

Analysis of expressed sequence tags generated from the posterior silk gland cDNA clones of *Antheraea yamamai*

Eun Young Yun, Tae Won Goo, Seok Woo Kang, Hae Won Lee, Jae Sam Hwang and Ho Rak Kim

Dept. of Sericulture and Entomology, NIAST, RDA, Suwon 441-100, Korea

In order to understand molecular events during silk synthesis and provide genetic resources for molecular breeding, we had constructed the cDNA library from posterior silk gland of *Antheraea yamamai*, and partially sequenced 276 randomly selected genes from the cDNA library. Database comparisons of the expressed sequence tags (ESTs) revealed that 32 non-redundant clones showed a high similarity with previously identified genes. Among them, 19 clones exhibited a homology with previously identified insect genes and 12 were identical to genes that were previously identified from other organisms. A functional categorization showed that silk synthesis-, defense- or stress-related genes, as well as genes involved in the metabolic pathways and in the transcriptional or translational apparatus are represented. In this report, the clone (AY479) which had high similarity with fibroin from *Antehraea pernyi* was particularly analyzed in detail. AY479 clone was carboxyl terminal region of fibroin. The 472 bp cDNA had 123 amino acids that shared 85% homology with the fibroin from *Antheraea pernyi*, and its deduced peptide had unique feature, that is, sites of alanine rich residues.