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Plant Gene Register

The *gdcsPA* Gene from *Flaveria pringlei* (Asteraceae)[1]

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GDC is the key enzyme of Gly catabolism in bacteria, animals, and plants. In higher plants this mitochondrial multienzyme complex, cooperating with other enzymes of the photorespiratory carbon oxidation cycle, catalyzes the salvage of carbon skeletons withdrawn from the Calvin cycle by the oxygenation of ribulose-1,5-bisphosphate. The GDC, together with Ser hydroxymethyltransferase, converts two molecules of Gly into Ser, CO_2, and NH_3 (Sarojini and Oliver, 1983). The enzyme complex is comprised of the four subunits P-protein (pyridoxal phosphate binding), H-protein (lipoamide-containing aminomethylenetransferase), T-protein (tetrahydrofolate-dependent methylenetransferase), and L-protein (lipoamide dehydrogenase), with a stoichiometry of $1L_2$:$2P_2$:27H:9T (Oliver et al., 1990). The biosynthesis of the P-protein as well as the other GDC components has been shown to be light regulated in leaves (Kim et al., 1991). cDNA sequences for P-subunits from chicken and human (Kume et al., 1991) have been published. Among plants cDNAs of the P-protein have been cloned and analyzed from pea and *Flaveria pringlei* (Turner et al., 1992; Kopriva and Bauwe, 1994). However, until now there exist no reports concerning the corresponding eukaryotic genes.

Here we report the cloning and sequencing of the *gdcsPA* gene, one of six members of the *gdcsP* gene family from *F. pringlei*, a C_3 species (Table I). The cloned fragment of 8.5 kb covers the complete gene and includes approximately 2 kb of the 5′ flanking region and 600 nucleotides of the 3′ flanking sequence. The derived transcript corresponds perfectly with a cDNA isolated earlier in our laboratory (Kopriva and Bauwe, 1994). Therefore, we conclude that the gene is transcriptionally active in leaves. It consists of 16 exons, which, with the exception of the first one (1306 bp), have lengths between 281 and 68 bp. All exon-intron junctions strictly follow the GT. . .AG consensus. Although the transcription start has not yet been precisely mapped, a computer analysis shows correlated CCAAT box, GC box, and TATA box motifs. Two putative cap sites are located at positions −223 and −214 from translation start.

We found that the protein contains a strongly conserved Leu zipper pattern, which, as a general dimerization domain, might facilitate the association of two P polypeptides to the dimeric form existing in the enzymatically active GDC complex.

Table I. *Characteristics of the gdcsPA gene encoding one of the P-isoproteins of the GDC multi-enzyme complex from F. pringlei*

Organism:	*Flaveria pringlei* (Asteraceae, C_3).
Isolation:	Screening of a genomic library constructed in λ GEM11 with a full-length cDNA probe from *F. pringlei*.
Sequencing:	Both strands by nested deletions using three subfragments.
5′ Flanking and Nontranslated Region:	2040 bp with correlated CCAAT box, GC box, and TATA box motifs at positions −360, −353, and −255, respectively, from translation start. Two putative cap sites are located at positions −223 and −214.
Transcribed Region:	16 exons on a transcribed stretch of 6045 nucleotides including 214 to 223 and 186 nucleotides of nontranslated leader and trailer sequences, respectively.
Protein:	mRNA encodes a precursor protein with 1037 amino acids. The mature protein (106 kD) consists of 971 amino acids.
Cellular Localization:	Mitochondrial matrix.
Gene Localization:	Nuclear, multigene family with six members.

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Abbreviation: GDC, glycine decarboxylase.

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