

D21

Construction of cDNA microarray during early embryo of *Bombyx mori*

Sun Mee Hong¹, Seok Woo Kang², Tae Jung Oh³, Nam Soon Kim⁴, Jin Sung Lee⁵, Tae Won Goo², Kwang Ho Choi² and Si Kab Nho¹

¹College of Agriculture and Life Sciences, Kyungpook National University, Daegu 1370, Korea, ²Department of Sericulture and Entomology, NIAST, RDA, Suwon 441-100, Korea, ³GenomicTree Incorporation of DaeDuk-Biocommunity, Jonmin-Dong Yusong Taejon 353-390, ⁴KoreaGenome Research Center Korea Research Institute of Bioscience and Biotechnology, Taejon 305-333, Korea and ⁵CoreBio Research Institute of Lifescience Biotechnology Seoul, Korea 461-6.

Embryogenesis is a complex process that requires the interaction of large groups of genes and is accompanied by changes in gene expression. To identify and analyze the expression patterns of *Bombyx mori* during embryogenesis, we constructed a *Bombyx* cDNA microarray containing 2446 unique genes identified from normalized and subtracted embryo cDNA libraries. We examined the patterns of gene expression during early embryo development in the *Bombyx* between six time points relative to unfertilization(0hr), fertilization(2-4h after oviposition), Blastoderm formation(8-10hr), Germband formation(24hr, HCl treatment for artificial hatching at this time), Spatula stage(48hr) and the abdominal leg appendages formation(72hr). On the basis of two repeated experiments, a student's t-test was performed and then we chose ≥ 2.0 as the cutoff value for up-regulated genes and ≤ 0.5 for down-regulated genes. A total of 241 genes exhibited signal intensity. Differentially expressed genes can be grouped into two categories, early genes that are expressed until 24hr and lately genes expressed at 48/72hr. Of those, many genes of unknown function were identified that may be involved in the control and execution of development. Genes of known function were cataloged molecular function, biological process and cellular component. Our study provides the first utilization of cDNA microarray in the *Bombyx* and reveals changes in levels of gene expression in relative to early embryo development.