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Gene expression of chloroplast translation elongation factor Tu during chloroplast biogenesis in *Zea mays* L.

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We have investigated the expression of a maize nuclear *tuf* gene (*tuf*A) coding for the chloroplast translation elongation factor EF-Tu during chloroplast biogenesis. The steady-state level of the *tuf*A mRNAs was similar in both continuous light- and dark-grown seedlings. The level of the *tuf*A mRNAs also maintained at relatively same level during light-induced greening of etiolated seedlings and all examined developmental stages. These results indicate that the gene expression of the maize chloroplast EF-Tu is rarely light-regulated at its transcript level during chloroplast biogenesis. The monocot leaf such as a maize leaf is an excellent model system for the study of chloroplast development, because it shows the developmental gradient of chloroplast from the leaf base to the leaf tip. Therefore, we are currently examining the positional gradient of cellular differentiation in developing maize leaves to study the accumulation of *tuf*A mRNAs.

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3'-RACE PCR for cloning of *tuf* gene families in maize (*Zea mays* L.)

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The translational elongation factor is an essential part of the protein synthesis apparatus in prokaryotes and eukaryotes. Similary, eukaryotic organelles utilize EF-Tu (*tuf*) proteins for their own protein synthesis. Like many other mitochondrial and plastid proteins, the organellar elongation factors of higher plants are encoded by nuclear genes as a result of evolutionary gene transfer. The chloroplast *tuf* gene families were identified in the tobacco and the soybean. In addition, Kuhlman and Palmer have recently identified a nuclear gene (*tuf*M) coding for the mitochondrial elongation factor Tu, which is present in one copy in *Arabidopsis* but in several copies in other *Brassica* species. Therefore, we designed degenerative primer and tried 3'-RACE PCR to amplify various *tuf* genes in maize. 3'-RACE PCR approach was used for the following purposes : 1) Chloroplast *tuf* gene families (*tuf*A and *tuf*B) have divergency in the C-terminal coding part and the 3'UTR. 2) Two organellar *tuf* genes (*tuf*A and *tuf*M) are two sequence elements distinctive with each other in the C-terminal region. We obtained putative *tuf* clones (about 1.3 kb product) from maize leaf cDNA library using 3'-RACE and sequenced a portion of positive clones. Partially sequenced fragments showed 70% and 85% sequence identity on the nucleotide and amino-acid level with soybean chloroplast *tuf*A gene, respectively. This data indicates a PCR-based approach for isolating various *tuf* gene families using degenerative *tuf* gene primers is productive. By using genomic Southern analysis, we are currently examining that these clones include various EF-Tu genes.