F822 The Study of Fibroin Gene Expression by using Transgenic Silk Worm

Eun-Young Kang*, Seung-Hyun Sung, Hyung-Wook Jeon
and Dong-Sang Suh
Department of Genetic Engineering, Sungkyunkwan University

The fact that we found out tissue specific expression regulation mechanism of a gene is important to understand development and cell differentiation mechanism. The transcription of fibroin gene occur only at the posterior silk gland. Particularly, it is expressed very strongly at the latest age of the fifth instar, and produces fibroin that accounts for about 20 % of the body weight. Like above, it is supposed to provide a significant clue for the study of genetic expression regulation mechanism to explain a strong tissue-specific expression regulation mechanism of fibroin. The firefly luciferase gene was used as a reporter of gene expression. The pLuc vector was microinjected into the fertilized eggs and we had transgenic silk worms. Hatching rate is about 1%. We have resolved the generation of F1 by Luciferase assay. Consequently, we have found out that the firefly luciferase gene was expressed up to progeny. In addition, we gained transformants in terms of inserting pFPLuc vector containing fibroin light chain promoter by using microinjection which has already been resolved. We are analyzing in order to examine the degree of the activation of fibroin promoter. It is expected that the results make it possible to study the strong promoter and production of the useful substances in eukaryotes.

F823 Tissue-Specific of Alpha-Amylase Gene Expression of Amy variants in *Drosophila melanogaster*

Jong Kil Choo, Hyung Chan Son, and Chi Hyun Ahn
Department of Biology, College of Natural Science, Chungang University

In *Drosophila melanogaster Amy* variants were screened for spatial variation in adult and larva midgut α-amylase(E.C. 3.2.1.1; *Amy*). Enzyme activity was detected by DNSA method during 10 generations in each food component for dietary control. Every strain revealed a different activity in each restricted medium, indicating that each strains have different adaptation ability to carbon source. The relationship of *Amy* genotype and midgut amylase-activity pattern(*Map*) analysis was shown expression of *Map*P indicated highly enzyme activity at anterior parts of region than that at posterior. This suggests that somehow *Amy* genes, or their products, are differentially recognized by products of the *Map* gene in addition to being differentially recognized in different parts of the midgut.