F205 Cloning of the Arginine Decarboxylase Gene from Carnation Flower and its Expression

Kwang-Suk Chang*, Myeong-Min Lee, Ky-Young Park[1] and Sun-Hi Lee
Department of Biology, Yonsei University, [1]Department of Biology, Sunchon Unversity

Argine Decarboxylase(ADC) is one of the key enzymes in the synthesis of putrescine in plants and it has been well known that the ADC activity is regulated depending on the physiological conditions. For example, ADC activity increases during cell elogation and in various stress condition such as acid stress, anaerobiosis, osmotic stress and deficiency of K^+ ion. However, the mechanism which regulates the ADC activity is poorly understood. To study the regulation of polyamine biosynthesis, we have isolated a cDNA clone(GenBank Acession NO U63832) which encodes ADC from carnation(*Dinathus caryophyllus* L. White sim) petal. Using two degenerate oligonucleotide primers based on the amino acid sequence of the conserved regions of tomato and oat ADC, we amplified a DNA fragment encoding carnation ADC by PCR and isolated a cDNA clone encoding ADC using a probe generated by PCR and rapid amplified of cDNA ends. An ADC cDNA clone (2586 bp) contains one complete open reading frame (2178 bp), 143 bp of 5′ untranslated region and 266 bp of 3′ untranslated region. The coding region is capable of encoding a protein which has a calculated molecular mass of 77.6 KD (726 amino acid). The deduced amino acid sequence of the carnation ADC show strong sequence identity to those of the cloned ADCs from dicotyledonous plants, tomato ADC (74.3 %), soybean ADC (67.6 %) and pea ADC (62.9 %). but, showed only 43.8 % amino acid sequence identity to that of the oat ADC which is a monocotyledone. We have investigated the regulation of ADC gene expression in carnation organs.

F206 The Light-Regulated Expression of a Maize (*Zea mays* L.) Chloroplast EF-Tu Gene

Jeong-Hwan Lee*, Kyu Lee Choi, Woong Seop Sim, and Jeong-Kook Kim
Department of Biology, Korea University

The chloroplast elongation factor EF-Tu(*tuf*) plays an essential role in protein synthesis. Although it is known about light regulation of chloroplast-encoded elongation factor in photosynthetic algae, little is known about light regulation of nuclear-encoded elongation factor. We investigated the expression patterns of the elongation factor(EF-Tu) by light and compared them with those of the *rbcL* gene and the 25S rRNA in a maize. For the detection of maize *tuf* transcripts, Northern hybridization was performed by using heterologous probes(*tufA* and *tufB* gene of *Nicotiana sylvestris*). The level of *tuf* mRNAs was much higher in light-grown seedlings than in dark-grown seedlings. Also, the *tuf* mRNA level significantly increased up to level of light-grown condition in transition of darkness to light. Under the same condition, the level of *rbcL* mRNA increased about 1.5-fold, but the level of 25S rRNA did not changed in all conditions. These results indicate that maize chloroplast EF-Tu mRNA level can be light-regulated.