

F202 Structures and Expression Patterns of Two ω -3 Fatty Acid Desaturase from Red Pepper

Ji Hae Kwon* and Chung Sun AN
Biology Department, Seoul National University

Two cDNA clones encoding ω -3 fatty acid desaturases (CaFAD3 and CaFAD7) were isolated from a leaf cDNA library of red pepper (*Capsicum annuum*). The nucleotide sequence of 1116 bp in the CaFAD3 showed 78% identity with that of a microsomal ω -3 FAD from tobacco. The nucleotide sequence of 1317 bp in the CaFAD7 showed 87.5% identity with that of a plastid ω -3 FAD from tobacco. The nucleotide sequences between them were 71.4% identical. The CaFAD7 had a transit peptide for targeting to the chloroplast. Northern analysis indicated that CaFAD7 mRNA was present in leaves, but not detected in roots. The CaFAD7 mRNA levels in the leaves upon wounding increased rapidly and strongly to reach the highest levels between 40 min to 3 h, then decreased markedly between 6 h and 9 h, but increased again to give a second peak at 18 h. Putative functions of the two clones will be discussed along with the expression pattern of the CaFAD3.

F203 Isolation and Characterization of Three cDNAs Encoding Catalase from Small Radish (*Raphanus sativus* L. var *sativus*)

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

Three cDNA clones encoding catalase were isolated from a cDNA library of cold-treated seedlings of small radish (*Raphanus sativus* L.) using amplified PCR products as probes. All of the clones (RaCat1, RaCat2 and RaCat3), encoded 493 amino acid residues and had a transit peptide of 22 amino acids for targeting into the peroxysome. Molecular weights of the mature proteins were 57 kDa - 58 kDa. The amino acid sequences of RaCat2 and RaCat3 were very similar each other with 97.5% identity, while that of RaCat1 was 75% identical to those of RaCat2 and RaCat3. Genomic Southern hybridization showed that three catalase genes were present as a small multigene family. Results from enzyme activities on native PAGE, Northern hybridizations and *in situ* hybridizations will also be presented to show differential expression patterns of the three catalase genes.