodes the plastid EF-Tu, and does not contain sequence elements found in all cyanobacterial and plastid *tufA* genes. However, the predicted amino acid sequence includes an N-terminal extension which resembles an organellar targeting sequence and shares three unique sequence elements with mitochondrial EF-Tu's, from *Arabidopsis thaliana*, *Saccharomyces cerevisiae*, and *Homo sapiens*, suggesting that this gene encodes the maize mitochondrial EF-Tu.