

ISOLATION AND CHARACTERIZATION OF GENES ENCODING HEAT SHOCK PROTEIN 70 FROM THE COELACANTH, *LATIMERIA CHALUMNAE*

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Under stress conditions, proteins unfold or misfold leading to the formation of aggregates. Molecular chaperones facilitate the proper folding of other proteins so that they arrive at a stable tertiary structure. Furthermore, they promote the refolding and degradation of denatured proteins after cellular stress. Heat shock proteins form one of the major classes of molecular chaperones. We are interested in determining if the coelacanth (*Latimeria chalumnae*) genome encodes a heat shock protein-based cytoprotection mechanism. We have isolated coelacanth genomic DNA of 50 kb and larger. From the alignments of several fish Hsp70 proteins, conserved regions at the N- and C-termini were identified. Codon usage tables were constructed from published coelacanth genes and degenerate primers were designed to amplify the full-length *hsp70* encoding gene and regions encoding the ATPase and the substrate binding domains. Since it is known that the tilapia and *Fugu* inducible *hsp70* genes are intronless, we proceeded on the assumption that the coelacanth *hsp70* is also intronless. Both the 1900 bp fragment encoding the full-length *hsp70* gene and two fragments, 1048 bp and 873 bp, encoding the ATPase and substrate binding domains, respectively, were amplified. Protein sequences translated from both nucleotide sequences were highly identical to typical Hsp70s. This is the first study to provide evidence for a cytoprotection mechanism in the coelacanth involving an inducible Hsp70.

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