

1-11. cDNA microarray profiling of *Bombyx mori*(kl20) during early embryogenesis

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The development of cDNA microarray has permitted the analysis of thousands of genes simultaneously. cDNA microarray has been used to analyze gene expression profiles during developmental stage in both single and multicellular organisms. Two significant factors contributing to the limitation of the development of cDNA microarray in the *Bombyx mori* are the shortage of accessible repositories of cDNA clones and ESTs and the relative scarcity of facilities to produce microarrays and analyze the data generated. In this study, we constructed a *Bombyx mori* cDNA microarray containing 1468 unique genes identified from *Bombyx mori* embryo cDNA libraries. We examined the patterns of gene expression during embryo development in the *Bombyx mori* between five time points relative to fertilization(2-4 hours after oviposition), blastoderm(8-10hrs), germband(24 hrs), mesoblast(48hrs), blastokinesis(120 hrs). Of these ESTs 247 showed significant perturbation during the embryo development. Differentially expressed gene can be grouped into three categories. 120 ESTs whose expressions up-regulated during early stage (fertilization/blastoderm

/germband) contained heat-shock protein, cell nuclear protein. hypothetical protein, lectin etc. 53 ESTs whose expression up-regulated during late stage (mesoblast/ blastokinesis) contained activating transcription factor, ribosomal protein etc. 6 ESTs whose expression fluctuated during all stage (fertilization/germband) contained PIN2/TRF1 interacting protein, homeodomain transcription factor. In the present study, we monitored the up-regulated and down-regulated genes expressed in the each stage during early embryo development.