(05-1-133)

Identification of regulatory elements involved in seed and pollen-specific expression of *PfFAD3* gene from *Perilla frutescens*

Hyang Hwa Lee¹, Chung-Han Chung², Nam-In Hyung³, Mi-Chung Suh⁴ and Jaeho Pyee¹*

Department of Molecular Biology & Institute of Nanosensor and Biotechnology, Dankook University, Seoul 140-714

Department of Biotechnology, Dong-A University, Pusan 604-714

Department of Plant Science and Technology, Sangmyung University, Cheonan 330-720

Division of Applied Plant Science and Agricultural Plant Stress Research Center, Chonnam National University, Gwangju 500-757

Introduction of an exogenous gene encoding linolenic acid desaturase (FAD3) into oil seed plants containing a limited amount of linolenic acid has been pursued to improve seed oil quality. To understand underlying the mechanism of the expression of the exogenous *PfFAD3* cDNA incorporated into sesame (*Sesamum indicum*), a genomic clone containing the regulatory regions was amplified from *Perilla frutescens* by GenomeWalk PCR. To assess regulatory regions involved in spatial and temporal expression and environmental response of *PfFAD3* gene, the 5' flanking region fused to the bata-glucuronidase gene was incorporated into *Arabidopsis thaliana*. Histochemical assay showed that GUS expression under the *PfFAD3* promoter was restricted to seed and pollen. In order to identify the regulatory elements involved in response to environmental factors, transgenic *Arabidopsis* plants containing deletion series of the 5' flanking region were treated with various photo period and light intensity. Our results showed that the cis-elements in the -1095/-955 and -510/-236 regions were required for seed-specific and pollen-specific expression of the *PfFAD3* promoter, respectively.

^{*} Corresponding author: Jaeho Pyee, TEL: 02-709-2818, E-mail: jpyee1@dankook.ac.kr