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Comparison of Gene Representation in the Posterior Silk Gland of Silkworm using ESTs and SAGE Tags

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The silkworm *Bombyx mori* larvae have a pair of posterior silk glands (PSGs). The PSGs exclusively synthesize the silk fibrous protein (fibroin H- and L-chain), which provides an excellent model to study differential gene expression. In this study, in order to understand the overall biosynthesis mechanism of fibrous protein in the PSG of silkworm, we have obtained a set of qualitative and quantitative information of expressed genes of the PSG. Firstly, we constructed and analyzed a full-length cDNA library from the PSGs at day 4 of the 5th instars. A total of 3,840 clones were randomly selected, and the 5'ends of the inserts were sequenced to generate ESTs. 544 unigenes were generated after the assembly of 2,867 high-quality ESTs. Functional groups of these sequences with matches in the database were constructed according to their putative biological function. Additionally, we have generated and analyzed a SAGE tag library from the PSGs. SAGE is a sequenced-based approach that identifies which genes are expressed and quantifies their level of expression. This SAGE catalog of gene expression for a given cell or tissue is defined as the 'transcriptome'. In this study, a total of 2,427 SAGE tags were analyzed, representing 682 unique transcripts. Finally, we discussed the comparative analysis of the transcript abundance between the cDNA sequences and the SAGE tags.