Sequence of a cDNA Encoding Rice (Oryza sativa L.) Leaf Ferredoxin-NADP+ Reductase

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FNR (EC 1.18.1.2) catalyzes the final step in the oxygenic photosynthetic electron transport. The enzyme has been purified and extensively characterized (Knaff and Hirasawa, 1991). The enzyme's amino acid sequences have been described for spinach (Karplus et al., 1984; Jansen et al., 1988), pea (Newman and Gray, 1988), and ice plant (Michalowski et al., 1989) as well as other photosynthetic organisms. However, the primary sequences from higher plant FNR are limited to those from the dicotyledonous plants. During the course of cDNA cloning of rice root FNR (Aoki and Ida, 1994), we isolated a full-length cDNA clone encoding the rice (Oryza sativa L.) leaf enzyme. We report here the complete nucleotide sequence of a cDNA for leaf FNR from rice (Table I).

A rice leaf cDNA library was constructed in λgt11 from poly(A)+ RNA of nitrate-induced greening rice seedlings (Matsui et al., 1990). The library was screened with a rabbit polyclonal antiserum raised against the leaf FNR. The leaf enzyme was purified to homogeneity by butyl-Toyopearl and Fd-Sepharose chromatography (Shin et al., 1990) from an FNR fraction obtained during the purification of rice leaf nitrite reductase (Ida et al., 1989).

The cDNA is 1400 bp long and contains an open reading frame of 1086 bp and 81-bp 5' and 233-bp 3' noncoding regions. In the 3' untranslated region, there are two possible hexameric polyadenylation signals, AATAAT, that are contiguous. The first 58 amino acids of the amino-terminal stretch was assigned as a putative transit peptide, because the amino terminus of the isolated protein starts with Ala at position 59. The transit peptide contains a high proportion of Ala (18 residues) and a single Asp but no Glu. Such salient features are characteristic of the chloroplast transit peptides (Archer and Keegstra, 1990). Although there are a few identical amino acids in the transit peptides, comparison of the predicted amino acid sequences of the deduced mature proteins revealed extensive homology among the photosynthetic FNRs from higher plants. Thus, the rice leaf enzyme has 86, 85, and 83% identity with FNR from ice plant (Michalowski et al., 1989), pea (Newman and Gray, 1988), and spinach (Jansen et al., 1988), respectively. The similarities found among the FNR sequences suggest that their structural genes are highly conserved irrespective of whether plants are dicotyledonous or monocotyledonous. Despite high degrees of identity of leaf FNRs, there is only 49% homology between rice leaf and rice root FNR, as we reported recently (Aoki and Ida, 1994), suggesting that the two enzymes are expressed separately in photosynthetic and nonphotosynthetic tissues of the rice plant.

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**Table I. Characteristics of a cDNA encoding leaf FNR from rice**

| Organism: Rice (Oryza sativa L.) cv Kinmaze. |
| Genome Location: Nuclear genome. |
| Gene Product: FNR (EC 1.18.1.2) |
| Source: cDNA library in λgt11 constructed from poly(A)+ RNA isolated from greening shoots of rice seedlings. |
| Techniques: Immunoscreening, restriction fragment subcloning into pBluescript II SK++, dideoxy sequencing of both strands from progressive deletion. |
| Methods of Identification: Comparison of the published amino acid sequences and the amino-terminal amino acid sequence of the isolated protein. |
| Features of cDNA Structure: Total length of 1400 bp, open reading frame from nucleotide 82 to 1167, representing a full-length clone. |
| Features of the Deduced Protein: Open reading frame encodes a polypeptide of 362 amino acid residues. The first 58 amino acid stretch represents a putative chloroplast transit peptide, suggesting a mature protein of 304 residues (M, = 34310.73). Homology to the mature protein of ice plant (86%; Michalowski et al., 1989), pea (85%; Newman and Gray, 1988), spinach (83%; Jansen et al., 1988), and rice root FNR (49%; Aoki and Ida, 1994). |

Abbreviation: FNR, ferredoxin-NADP+ oxidoreductase.
The DDBJ accession number for the sequence reported in this article is D17790.

LITERATURE CITED


