

D-43 Cerebral Ischemia/Reperfusion Injury and Stress Response
in Mongolian Gerbil (*Meriones unguiculatus*)

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Oxidative stress are increasingly being implicated in cerebral cell injury upon ischemia/reperfusion (I/R). It has also been suggested that the induction of HSP70 in the pretreated brain play a protective role against tissue injury. In this study, we have attempted to quantitate oxidative cell damage in hippocampus and cortex and to evaluate the possible role of HSP70. We have produced experimental I/R to the brains of gerbil by transient occlusion and release of common carotid arteries. To monitor the oxidative stress associated with I/R, we measured the amount of oxidized glutathione/ total glutathione pool by high pressure liquid chromatography. We then measured oxidative cell damage in membrane and DNA by quantitating lipid peroxides (LPO) and the oxidative DNA damage product, 8-hydroxy-2'-deoxyguanosine (oh⁸dG), respectively. We found an increase of LPO and oh⁸dG at early phase of reperfusion that followed ischemia. The magnitude of increase was more pronounced in hippocampus than in cortex. These results are in parallel with those obtained from glutathione oxidation. We noted that the induction of HSP70 in hippocampus was not as obvious as that seen in cortex. We speculate that the signal transduction pathways activating the heat shock response may be less active or impaired in cells in hippocampus.

D-44 cDNA sequences encoding the antibacterial peptides from
Spodoptera litura

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The partial cDNA sequences, possibly encoding the cecropin-like antibacterial peptides, were obtained from analysis of DNA fragment which were amplified by use of RT-PCR and subcloned into the T-vector. Three different kinds of degenerated primers were used in this study: two of them are located on the presequence and the remaining is on the 5'-end of the structural gene of the antibacterial gene. The new cDNA sequences show 40-87 % homologies to the cecropins, based on the amino acid sequence deduced from cDNA. Especially, the highly conserved amino acid residues through different kind of cecropins were also well conserved in these sequences. However, they do not match with any of antibacterial peptides purified from *Spodoptera litura* even if they show higher amino acid homologies to the spodopsins, the antibacterial protein purified from *Spodoptera litura*. This fact implies that there will be more genes for the antibacterial activities. The NH₂-terminal domain seems to be more conserved than the COOH-terminal domain which is believed to confer the spectrum of antibacterial activities.