

3-4-9. Expressed Sequence Tags Analysis of *Bombyx mori* (Chosunjaelaeam, *kl20*), Embryo

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A cDNA library was constructed from fertilized eggs, *Bombyx mori* (*kl20*, Chosunjaelaeam, Korean native strain) collected after oviposition (24~48hr) with mating. Korean strain, *kl20* was reported that distinguished from Korean strains by isozyme experiment and RAPD analyses. We thought that ESTs provide an economical approach to identifying large numbers of genes that can be used in gene expression during embryogenesis. We used to a method for efficiently constructing high-content full-length cDNA libraries based on chemical introduction of biotin group of the cap structure of eukaryotic mRNA, followed by RNaseH treatment to select full-length cDNA. Expressed sequence tags (ESTs) of the 5-end of more than 5000 clones were determined and the clones were categorized into independent clusters using the assembly program. Of the 1469 assembled ESTs, 1131 ESTs were singlet and 338 assembled ESTs contained more than 2 ESTs. A total of 1469 ESTs were analyzed in detail of their sequences against a BLASTX search. The average length of sequences was 578nt and full-length cDNA was 1143 ESTs. These genes were categorized into 12 groups according to their biological functions. The group was the genes involved in cellular organization (28.8%), transcription (10.8%), cell cycle and DNA processing (10.2%), regulation of / interaction with cellular environment (1.2%), metabolism (8.5%), cellular communication/signal transduction (1.7%), cellular transport and transport mechanisms (5.9%), energy (2.2%), protein fate (6.5%), protein synthesis (5.7%), cell fate (0.009%) and unclassified genes (18.8%).