11 Characterization of Promoter and 5′-UTR of *S*-adenosylmethionine decarboxylase Gene in its Expression.

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S-adenosylmethionine decarboxylase(SAMDC) gene is a rate-limiting step of polyamine biosynthesis. By sequence analysis of genomic clone, we identified that putative light-regulated elements and other various putative elements for hormonal recognition and developmental control are in promoter region. Also there were two introns and a 54-codon upstream open reading frame(uORF) in 5′-UTR. Using transgenic tobacco plant, we found that the leader intron of SAMDC gene has a role for post-transcriptional control in determining spatial pattern of SAMDC expression. Element related pollen-specific expression(TCATCTTCTATAAA) of SAMDC gene locates between -1073bp and -1060bp of promoter region. Two kinds of components, enhancer and silencer, related to anther-specific expression of SAMDC gene locate between -1824bp and -724bp, -723bp and -274bp, respectively, of promoter region. Element for anther, and stigma-specific expression of SAMDC gene locates downstream -273bp of promoter region. Now we are studying expression pattern of SAMDC gene with circadian rhythm and roles of promoter and 5′-UTR in regulation of SAMDC expression. Also, we confirmed that the uORF repress translation of the downstream GUS reporter gene both in the wheat germ extract translation system and in transgenic tobacco plant. In *in vitro* experiments, we found that the translation of the uORF region was required for repression of downstream main ORF, and several point-mutations in the nucleotide sequences of uORF nulled the respression. Using in vivo system, we demonstrate that deletion of uORF sequence unaffect tissue-specific expression of GUS gene and uORF provides the translational control in determining an inducibility.

Keywords: polyamine, SAMDC, uORF