

Plant Gene Register

A cDNA Encoding a Metallothionein I-Like Protein from Coffee Leaves (*Coffea arabica*)¹

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Metallothioneins are small, high-Cys-containing proteins present in a wide variety of organisms including vertebrates, invertebrates, fungi, cyanobacteria, and higher plants (Hamer, 1986). Metallothioneins play a role in heavy metal detoxification, especially in respect to cadmium, copper, and zinc (Hamer, 1986). Gene disruptions of the bakers' yeast *Cup1* locus that encodes a metallothionein and the mouse metallothionein I and II genes result in hypersensitivity to copper and cadmium (Hamer et al., 1985; Michalska and Choo, 1993). Metallothioneins might also be involved in regulation of cellular availability of required heavy metals, especially copper and zinc (Hamer, 1986).

Metallothionein-like proteins and genes have been isolated from a number of higher plants, including both monocots and dicots (Lane et al., 1987; De Framond, 1991; Kawashima et al., 1991; Robertson et al., 1992; Zhou and Goldsbrough, 1994; K. Takahashi, GenBank accession No. X62818; Weig and Komor, GenBank accession No. L02306). Plant metallothioneins are also involved in heavy metal tolerance. Evans et al. (1992) have shown that expression of a pea metallothionein-like gene using a cauliflower mosaic virus 35S promoter to drive expression results in increased accumulation of copper in transgenic *Arabidopsis thaliana*. In addition, two different *A. thaliana* metallothioneins are capable of complementing a deletion of the bakers' yeast metallothionein gene *Cup1* (Zhou and Goldsbrough, 1994). This is consistent with a role in heavy metal detoxification. Also, in wheat high levels of metallothionein are found in embryos, as might be expected if it has a role in metal ion homeostasis (Kawashima et al., 1992).

We now report the isolation of a full-length cDNA from immature coffee (*Coffea arabica*) leaves encoding a metallothionein I-like protein (Table I). The deduced coding region encodes an 80-amino acid protein with 64% identity to a *Ricinus communis* metallothionein. One unusual characteristic of this cDNA is a 684-base 3' untranslated region. The *A. thaliana* and *R. communis* metallothionein mRNAs also

Table I. Characteristics of a coffee metallothionein I cDNA

Organism:	<i>Coffea arabica</i> .
Gene Product:	Metallothionein I-like protein.
Source:	cDNA library constructed from mRNA isolated from immature leaves in λZAP.
Sequencing Methods:	Automated sequencing using the Applied Biosystems (Foster City, CA) model 373A automated sequencer. Primers used in sequencing were homologous to T7 and T3 promoter sites in the vector and internal to the cDNA.
Features of the cDNA:	Total size is 764 bases with a 47-base 5' untranslated region, a 240-base coding region, and a 684-base 3' untranslated region.
Features of the Deduced Protein:	The open reading frame encodes an 80-amino acid protein with a molecular mass of 7913.95 D. The deduced protein is high in Cys (17.5 mol%) and has high similarity to metallothionein I proteins.

contain relatively long 3' untranslated regions of 258 and 301 bases, respectively. The sequences of the 3' untranslated regions of these genes are not similar. One interesting motif found in the coffee metallothionein mRNA 3' region is a 7-fold "TAG" tandem repeat. The 3' region does not show significant similarity to other sequences in GenBank, except for several apparently unrelated sequences that also contain TAG tandem repeats.

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The GenBank accession number for the sequence reported in this article is U11423.

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