F206 Characterization of 5'-Flanking Region of Carnation Genomic Clone Encoding *S*-adenosylmethionine Decarboxylase.

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S-adenosylmethionine Decarboxylase(SAMDC) is a rate-limiting step in polyamine biosynthesis. In order to study the regulation of SAMDC gene expression, we made several constructs in which the various length of 5'-flanking regions of genomic SAMDC gene were fused GUS reporter gene and these constructs were transformed into tobacco leaf discs using *Agrobacterium*. GUS activity of tobacco leaves transformed with the construct containing full-length(1824 bp) of promoter and first leader intron was the highest among those with other constructs. However, when transformants were incubated with 1mM methyljasmonate or 3% sucrose, GUS activity was stimulated only in the transformant having the construct containing promoter and full-length of 5'-untranslated region(two leader intron and upstream open reading frame). According to the results of histochemical GUS staining of transformants, GUS gene of transformant having construct with 1824 bp promoter and 5'-untranslated region(UTR) was expressed mainly in petal, anther and stigma but that of transformant having the construct deleted 5'-UTR was only expressed in stigma. And GUS gene of transformant having construct with 724 bp promoter and 5'-UTR was expressed in petal and stigma Based upon these data, we propose that 5'-UTR confer the responsiveness to inducer and tissue-specificity on SAMDC gene expression. Also, the element related to pollen development locate at between -1824 bp and -724 bp in promoter region.

F207 Characterization of Rice Chloroplast Elongation Factor Tu cDNA

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The chloroplast translational elongation factor Tu is one of proteins that encoded on nuclear DNA and imported into chloroplast for chloroplast protein synthesis. Elongation factor Tu forms ternary complex with aminoacyl-tRNA and GTP that promotes the binding of the aminoacyl-tRNA with the A site of ribosomes, and consequently directs the elongation of polypeptides on ribosome. In this study, we have isolated a partial cDNA clone for the chloroplast translational elongation factor Tu gene in *Oryza sativa* L. and determined its entire mature peptide sequences and a part of transit peptide sequence. The clone was obtained from a leaf cDNA of *Oryza sativa* L. using the RACE-PCR (Rapid Amplification of cDNA ends-Polymerase Chain Reaction). The rice chloroplast EF-Tu has four consensus amino acid sequence(GHVDHGK, DCPG, NKKD and SAL) involved in GTP interaction, two chloroplast EF-Tu signature regions and about 283 nucleotides in 3'UTR. It shows 83-86% amino acids identity with that of tuf genes of soybean, tobacco, arabidopsis and pea.