

Gene Discovery through Expressed Sequence Tag Sequencing of the Immune Response Genes from the *Bombyx mori*

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Insects lack an acquired immune system but have a well-developed innate response. Dividing the insect immune system into cellular and humoral responses is somewhat arbitrary, as many humoral factors affect hemocyte function and hemocytes are an important source of many humoral molecules. There also is considerable overlap between humoral and cellular defenses in processes like the recognition of foreign intruders.

To screen genes related immune of *Bombyx mori* as model species, I constructed three cDNA libraries using larvae infected gram-positive, gram-negative and fungi. Here, we describe a collection of genes from the silkworm expressed during the switch from pathogenic. Each 2,304 expressed sequence tags were annotated. A total of 6,912 expressed sequence tag (EST) clones were generated from the three libraries; 2,304 from the non-normalized library and 4,608 from the normalized library. A total of 6,590 of the EST clones were identified to share significant sequence identity in GenBank, representing at least 3,977 different *Bombyx* genes. Also, these genes are categorized into 7 groups of biological process by Geneontology (GO). Some of these may be useful candidates for markers of the larvae infected *Bombyx*.