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Plant Gene Register

A cDNA Clone Encoding a Rice Catalase Isozyme

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Catalase (H_2O_2: H_2O_2 oxidoreductase, EC 1.11.1.6) is a heme-containing enzyme that converts H_2O_2 into oxygen and water. In plants, catalase is involved in scavenging H_2O_2, which is generated during the course of photorespiration and β-oxidation of fatty acids. It also plays an important role in detoxification of active oxygen species that are generated by various environmental stresses (Scandalios, 1990).

Many higher plants have multiple isoforms of catalase. Maize catalase is encoded by three distinct genes whose expression is regulated differentially in response to changes in either developmental phase or environmental conditions (Redinbaugh et al., 1988; Scandalios, 1990). Two isozymes of cotton catalase also exhibit different patterns of expression (Ni and Trelease, 1991a).

A rice catalase cDNA (*CatA*) has been isolated from immature seeds (Mori et al., 1992). Here we report the sequence of another rice catalase cDNA, which covers nearly the full length of its corresponding mRNA, 282 nucleotides of which are identical with those found in a partial cDNA sequence from suspension-cultured rice cells reported as accession number D10425 (Uchimiya et al., 1992).

A cDNA library in λZapII vector was constructed from poly(A)$^+$ RNA prepared from rice seedlings grown in the dark for 4 d. PCR was performed on cDNAs prepared as described above using oligonucleotide primers synthesized on the basis of the conserved sequences of catalases from maize (Redinbaugh et al., 1988), cotton (Ni and Trelease, 1991b), pea (Isin and Allen, 1991), and sweet potato (Sakajo et al., 1987). A PCR product with an expected size of 550 bp was obtained. Partial sequencing of this product revealed that it was highly homologous but not identical with rice *CatA*. Using this fragment, the cDNA library was screened. Three positive clones were isolated, one of which (named *CatB*) was sequenced (Table I).

It is 1854 bp long and contains an open reading frame encoding a protein of 492 amino acids. The nucleotide sequence is 63.6% identical with rice *CatA* and 80.7% with maize *Cat1*. It contains a segment completely identical, except for one base, with that in a partial sequence (accession No. D10425) of a rice catalase gene. The deduced amino acid sequence shows high homologies of 71.1, 93.3, 63.3, and 67.4% to rice CATA, maize CAT1, CAT2, and CAT3, respectively. All of the amino acid residues involved in catalytic activity (His^{74}, Ser^{113}, Asn^{147}) and heme binding (Val^{73}, Arg^{111}, Tyr^{114}, Phe^{150}, Pro^{335}, Arg^{353}, Tyr^{357}) (Fita and Rossman, 1985) are conserved in rice CATB as well as the published sequences of other plant catalases. A tripeptide Ser-Arg-Leu, which is reported to be a peroxisomal targeting signal located at or near the C terminus (Gould et al., 1989), is found six residues upstream of the C terminus, but its function is unknown.

Table I. *Characteristics of rice CatB*

Organism:
Rice (*Oryza sativa* L. cv Nipponbare).
Function:
Encoding a subunit of catalase, which catalyzes the dismutation of H_2O_2 into water and oxygen.
Source:
cDNA library in λZapII vector constructed from mRNA isolated from rice seedlings grown in the dark for 4 d.
Techniques:
Amplification of rice catalase cDNA with PCR using synthetic oligonucleotide primers, hybridization screening with an amplified cDNA, restriction fragment subcloning, and dideoxy sequencing of both strands.
Method of Identification:
Sequence comparison with rice *CatA* and maize *Cat1*.
Structural Features of Protein:
The deduced protein sequence consists of 492 amino acid residues with a calculated molecular mass of 56.5 kD.
Expression Characteristics:
Approximately 2-kb transcript.

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The EMBL/GSDB/DDBJ/NCBI accession number for the sequence reported in this article is D26484.

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