## Plant Gene Register

## A cDNA Clone Encoding Chlamydomonas reinhardtii Preferredoxin

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Fd's are ubiquitous low mol wt proteins containing iron sulfur center(s) involved in numerous electron transfer reactions. In plants, one of the major functions of Fd is to provide the reducing power for chloroplastic NADP photoreduction. In addition, Fd is also needed for nitrite, ammonia, and sulfite assimilation as well as for pseudocyclic electron flow and fatty acid metabolism and for the light regulation of chloroplastic enzymes (Orme-Johnson, 1973). This protein is encoded by nuclear genes and is, therefore, produced as a precursor that is subsequently cleaved inside the chloroplast (Smeekens et al., 1985). We have previously purified Chlamydomonas reinhardtii Fd and determined its primary structure by direct amino acid sequencing (Schmitter et al., 1988). Based on this sequence and using the polymerase chain reaction, we have isolated a nucleotidic sequence coding for the mature portion of C. reinhardtii Fd and shown that the deduced amino acid sequence was identical with only one substitution Thr7 to Ser (Table I). In addition, we demonstrated that Escherichia coli cells were able to direct the synthesis of C. reinhardtii Fd polypeptide and to reassemble it together with an iron-sulfur center (Rogers et al., 1992).

In this paper we report the sequence of a cDNA encoding *C. reinhardtii* preferredoxin. A  $\lambda$ gt11 cDNA was sequenced (527 bp) and found to encode a 126-amino acid precursor with a molecular mass of 13,250 D, compared to the mature form, which contains 94 amino acids and has a molecular mass of 9,908 D. The deduced amino acid sequence was completely homologous to the sequence reported by Schmitter et al. (1988). In addition, the sequence revealed the structure of the 32-amino acid transit peptide (molecular mass 3342 D), which is as follows: MAMAMRSTFAARVGAKPA-VRGARPASRMSCMA.

Several lines of evidence indicate that the first ATG is the initiation codon. First, it is preceded by TCA and AAA, triplets theoretically coding for Ser and Lys but rarely if ever used for nuclear genes in *C. reinhardtii*. Second, the flanking sequence surrounding the initiation codon (AAAAATGGC) fits well the eukaryotic translation initiation consensus (Wedel et al., 1992). Finally, the beginning of the transit peptide (MAMAM) is highly similar to the MAQM sequence reported by Wedel et al. (1992) and to the MAMAT of Hoffmann et al. (1988), and the dipeptide MA is overwhelm-

Org	anism:
C	hlamydomonas reinhardtii.
Fun	iction:
E	ncodes the precursor for Fd, a protein essential for chloroplas- tic NADP photoreduction.
Clo	ne Type, Designation:
с	DNA, Fd 9.
Sou	irce:
	DNA library (λgt11), a gift from Michel Clermont-Goldschmidt. thod of Identification:
A	mino acid sequencing, polymerase chain reaction cloning,
	screening of the $\lambda$ gt11 library with labeled polymerase chain
	reaction fragment.
Seq	uencing Strategy:
Р	lasmid sequencing in Bluescript SK+.
Fea	tures of cDNA Structure:
S	ixty-five percent homology to <i>Silene pratensis</i> cDNA (relates to the 288 nucleotides coding for the mature protein).
Stru	actural Features of the Deduced Protein:
le	dentical with the direct amino acid sequencing of <i>C. reinhardtii</i> Fd. About 70% homology to higher plant Fd's.
Exp	ression
R	tecombinant ferredoxin can be expressed in <i>E. coli</i> reassociated with its iron-sulfur center (Rogers et al., 1992).
Ant	ibodies:
N	lone available.
Sub	ocellular Localization:
C	Chloroplast.

Table I. Characteristics of a aDMA along andian for

ingly found to start chloroplastic transit peptides (von Heijne et al., 1989).

The putative transit peptide displays a very high content of Ala, Met, and Arg. Nine amino acid residues are absent, most notably the acidic residues Asp and Glu, as well as the hydrophobic residues Ile, Leu, Trp, and Tyr. Hydroxylated residues are present, but their content is not higher than in mature Fd. Overall, the peptide is very positively charged; no clear homology to other Fd transit peptides and no obvious secondary structure can be deduced as observed by Pilon et al. (1992). From the NH<sub>2</sub>-terminal sequence of mature Fd, we can deduce that the processing of *C. reinhardtii* preferredoxin occurs between Ala and Tyr residues, Ala being often found next to the processing site of chloroplastic precursor proteins (Keegstra et al., 1989).

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