

P 73 Expression of an Evolutionarily Distinct Novel BiP Gene during the Unfolded Protein Response in *Arabidopsis thaliana*

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Objectives

Compared to mammals, little is known about the unfolded protein response (UPR) in plants. In order to characterize the UPR in plant, we investigated the change of the expression profile of *Arabidopsis* genes upon tunicamycin treatment.

Methods and Results

Using an oligonucleotide array comprising up to 8200 *Arabidopsis* genes we investigated the effect of endoplasmic reticulum (ER) stress on gene expression. Expression of 25 genes increased, including at least nine whose products act in the ER. The data were consistent with the hypothesis that UPR in eukaryotes increases the ability of the ER to cope with the increased amounts of unfolded

/misfolded proteins that accumulate during stress. Transcription activation of the ER-related genes was confirmed. Among the upregulated genes was a novel BiP we termed BiP-L, whose expression appeared to be regulated by two promoter sequences perfectly matching mammalian ERSE. Cloning and sequencing of full-length BiP-L cDNA showed it contained a signal peptide sequence and the ER retention signal (HDEL). Interestingly, BiP-L was substantially different from the other two *Arabidopsis* BiP genes in genomic organization and sequence homology. Furthermore, phylogenetic analysis showed that the BiP-L protein is the most distal form among the reported plant BiP proteins. Interestingly, levels of BiP-L were very low in various mature *Arabidopsis* plant organs (leaf, stem, root, flower and silique), with significant levels of BiP-L only observed in stressed (tunicamycin-treated) seedlings. Transcription of BiP-L during ER stress was shown to be regulated by a feedback loop.