

## Gene Discovery through Expressed Sequence Tag Sequencing in *Bombyx* brain

Sun Mee Hong<sup>1</sup>, Si Kab Nho<sup>1</sup>, Nam Soon Kim<sup>2</sup>, Jin Sung Lee<sup>3</sup>,  
Jae Hoon Eum<sup>4</sup>, Tae Won Goo<sup>4</sup>, Kwang Ho Choi<sup>4</sup> and Seok Woo Kang<sup>4</sup>.

<sup>1</sup>College of Agriculture and Life Sciences, Kyungpook National University, Daegu 1370, Korea <sup>2</sup>Korea Research Institute of Biotechnology, Taejon 305-333, Korea <sup>3</sup>CoreBio Research Institute of Lifescience Biotechnology Seoul, 461-6, Korea and <sup>4</sup>National Institute of Agricultural Biotechnology, NIAST, RDA, Suwon 441-100, Korea,

In the present study, cDNA library from *Bombyx* brain was constructed and a total of 7392 expressed sequence tag (EST) clones were generated from the two libraries; 2,784 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. The brain cDNA library has been partially sequenced and functionally annotated searching the nucleotide and protein databases in the GenBank and other public sources using BLASTX. The average length of sequences was 506nt. Most of the best matches originated from insects. They are *Drosophila melanogaster* and *Anopheles gambiae*. Also, these genes are categorized into 7 groups of biological process by Geneontology (GO). Groups that expressed at high level are physiological process (82%), cellular process (13%), regulation of biological process (3%), development, biological process unknown, behavior, viral life cycle. Some of these may be useful candidates for markers of the spinning stage of *Bombyx* brain.