A7

Construction of the cDNA Library and Selection of Differentially Expressed Clones from *Bombyx mori* Bm5 Cell Line Inhibited N-glycosylation by Tunicamycin Treatment

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Accumulation of unfolded proteins in the endoplasmic reticulum (ER) triggers the transcriptional induction of molecular chaperones and folding enzymes localized in the ER. Thus, eukaryotic cells possess an intracellular signaling pathway from the ER to the nucleus, called the unfolded protein response (UPR) pathway. To obtain genes related to UPR from *Bombyx mori* Bm5 cell, the cDNA library was constructed with mRNA isolated from Bm5 cell line in which N-glycosylation was inhibited by tunicamycin treatment (5 ㎍/㎖). From the cDNA library, we selected 40 clones that differentially expressed when cells treated with tunicamycin, and produced expressed sequence tags (ESTs). Among these clones, we have isolated TmInc329 clone showing high similarity with ATF (encodes a bZIP transcription factor) of *M. muscululs*. Basic-luecine zipper (bZIP) domain in amino acid sequences of TmInc329 shared homology with several transcription factors, yeast Haclp, human CREB and mouse ATF. Also, TmInc329 clone is up-regulated when N-glycosylation of newly synthesized proteins in the ER is inhibited by tunicamycin treatment. Therefore we suggest that TmInc329 clone is a gene responding to accumulation of unfolded proteins in the ER.