cDNA cloning of a Putative ApolipophorinⅢ from the Silkworm, *Bombyx mori*

Eun Young Yun, Tae Won Goo, Sung Wan Kim, Kwang Ho Choi, Jae Sam Hwang, O-Yu Kwon[1] and Seok Woo Kang

Department of Sericulture and Entomology,
The National Institute of Agricultural Science and Technology, RDA, Suwon 441-100, Korea
[1]Department of Anatomy, College of Medicine, Chungnam National University,
Taejon 301-131, Korea

ApolipophorinⅢ (apoLp-Ⅲ) is a protypical exchangeable apolipoprotein that is abundant in hemolymph of many insect species. Its function lies in the stabilization of low-density lipophorin particles (LDLp) crossing the hemocoel in phases of high energy consumption to deliver lipids from the fat body to the flight muscle cells. But, recent studies with naive *Galleria mellonella*-apoLp-Ⅲ gave first indications of an unexpected role of that protein in insect immune activation (Niere *et al.*, 1999). In this research, to identify novel genes that are expressed specifically or preferentially in immunized-*B. mori*, we constructed a cDNA library using whole bodies of *B. mori* larvae injected with *E. coli*, carried out the differential screening using cDNA synthesized with total RNA from *B. mori* injected with *E. coli* or not, respectively, and selected the up-regulated clones. Among these clones, we focused on the cDNA showing the significant similarity with apolipophorinⅢ from other insects, analyzed the nucleotide and deduced amino acid sequences. The pupative *B. mori* apoLp-Ⅲ cDNA (GenBank Acc. No. AY341912) contained 1,131 bp encoding 186 amino acid residues. The *B. mori* Jam123 apoLp-Ⅲ showed 99%, 98%, 99%, 65%, 64%, 59%, 63%, 15% and 9% nucleotide sequence identity to the *B. mori* P50, *B. mori* N4, *B. mandarina, M. sexta, S. litura, G. mellonella, E. postvittana, L. migratoria and A. domesticus*, respectively. Phylogenetic analysis revealed that the nucleotide and amino acid sequences of the *B. mori* apoLp-Ⅲ cDNA formed a highly inclusive subgroup with Bombycidae. But, it was interesting that *B. mori* Jam 127 is closer to *B. mandarina* than *B. mori* P50 and *B. mori* N4. Northern blot analysis showed a signal in the fat body, posterior silkgland and mid-gut.