

Cloning of the Fibroin Gene from the Oak Silkworm, *Antheraea yamamai* and Its Complete Sequence

**Jae-Sam Hwang¹, Jin-Sung Lee¹, Tae-Won Goo¹, Eun-Young Yun¹,
Kwang Ho Choi¹, Kwang-Sik Lee², Yong-Sung Kim³, Byung-Rae Jin²,
Sang-Mong Lee⁴, Keun-Young Kim¹, Seok-Woo Kang¹ and Dong-Sang
Suh⁵**

¹*Department of Sericulture and Entomology, National Institute of Agricultural Science and Technology, RDA, Suwon 441-100, Korea,* ²*College of Natural Resources and Life Science, Dong-A University, Pusan 604-714, Korea,* ³*Genome Center, Korea Research Institute of Bioscience and Biotechnology, Taejeon 303-333, Korea,* ⁴*Department of Sericultural & Entomological Biology, Miryang National University, Miryang, Kyung-Nam 627-130, Korea, and* ⁵*Department of Genetic Engineering, Sungkyun Kwan University, Suwon 440-746, Korea*

The nucleotide sequence containing an entire genomic region and 5' upstream region of *A. yamamai* fibroin gene have been determined. The gene consists of an initial exon encoding 14 amino acids, an intron(150 bp), and a long second exon coding for 2641 amino acids. One interesting feature of the deduced amino acid analysis of *A. yamamai* fibroin is that it is extremely rich in three amino acids, alanine, glycine and serine, and these three amino acids take up almost 80% of *A. yamamai* fibroin amino acid composition. Exon 2 of this gene is composed of 80 repetitives with each pair composed of one polyalanine motif [(A)₁₀₋₁₂, (PAM)] and one non-polyalanine motif (NPAM). The amino acid sequence of NPAM shows a higher hydrophobic pattern than PAM sequence, and thus, *A. yamamai* fibroin shows the characteristic of the regular repetition of a hydrophilic region and a hydrophobic region. Northern blot analyses confirmed that fibroin gene is actively expressed in the posterior silk gland of the final instar larvae of *A. yamamai*.