Identification of Unfolded Protein Response (UPR) Relevant Genes from *Bombyx mori* Cell Lines by a Subtractive Hybridization Approach

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The Unfolded Protein Response (UPR) is an integrated intracellular signaling pathway that transmits information about the protein folding status in the ER lumen to the cytoplasm and the nucleus. For studies of UPR, we isolated differentially expressed genes in Bm5 cell line induced with treatment of tunicamycin, the synthesis inhibitor of N-linked oligosaccharides in cells and constructed the subtractive cDNA library enriching UPR-related genes. A total of 459 subtractive clones were isolated in this study. Of the 459 ESTs, 315 ESTs were singletons and the remaining 144 ESTs were assembled into 51 contiguous sequences (contigs) with an overall EST redundancy of 31% (number of ESTs in contigs/number of ESTs). Based on the BlastX annotation, 366 unique genes were identified, 125 of which were novel sequences having no BlastX match. Overall, about 66% of the identified genes encode polypeptides database. The remaining sequences fall into the unclassified category of proteins with unknown function (e.g., expressed, putative or hypothetical proteins) or with no BlastX match. Among 241 known genes, 21 (8.7%) clones showed significant similarity to the previously reported genes from *B. mori*. One hundred-five (43.6%) clones showed similarity to the genes from insects containg *B. mori*, 136 clones (56.4%) showed similarity to the genes from other kingdoms, including monera (5.4%), protista (2.5%), plantae (2.5%), vertebrates (36.9%), and others (9.1%). Functional categorization of the database-matched clones through database search indicated that 60 UPR-related genes (18%) and 4 glycosylation-related genes (1.2%).