

3-4-7. Construction of the cDNA Library and Selection of Differentially Expressed Clones from *Bombyx mori* Bm5 Cell Line Inhibited N-glycosylation by Tunicamycin Treatment

Tae Won Goo, Eun Young Yun, Jae Sam Hwang, Seok Woo Kang, Jin Sung Lee, Soo Jung Park¹, Kwang Sik Lee² and O-Yu Kwon³

Department of Sericulture and Entomology, the National Institute of Agriculture Science and Technology, R.D.A., Suwon 441-100, Korea,

¹Department of Biology, College of Natural Science, Chungnam National University, Taejon 305-010, Korea,

²College of Natural Resources and Life Science, Dong-A University, Pusan 604-714, Korea,

³Department of Anatomy, College of Medicine, Chungnam National University, Taejon 301-131, Korea

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 $\mu\text{g}/\text{ml}$). 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. musculus*. Basic-lucine zipper (bZIP) domain in amino acid sequences of TmInc329 shared homology with several transcription factors, yeast Hac1p, 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.