F810 Molecular cloning of Fibroin Heavy Chain (FHC) Gene from *Antheraea yamamai* and Its cDNA Ends Analysis

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Fibroin heavy chain (FHC) gene product is the major component of the silk protein, which is structurally and functionally diverse in insects. Only partial fibroin nucleotide sequences have been clarified owing to their repetitive structure and the large sizes (10 kb). We have characterized a genomic and cDNA ends of FHC gene containing exon 1, intron 1, partial exon 2 and poly A upstream region using cosmid genomic library, cDNA library and RT PCR technology from korean oak silkmoth, *Atheraea yamamai* (*Ay*). The 5′ genomic clone of *Ay* FHC consists of the first exon that encodes only 14 amino acid residues, a short intron (151 bp) and partial second exon encoding 328 amino acid residues. The 3′ end cDNA clone of 612 bp has termination codon (TAA), poly A signal (AATAAA) and 28 nt poly A tail. The nucleotide sequences similarity to the FHC of domesticated silkworm, *Bombyx mori* (*Bm*) is limited to small region of exon 1 because *Bm* FHC lacks polyalanine-rich motifs. Extensive homology was observed within the gene. A kind of concerted evolution was estimated. The alanine-rich blocks of the motif were well conserved, although the block among the motifs was a little different. The properties of the whole fibroin gene will provide highly useful information for understanding the dynamic aspects of molecular evolution of silk-producing insects and for genetically modified silk products.

F811 Cloning and Sequencing Analysis of Inverted α-Amylase Gene in *Drosophila melanogaster*

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In *Drosphila melanogaster*, α-amylase(AMY) is an 54,500 dalton monomeric enzyme that hydrolyzes α-1,4 glycosidic bond in starch. The α-amylase structural gene locus contains two duplicated genes called Amy-p(proximal gene) and Amy-d(distal gene). It is located in the right arm of chromosome 2 and two duplicated genes are approximately 4kb apart and inverted. In order to detect intergenic inversion of Amy gene, inversion mutant in Suwon natural population was analyzed by PCR method with selected primers from the different site at the highly divergent region in flanking regions of Amy-p and Amy-d. For genetic analysis, 6 lines of mutants were made by mating with *Cy/Pm* and genomic DNA of inversion mutant was cloned into bacteriophage vector and the inverted Amy locus out of screened genomic library was amplified by PCR method and the obtained products of two proximal genes were cloned in pGEM-Tvector. Furthermore, We plan to analyze the sequences compared with wild type to confirm gene exchange as well as inversion between two duplicated genes and add the experimental improvement of the fact that concerted evolution is caused by frequent recombination exchange in natural population.