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The Involving of Phosphorylation in Distinct Mechanisms of Translational Regulation by Upstream Open Reading Frame of SAMDC Gene

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S-adenosylmethionine decarboxylase (SAMDC; EC 4.1.4.50) is a key enzyme in the biosynthesis of the polyamines spermidine and spermine. Carnation *SAMDC*genes have an upstream open reading frame (uORF) of 52 or 54 amino acids in 5'-leader sequences with an extensive stem-loop structure (ΔG > -65 kcal/mol, mfold). SAMDC uORF sequence induced a real protein of 5.8-kDa, which was provided the direct evidence of peptide synthesis from the SAMDC uORF using an *in vitro* translation system. To test whether the uORF protein was functional, we performed *in vitro* phosphoryation assay. In this paper we show the uORF protein specifically is phosphorylated by unknown kinase. It was first reported that phosphorylation of uORF functions as a crucial effect for downstream ORF translation. In addition, the nuclear localization of uORF protein will examine byconstructing the uORF-GFP fusion protein, the expression of which is controlled by the cauliflower mosaic virus 35S promoter. In order to elucidate action mechanism of SAMDC uORF, we have used a primer extension inhibition assay to determine the location and stability of translating ribosomes on the SAMDC uORF. Our results might imply the distinct mechanism of SAMDC uORF, which was regulated by ribosomal stalling and reinitiation.

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The Response to a Various Stresses in Transgenic Tobacco Plants Expressing the Antisense Genes of Biosynthesis for Ethylene

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Tolerance to a wide variety of environmental stress conditions has been correlated with increased level of antioxidative properties. We have investigated the tolerance against abiotic and biotic stresses by determining the gene expression of antioxidant enzymes using transgenic tobacco plant, in which cellular contents of polyamines were increased by anti-expression of ethylene-biosynthesis genes, 1-aminocyclopropane-1-carboxylic acid (ACC) synthase and ACC oxidase. Transcript levels for antioxidant enzymes, glutathione-*S*-transferase (GST), ascorbate peroxides (APX) and manganase-superoxide dismutase (Mn-SOD), were induced more significantly in transgenic plants than wild-type plant after treatment with hydrogen peroxide (H2O2). We also examined the accumulation of H2O2 by 3,3-diaminobenzidine (DAB) polymeration in response to abiotic stress (NaCl) and ABA treatment. In result, considerably more H2O2 was detected in the main vein surrounding region of the leaf. And then, strong color develops at wild type plants than transgenic plants. To confirm, H2O2acts as a second messenger for the induction of defense genes in response to abiotic stresses, we were measured the ethylene production after treatment with the NADPH oxidase inhibitor diphenylene iodonium (DPI) and antioxidants (BHT, DTT, iodine).

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Structure of Ribosomal Protein Genes and Expression Pattern under Drought Stress in Hot Pepper (*Capsicum annuum*)

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Exposure to environmental stresses such as low temperature, high temperature, salinity, and drought causes adverse effects on the growth and productivity of crops. We built a cDNA library from drought-stressed hot pepper plants (*Capsicum annuum* cv. Pukang). Differential screening of the cDNA library using probes prepared either from 15-days non-watered hot pepper plants or nonstressed hot pepper plants. Isolated 1430 cDNA clones that probably represent preferentially expressed transcripts under dehydration stress. Partial uni-directional nucleotide sequencing of the clones selected five clones for ribosomal proteins. To analyse expression level of ribosomal proteins at the transcript level under dehydration stress, RNA blot analysis was performed for transcripts under three different levels of dehydration stress. All the five cDNA clones showed a dramatic reduction of the transcripts upon exposure to the dehydration stress. However, transcript levels of four clones increased as the duration of dehydration stress prolonged. This increase of transcripts under severe dehydration stress suggests function of ribosoaml proteins during the adaptation process to the dehydration stress.