F204 Genomic Cloning and Characterization of *tuf*M Gene from Maize (*Zea mays* L.)

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We have characterized a mitochondrial elongation factor Tu (EF-Tu) gene (*tuf*M) in maize. A 8 kb *Bam*H I fragment of maize DNA was hybridized with a partial chloroplast EF-Tu gene of tobacco as a probe. Therefore, various DNA fragments in the region of 8 kb *Bam*H I fragment were isolated and ligated into the vector EMBL3. One genomic clone coding for a maize mitochondrial EF-Tu protein was isolated by plaque hybridization. Restriction enzyme digestion and Southern blot analysis was carried out for further characterization. The 8 kb *Bam*H I fragment which was hybridized with the partial chloroplast EF-Tu gene of tobacco as a probe was subcloned into a plasmid vector pBluescript SK II. Nucleotide sequence of the clone was determined. The gene consists of 12 exons and 11 introns spannig over 5 kb and encodes 508 amino acids. The nucleotide sequence show 66.8 % and 52.1 % identity with the *Arabidopsis thaliana* mitochondria and chloroplast EF-Tu sequence, respectively. The deduced amino acid sequence show 85.2 % and 61.4 % identity with that of *Arabidopsis thaliana* mitochondria and chloroplast EF-Tu, respectively. The consensus amino acid sequences, GXXXXGK, DXXG, NKXD and SAL, known to be involved in GTP interaction, an N-terminal extension which resembles an organellar targetting sequence and three unique sequence elements which are present in *Arabidopsis thaliana, Saccharomyces cerevisiae* and *Homo sapiens* mitochondrial EF-Tu, were present in the clone. According to the above-mentioned results, it is concluded that this gene encodes the maize mitochodrial EF-Tu.

F205 Partial cloning and characterization of cytokinin-induced genes from Maize (*Zea may* L.)

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Cytokinins are important growth hormones that control the proliferation and differentiation of plant. Rapid changes in gene expression were studied during incubation of maize cotyledons with cytokinin in darkness. cDNA fragments for mRNA whose levels increased in 4h of treatment with N^6-benzyladenine(BA) were synthesized by differential display RT-PCR and these cDNA fragments were inserted into pCR2.1-TOPO. One of them is named CI8and its size was about 200 bp. CI8 hybridized with 3.1-3.2Kb mRNA by northern blot analysis. The amount of CI8 mRNA was increased 1.5 fold in BA-treated maize cotyledons compared with control. Treatment of the cotyledons with BA was shown to modulate CI8 mRNA levels in a dose- and time- dependent manner. These result suggest that a gene including CI8 is in part controlled at transcriptional level by cytokinin.