E241 Molecular Cloning and Characterization of a Gene Encoding Hot Pepper Ascorbate Peroxidase

Sung Chae Moon*, and Chung Sun An
Department of Biology, Seoul National University

Ascorbate peroxidase (APX) plays a significant role in scavenging the hydrogen peroxide which is produced during normal metabolism or after environmental stresses. APX isozymes are localized in three distinct cell compartments of higher plants: cytosol, cholroplasts and microbodies. Screening of a hot pepper cDNA library with partial APX cDNA(CFR4-EST) as a probe resulted in a cDNA which encodes a putative peroxisomal APX isoform. DNA sequencing of 1052 nucleotides revealed that it encodes 252 amino acids(27.39kDa). The deduced amino acid sequences shares 89% and 88% identities with *Nicotiana tabacum* and *Capsicum annuum* cytosolic APX, respectively. However N-terminal sequence showed homology with peroxisomal APX of *Arabidopsis thaliana* and the presence of the peroxisomal targeting sequences imply that this APX isoform is peroxisomal form. To characterize the expression of APX the transcripts and isoforms of APX were examined in total RNA and protein exracts from four different tissues, respectively.

E242 Cloning, Expression and Genomic Characterization of Superoxide Dismutases (SODs) from Small Radish (*Raphanus sativus* L.)

Soon Il Kwon*, and Chung Sun An
Department of Biology, Seoul National University

We have isolated three types (cytosolic Cu/Zn, Mitochondrial Mn, and Fe) superoxide dismutases clones from cold-treated seedling cDNA library of small radish through PCR method. Their nucleotide and amino acid sequences showed the highest homology with those of *Arabidopsis*. Small radish superoxide dismutase could be resolved into four isozyme forms during developmental stages by nondenaturing polyacrylamide gel staining. Southern-blot analysis of genomic DNA showed that Cu/ZnSOD is small multi-gene family, while MnSOD is a single-copy gene. Northern analysis of SODs expression was performed on RNAs extracted from different tissues. The expression of SODs was developmentally regulated and influenced by various chemicals (paraquat, plumbagin, cercosporin, sucrose, mannitol, salt, arsenate, aluminum..), hormones (ABA, IAA) and light sources (white light, U.V.). Mn- and Fe-SOD genomic clones have been isolated and their DNA sequence was determined. Six and five introns were identified in FeSOD and MnSOD coding regions, respectively. We are in the process of promoter analysis.