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Transcriptome Analysis of the Posterior Silk Gland of *Bombyx mori*

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The *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. We have generated and analyzed 3,840 expressed sequence tags (ESTs) from PSGs at day 4 of the 5th instars. Of these, 2,930 high-quality ESTs analyzed correspond to 552 unique genes. The most frequently represented genes in the library were elongation factor 1-alpha (gil232082), fibroin L-chain (gil19850) and heat shock cognate protein (gil20563125), which appeared 328, 137 and 125 times, respectively. Functional groups of these sequences with matches in the database were constructed according to their putative biological function. Additionally, to understand the gene expression quantification we analyzed the transcriptome of the PSGs using the SAGE method (Serial Analysis of Gene Expression – Velculescu et al., 1995) which allows to study the redundancy of mRNA. SAGE library have been constructed from mRNA isolated from posterior silk land at day 4 of the 5th instars. Presently, 114 concatemer clones were sequenced, and these represented 1,604 tags sequence information. However, there are two problems when applying the SAGE method for gene identification. The first one is that many SAGE tags identified have no match to known sequences in database. The second problem is that certain SAGE tag sequences have multiple matched with sequences in the databases.